

10336256.txt

SEQUENCE LISTING

<110> Michelle Cayouette
 Connie Jo Hansen
 Amy McClure
 Mark Dyaico
 Svetlana Gramatikova
 May Sun
 Nelson Barton
 Justin Stege
 Nahla Aboushadi

<120> Proteases, Nucleic Acids Encoding Them
 and Methods For Making and Using Them

<130> 09010-093W01

<140> not assigned

<141> 2003-10-10

<150> 60/418,467

<151> 2002-10-10

<150> 60/471,423

<151> 2003-05-16

<160> 255

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1305

<212> DNA

<213> Bacteria

<400> 1

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gccaccccac	acgtgagcgg	cacagtgcgc	ctaattcagg	cagccaggct	cgcccagggc	1140
ctaccactac	taccaccagg	cacagaggac	gacctaacca	cagacaccgt	gagaggcatc	1200
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<212> PRT

<213> Bacteria

<220>

<221> SIGNAL

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<222> (1)...(37)

<400> 2

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 20      25      30
Pro Val Ala Thr Ala Val Ser Tyr Lys Thr Leu Ile Val Lys Ile Asp
 35      40      45
Arg Ala Lys Phe Asp Pro Glu Arg Val Lys Gly Leu Gly Gly Arg Val
 50      55      60
Val Tyr Val Ala Gln Leu Ala Pro Val Ala Ile Leu Val Val Pro Ala
 65      70      75
His Ala Ala Glu His Val Lys Lys Leu Pro Gly Val Leu His Val Ser
 85      90      95
Glu Asp Gly Glu Val Lys Ala Phe Ala Val Arg Val Ser Leu Thr Gln
100      105      110
Pro Pro Gln Thr Met Pro Trp Gly Val Asp Tyr Ile Asp Ala Glu Gln
115      120      125
Val Trp Ser Ile Thr Lys Gly Phe Val Asp Val Asn Gly Asp Gly Asp
130      135      140
Ser Glu Ile Glu Val Ala Val Ile Asp Ser Gly Val Asp Leu Asp His
145      150      155
Pro Asp Leu Ala Asp Asn Ile Lys Trp Cys Val Ala Val Leu Asn Gly
165      170      175
Arg Ile Ser Asn Arg Cys Ser Asp Val Asn Gly His Gly Thr His Val
180      185      190
Thr Gly Thr Ile Ala Ala Leu Asp Asn Glu Ile Gly Val Val Gly Val
195      200      205
Ala Pro Glu Val Glu Ile Tyr Met Ile Lys Ala Leu Lys Asn Ser Gly
210      215      220
Ser Gly Ser Trp Ser Asp Leu Ile Ile Ala Ile Asp Leu Ala Val Arg
225      230      235
Gly Pro Asp Gly Val Ile Asp Ala Asp Gly Asp Gly Val Ile Val Gly
245      250      255
Asp Pro Glu Asp Asp Ala Pro Glu Val Ile Ser Met Ser Leu Gly Gly
260      265      270
Tyr Asp Pro Pro Glu Leu Gln Glu Val Ile Ala Ala Ala Tyr Ser
275      280      285
Tyr Gly Ile Val Ile Val Ala Ala Ala Gly Asn Glu Gly Leu Asp Thr
290      295      300
Pro Ala Tyr Pro Ala Ala Tyr Pro Glu Val Ile Ala Val Gly Ala Ile
305      310      315
Asp Glu Asn Ala Thr Val Pro Asp Trp Ser Asn Arg Asn Pro Glu Val
325      330      335
Thr Ala Pro Gly Val Asp Ile Leu Ser Thr Tyr Pro Asp Asp Ser Tyr
340      345      350
Ala Val Leu Ser Gly Thr Ser Met Ala Thr Pro His Val Ser Gly Thr
355      360      365
Val Ala Leu Ile Gln Ala Ala Arg Leu Ala Gln Gly Leu Pro Leu Leu
370      375      380
Pro Pro Gly Thr Glu Asp Asp Leu Thr Thr Asp Thr Val Arg Gly Ile
385      390      395
Leu His Leu Thr Ala Val Asp Leu Gly Asp Pro Gly Tyr Asp Thr Leu
405      410      415
Tyr Gly Tyr Gly Val Ile Asn Ala Tyr Asp Ala Val Leu Thr Ala Leu
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Asn Ser

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<210> 3

<211> 1572

<212> DNA

<213> Bacteria

<400> 3

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60

120

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aagatcaagc ggacctacac ctcgggccgt aacgggtacg ccgtcgaact ctccgaggcc 300
caggcgaaga agctcgcggc cgaccccgcc gtgacctcgg tcgtccagaa ccgctcttc 360
cacgtcgacg gcacgcagcc ctccccgccc tcctgggggtc tggaccggat cgaccagaag 420
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tacatcatcg acaccggcgt acgcatcacc cacagcgact tcggcgggcg cgcctcctac 540
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gtcgcgggca cggtcgcggg cacctcgtac ggctcgcca agaaggcgaa gatcgtcggc 660
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<212> PRT
<213> Bacteria

<220>
<221> SIGNAL
<222> (1)...(36)

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35 40 45
Glu Gly Thr Ile Ala Gly Ser Tyr Ile Val Thr Leu Asp Glu Ser Ala
50 55 60
Gln Ala Glu Thr Ala Lys Gly Arg Ala Val Ala Ala Lys Phe Gly Ala
65 70 75 80
Lys Ile Lys Arg Thr Tyr Thr Ser Ala Val Asn Gly Tyr Ala Val Glu
85 90 95
Leu Ser Glu Ala Gln Ala Lys Lys Leu Ala Ala Asp Pro Ala Val Thr
100 105 110
Ser Val Val Gln Asn Arg Val Phe His Val Asp Gly Thr Gln Pro Ser
115 120 125
Pro Pro Ser Trp Gly Leu Asp Arg Ile Asp Gln Lys Ala Leu Pro Leu
130 135 140
Asn Gln Ser Tyr Thr Tyr Pro Asp Thr Ala Gly Gln Gly Val Thr Ala
145 150 155 160
Tyr Ile Ile Asp Thr Gly Val Arg Ile Thr His Ser Asp Phe Gly Gly
165 170 175
Arg Ala Ser Tyr Gly Tyr Asp Ala Ile Asp Asn Asp Asn Thr Ala Gln
180 185 190
Asp Gly His Gly His Gly Thr His Val Ala Gly Thr Val Ala Gly Thr
195 200 205
Ser Tyr Gly Val Ala Lys Lys Ala Lys Ile Val Gly Val Arg Val Leu
210 215 220
Asp Asn Ser Gly Ser Gly Thr Thr Glu Gln Val Val Ala Gly Ile Asp
225 230 235 240
Trp Val Thr Arg Asn Ala Val Lys Pro Ala Val Ala Asn Met Ser Leu
245 250 255

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Gly Gly Gly Val Asp Thr Val Leu Asp Ala Ala Val Arg Asn Ser Ile
 260 265 270
 Ala Ser Gly Val Thr Tyr Ala Val Ala Ala Gly Asn Asp Ser Ser Asn
 275 280 285
 Ala Ser Asn Tyr Ser Pro Ala Arg Val Thr Glu Ala Ile Thr Val Gly
 290 295 300
 Ser Thr Thr Asn Thr Asp Ala Arg Ser Ser Phe Ser Asn Tyr Gly Thr
 305 310 315 320
 Val Leu Asp Ile Phe Ala Pro Gly Ser Ser Ile Thr Ser Ser Trp Asn
 325 330 335
 Thr Ser Asp Ser Ala Thr Asn Thr Ile Ser Gly Thr Ser Met Ala Thr
 340 345 350
 Pro His Val Ala Gly Ala Ala Ala Val Tyr Leu Ala Gly Asn Pro Thr
 355 360 365
 Ala Thr Pro Ala Gln Val Ser Thr Ala Leu Thr Thr Ala Ala Thr Pro
 370 375 380
 Asn Val Val Thr Asn Pro Gly Ser Gly Ser Pro Asn Arg Leu Leu Tyr
 385 390 395 400
 Val Gly Gly Gly Thr Thr Thr Pro Pro Gly Pro Lys Phe Glu Asn Thr
 405 410 415
 Ala Asp Tyr Ala Ile Ala Asp Asn Ala Thr Val Glu Ser Pro Val Thr
 420 425 430
 Val Ser Gly Val Ser Gly Asn Ala Pro Ala Ala Leu Gln Val Pro Val
 435 440 445
 Asn Ile Val His Thr Tyr Ile Gly Asp Leu Gln Ile Gln Leu Ile Ala
 450 455 460
 Pro Asp Gly Ser Ala Tyr Thr Leu Lys Ala Phe Gly Thr Gly Gly Ser
 465 470 475 480
 Ser Asp Asn Ile Asn Thr Thr Tyr Ser Val Asn Ala Ser Ser Glu Val
 485 490 495
 Ala Asn Gly Thr Trp Lys Leu Arg Val Thr Asp Asn Ala Asn Ala Asp
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 <211> 3684
 <212> DNA
 <213> Bacteria

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<210> 6
 <211> 1227
 <212> PRT
 <213> Bacteria

 <220>
 <221> SIGNAL
 <222> (1)...(32)

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35      40      45
Ser Thr Thr Val Thr Leu Val Thr Gly Asp Arg Val Thr Leu Thr Asp
50      55      60
Leu Gly Gly Gly Arg Lys Thr Val Thr Val Asp Arg Ala Glu Gly Ala
65      70      75      80
Thr Gly Ala Ile Arg Ser Arg Ile Asp Asp Gly Arg Val Thr Val Val
85      90      95
Pro Asp Glu Ala Arg Pro Tyr Leu Asp Ser Gly Ala Leu Asp Pro Arg
100     105     110
Leu Phe Asp Val Thr Gly Leu Val Glu Gln Gly Val Thr Gly Glu Leu
115     120     125
Pro Leu Ile Val Thr Tyr Gly Gly Lys Thr Ala Arg Thr Ala Ala Ala
130     135     140
Ala Pro Arg Gly Ala Glu Thr Val Arg Pro Leu Pro Ser Ile Gly Gly
145     150     155     160
Ala Ala Val Thr Ala Thr Asp Pro Ala Ser Phe Trp Arg Gly Phe Thr
165     170     175

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Ala Ala Pro Thr Ala Arg Ala Ala Ala Pro Ala Lys Val Trp Leu Asp
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 Val 210 Leu Asp Thr Gly Ala 215 Asp Leu Ala His Pro 220 Leu Ala Gly Arg
 225 Val Thr Glu Ser Lys 230 Ser Phe Ile Ala Gly Gln Glu Val Ala Asp Arg
 Asn Gly His 245 Gly Thr His Val Ala Ser 250 Thr Val Gly Gly Ser 255 Gly Ala
 Gly Ser Asp 260 Gly Lys Glu Lys Gly 265 Val Ala Pro Gly Ala Thr Leu Ala
 Val Gly 275 Lys Val Leu Ser Asp 280 Glu Gly Ser Gly Ser 285 Glu Ser Glu Ile
 Ile Ala Gly Met Glu Trp 295 Ala Lys Asp Ile Asp Ala Lys Ile Val
 305 Ser Met Ser Leu Gly 310 Ser Arg Glu Pro Ser Asp Gly Thr Asp Pro Met
 Ala Leu Ala Val 325 Asn Thr Leu Thr Ala 330 Glu Thr Gly Ala Leu Phe Val
 Ile Ala Ala Gly 340 Asn Ser Gly Tyr 345 Pro Gly Ser Ile Gly Ser Pro Gly
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 Ala Ala Tyr Phe Thr 375 Ser Gln Gly Pro Arg Tyr 380 Gly Asp Gln Ala Leu
 385 Lys Pro Asp Leu Ser 390 Ala Pro Gly Val Asp 395 Ile Leu Ala Ala Arg Ser
 Gln Leu Leu Pro Gly 405 Ser Gly Leu Tyr Thr Ser Met Ser Gly Thr Ser
 Met Ala Thr 420 Pro His Val Ala Gly Val Ala Ala Leu Leu Ala Glu Arg
 His Pro Asp 435 Trp Thr Gly Ala 440 Gln Leu Lys Asp Ala 445 Leu Met Ser Ser
 Ser Lys Thr Leu Asp Ala 455 Ser Ser Tyr Ala Leu Gly Ser Gly Arg Val
 465 Asp Val Ala Ala 470 Ile Ala Ala Asn Val Thr Ala Thr Gly Ser Ala
 Asp Leu Gly Phe Val Ala Trp Pro Tyr 490 Ala Ser Ser Lys Pro Val Thr
 Lys Thr Val 500 Thr Tyr Thr Asn Ser 505 Ser Asp Ala Pro Val Glu Leu Asn
 Leu Ala Val Glu Gly Met Pro 520 Ala Gly Val Ala Ala Leu Ala Asp Thr
 Thr 530 Leu Thr Val Pro Ala 535 His Gly Thr Ala Ser Thr Thr Val Thr Gly
 545 Asp Gly Thr Lys Ala 550 Pro Val Gly Gln Ser Ser Gly Arg Ile Thr Ala
 Thr Ala Ala Gly 565 Thr Val Val Ala His 570 Thr Ala Leu Gly Leu Val Lys
 Glu Glu Glu Arg Tyr Thr Leu Thr Val His Val Lys Asp 585 Arg Asp Gly
 Ala Pro Thr Pro Ala His 600 Gly Val Lys Gln Leu Ala Glu Asp Thr
 Asp 610 Pro Phe Pro Ala Ala 615 Val Gly Asp Ser Gly 620 Leu Glu Leu Arg
 625 Leu Gln Pro Gly Thr Tyr Thr Val Asp Thr Phe Leu Asp Val Arg Gly
 Ser His Gly Glu 645 Asp Ser Leu Gly Leu 650 Gly Phe Leu Thr Ala Pro Glu
 Ile Thr Leu 660 Asp Arg Asp Arg Glu 665 Ile Thr Leu Asp Gly Arg Gln Leu
 Arg Glu 675 Ile Arg Ala Glu Val 680 Asp Arg Arg Thr Glu Thr Arg Gln Leu
 Leu Met Glu Phe Asp Arg 695 Lys Ala Asn Gly Ala Ser Tyr Gly Gly Ala
 705 710 715 720

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Lys	Pro	Met	Leu	Glu	Thr	Ser	Val	Asp	Gly	Ser	Arg	Leu	Ser	Gly	Ala
		755					760					765			
Thr	Pro	Gln	Ala	Gly	Ala	Thr	Leu	Leu	Glu	Gly	Arg	His	Arg	Leu	Gly
	770					775					780				
Leu	Val	Asp	Ala	Gly	Thr	Gly	Thr	Pro	Ala	Glu	Tyr	Thr	Gly	Arg	Asn
785					790					795					800
Val	Thr	Gly	Lys	Ala	Val	Leu	Val	Arg	Leu	Thr	Glu	Gly	Ala	Asp	Pro
			805						810					815	
Ala	Gln	Val	Ala	Gln	Thr	Ala	Gln	Asp	Ala	Gly	Ala	Lys	Ala	Leu	Phe
			820					825					830		
Val	Thr	Asp	Asp	Arg	Pro	Gly	Arg	Leu	Met	Glu	Trp	Phe	Gly	Thr	Ala
		835					840					845			
Asp	Tyr	Gln	Asp	Arg	Pro	Leu	Ala	Val	Ala	Thr	Val	Asn	Ala	Ala	Asp
	850					855					860				
Ala	Arg	Arg	Leu	Ala	Ala	Gly	Ala	Ala	Arg	Gly	Lys	Arg	Val	Asp	Leu
865					870					875					880
Thr	Gly	Thr	Arg	Phe	Thr	Pro	Phe	Thr	Tyr	Asp	Leu	Ser	Glu	Gly	His
				885					890					895	
Pro	Gly	Ala	Ile	Gly	Lys	Asp	Leu	Val	Phe	Arg	Pro	Asp	Glu	Asp	Glu
			900					905					910		
Leu	Ala	Thr	Val	Arg	Ser	Thr	Phe	His	Ala	Pro	Thr	Lys	Arg	Ala	Glu
		915					920					925			
Leu	Gly	Gly	Glu	Phe	Arg	Tyr	Ser	Ile	Thr	Asp	Thr	Phe	Pro	Ile	Gly
	930					935					940				
Phe	Gly	Phe	Lys	Glu	Trp	Ile	Ser	Phe	Pro	Ala	Glu	Arg	Thr	Glu	Tyr
945					950					955					960
Val	Ser	Thr	Gly	Thr	Gly	Gln	Arg	Trp	His	Glu	Ser	Val	Asp	Leu	Gly
			965						970					975	
Glu	Ser	Leu	Glu	Glu	Arg	Gly	Gly	Gln	Ser	Val	Tyr	Arg	Gly	Gly	Ser
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Arg	Val	Asp	Leu	Asp	Trp	Phe	Gly	Pro	Val	Trp	His	Pro	Trp	Leu	Gly
		995					1000					1005			
Thr	Gly	Leu	Gly	Trp	Gly	Gln	Gln	Arg	Thr	Gly	Asn	Asp	Leu	Arg	Phe
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			1045						1050					1055	
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			1060					1065				1070			
Asp	Ala	Pro	Ala	Glu	Glu	Ala	Ala	Tyr	Lys	Val	Val	Thr	Asp	Thr	Thr
		1075					1080					1085			
Leu	Asp	Pro	Ala	Arg	Trp	Arg	Leu	Ala	Thr	Lys	Gly	His	Ser	Glu	Trp
	1090					1095					1100				
Thr	Phe	Arg	Ser	Ala	Glu	Thr	Pro	His	Asp	Lys	Ile	Thr	Tyr	Leu	Pro
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Met	Leu	Asn	Leu	Gly	Phe	Asp	Val	Asp	Thr	Asp	Ile	Asn	Gly	Asp	Val
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Arg	Ala	Gly	Ser	Arg	Leu	Pro	Val	Gly	Ile	Ser	Ala	Glu	Tyr	Val	Lys
			1140					1145					1150		
Gly	Ala	Thr	Gly	Thr	Gly	Ser	Ile	Gly	Thr	Gly	Thr	Leu	Glu	Val	Ser
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Tyr	Asp	Glu	Gly	Arg	Thr	Trp	Thr	Lys	Val	Ala	Leu	Lys	Lys	Ala	Arg
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His	Gly	Ala	Ala	Trp	Asp	Gly	Glu	Leu	Arg	Val	Pro	Ser	Gly	Ala	Asp
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Ser	Val	Ser	Leu	Arg	Ala	Gly	Ala	Ser	Asp	Asp	Arg	Gly	Gly	Ser	Val
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<210> 7
 <211> 1332
 <212> DNA

10336256.txt

<213> Bacteria

<400> 7

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tgtaaaatta	gaaacgagtt	ctctatcatt	tcttgctgta	gtgccgatat	aacaccatca	300
gtcttagaag	aggttttaac	taattgtaac	catattaaaa	aggtgtattt	aaatcatgaa	360
gtgcgagctt	tattagatac	ggctgttata	tcagcaaagt	caaaaaatat	tgtgagaaat	420
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ccaaattctt	atttagacaa	atttcaaaaa	gggaatcgag	tggggtcaga	ctatttttct	1140
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cataatccaa	atgcaactcc	gcaagaggta	aaagacttat	taaaaagagg	aacggattta	1260
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<210> 8

<211> 443

<212> PRT

<213> Bacteria

<400> 8

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			20					25					30		
Lys	Trp	Thr	Pro	Cys	Phe	Leu	His	Lys	Met	Phe	Glu	Arg	Phe	Phe	Lys
			35				40					45			
Asn	Arg	Lys	Lys	Leu	Ser	Val	Ile	Ile	Glu	Phe	Glu	Ser	Asn	Cys	Tyr
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Gln	Glu	Gly	Cys	Leu	Glu	Val	Asn	Gln	Ala	Phe	Thr	Lys	Arg	Asn	Gly
65				70					75					80	
Cys	Lys	Ile	Arg	Asn	Glu	Phe	Ser	Ile	Ile	Ser	Cys	Cys	Ser	Ala	Asp
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Ile	Thr	Pro	Ser	Val	Leu	Glu	Glu	Val	Leu	Thr	Asn	Cys	Asn	His	Ile
			100					105						110	
Lys	Lys	Val	Tyr	Leu	Asn	His	Glu	Val	Arg	Ala	Leu	Leu	Asp	Thr	Ala
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Val	Ile	Ser	Ala	Asn	Ala	Lys	Asn	Ile	Val	Arg	Asn	Asn	Thr	Thr	Leu
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Thr	Gly	Lys	Gly	Ile	Thr	Ile	Ala	Val	Ile	Asp	Thr	Gly	Ile	Phe	Pro
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His	Thr	Asp	Leu	Ser	Gly	Arg	Ile	Ile	Asp	Phe	Val	Asp	Phe	Ile	Asn
			165						170					175	
Asp	Arg	Thr	Glu	Thr	Tyr	Asp	Asp	Asn	Gly	His	Gly	Thr	His	Cys	Ala
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Gly	Asp	Ala	Leu	Gly	Asp	Gly	Ser	Ala	Ser	Ser	Gly	Leu	Tyr	Met	Gly
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Pro	Ala	Pro	Glu	Ala	Asn	Val	Ile	Gly	Val	Lys	Val	Leu	Asn	Lys	Val
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Gly	Ser	Gly	Ser	Leu	Glu	Thr	Val	Met	Gln	Gly	Val	Asp	Trp	Cys	Ile
225				230						235				240	
Lys	Tyr	Asn	Asp	Gln	Asn	Pro	Asp	Gln	Lys	Ile	Asn	Ile	Ile	Asn	Met
			245						250					255	
Ser	Leu	Gly	Ala	Pro	Ala	Gln	Arg	Tyr	Glu	Asn	Glu	Asn	Asp	Asp	Pro
			260					265					270		
Met	Val	Lys	Met	Val	Glu	Lys	Ala	Trp	Glu	Asn	Gly	Ile	Val	Val	Cys

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275 280 285
 Val Ala Gly Asn Glu Gly Pro Glu Ala Ser Thr Ile Ala Ser Pro
 290 300
 Gly Val Ser Glu Gln Val Ile Thr Val Gly Ala Leu Asp Asp Lys Thr
 305 310 315 320
 Thr Ala Asp Thr Arg Ser Asp Asp Glu Val Ala Ser Phe Ser Ser Arg
 325 330 335
 Gly Pro Thr Ile Tyr Glu Lys Val Lys Pro Asp Ile Leu Ala Pro Gly
 340 345 350
 Val Asp Ile Ile Ser Leu Arg Ser Pro Asn Ser Tyr Leu Asp Lys Phe
 355 360 365
 Gln Lys Gly Asn Arg Val Gly Ser Asp Tyr Phe Ser Leu Ser Gly Thr
 370 375 380
 Ser Met Ala Thr Pro Ile Cys Ala Gly Ile Ala Ala Leu Ile Leu Gln
 385 390 395 400
 His Asn Pro Asn Ala Thr Pro Gln Glu Val Lys Asp Leu Leu Lys Arg
 405 410 415
 Gly Thr Asp Leu Trp Thr Asn Arg Asp Pro Asn Ile Tyr Gly Ala Gly
 420 425 430
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<210> 9

<211> 2181

<212> DNA

<213> Unknown

<220>

<223> obtained from an environmental sample

<400> 9

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ctgtccgatc	cttatttctg	gctgcgcgat	ccgagctatc	cggtcgtcga	tgacgcggac	240
gtcctcgatt	atgtgaaggc	cgaaaatgcc	tatttcgacg	cagcaatgaa	gccgcacgca	300
aagctcgtcg	agacgttggt	tcaggagatg	aagggccgca	tcaaggaggc	cgattcctcg	360
gtgcccagca	aggacggcga	ctggctctat	tggtatcgaat	atgacgaggg	cgccgaatat	420
aagaaatggt	accggaagcc	agcgtcaggc	tccggcgaga	cccagctcat	cctcgacgag	480
gtggcgatgg	ccgagggcaa	ggattatttc	cgctcgccgc	aactgtcgat	cagtccccgac	540
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aaatcggggc	gctggggctc	gctccacgag	gatgccgagg	agttcgccct	cgtgctgacg	2160
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 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1)...(28)

<223> obtained from an environmental sample

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 35 40 45
 Gln Arg Pro His Asp Val Thr Leu His Gly Lys Thr Leu Ser Asp Pro
 50 55 60
 Tyr Phe Trp Leu Arg Asp Pro Ser Tyr Pro Val Val Asp Asp Ala Asp
 65 70 75 80
 Val Leu Asp Tyr Val Lys Ala Glu Asn Ala Tyr Phe Asp Ala Ala Met
 85 90 95
 Lys Pro His Ala Lys Leu Val Glu Thr Leu Phe Gln Glu Met Lys Gly
 100 105 110
 Arg Ile Lys Glu Ala Asp Ser Ser Val Pro Gln Lys Asp Gly Asp Trp
 115 120 125
 Leu Tyr Trp Ile Glu Tyr Asp Glu Gly Ala Glu Tyr Lys Lys Trp Tyr
 130 135 140
 Arg Lys Pro Ala Ser Gly Ser Gly Glu Thr Gln Leu Ile Leu Asp Glu
 145 150 155 160
 Val Ala Met Ala Glu Gly Lys Asp Tyr Phe Arg Leu Ala Glu Leu Ser
 165 170 175
 Ile Ser Pro Asp Gly Arg Leu Met Ala Tyr Ser Phe Asp Asp Asn Gly
 180 185 190
 Ser Glu Arg Phe Glu Ala Arg Val Arg Asn Leu Glu Thr Gly Glu Leu
 195 200 205
 Leu Pro Asp Val Ile Pro Gly Thr Leu Ser Ser Leu Val Trp Thr Ser
 210 215 220
 Gly Asn Asp Ala Ile Leu Tyr Gly Leu Ala Asn Glu Asn Trp Arg Thr
 225 230 235 240
 Asp Asn Val Arg Leu His Lys Leu Gly Thr Pro Val Gly Gln Asp Lys
 245 250 255
 Leu Leu Tyr Lys Glu Pro Asp Ile Gly Phe Gly Val Gly Ile Gly Lys
 260 265 270
 Thr Ala Ala Asp Asn Tyr Ile Val Ile Gly Thr Gly Asp Asn Glu Thr
 275 280 285
 Asn Glu Val Tyr Leu Leu Pro Ala Asp Asn Pro Glu Ala Glu Met Gln
 290 295 300
 Leu Val Ser Ala Arg Gln Lys Gly Arg Glu Tyr Ser Val Asp Glu Arg
 305 310 315 320
 Asp Gly Thr Leu Tyr Ile Leu Thr Asn Asp Glu His Pro Asn Phe Arg
 325 330 335
 Val Ala Thr Ala Ser Ile Glu Ala Pro Gly Thr Trp Lys Thr Leu Ile
 340 345 350
 Pro Gly Ser Asp His Ser Tyr Ile Thr Gly Phe Ser Val Phe Arg Asp
 355 360 365
 Tyr Phe Val Leu Glu Ala Arg Glu Asp Gly Leu Asp Gln Val Asp Ile
 370 375 380
 Arg Lys Tyr Asp Ala Pro Leu Thr Pro Gly Arg Ile Glu Phe Pro Glu
 385 390 395 400
 Ala Thr Tyr Val Ala Gly Leu Gly Asp Asn Pro Glu Tyr His Gln Asp
 405 410 415
 Lys Leu Arg Leu Asp Tyr Glu Ser Met Val Thr Pro Asp Thr Val Tyr
 420 425 430
 Asp Tyr Asp Ile Ala Thr Gly Thr Leu Glu Thr Leu Lys Val Gln Glu

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435 440 445
 Ile Pro Ser Gly Tyr Asp Ala Thr Gln Tyr Val Thr Glu Arg Val Asn
 450 455 460
 Leu Pro Ser Arg Asp Gly Lys Thr Met Ile Pro Ala Ser Leu Val Tyr
 465 470 475 480
 Lys Lys Gly Thr Lys Arg Asp Gly Ser Ala Pro Met His Leu Tyr Ala
 485 490 495
 Tyr Gly Ser Tyr Gly Tyr Arg Ile Ala Pro Gly Phe Ser Thr Thr Arg
 500 505 510
 Leu Ser Leu Val Asp Arg Gly Met Ile Tyr Ala Ile Ala His Val Arg
 515 520 525
 Gly Gly Asp Asp Leu Gly Arg Ala Trp Tyr Leu Ala Gly Lys Thr Asp
 530 535 540
 His Arg Lys Asn Thr Phe Asn Asp Phe Ile Asp Val Ala Lys Gly Leu
 545 550 555 560
 Ile Ala Lys Gly Tyr Thr Ser Ala Gly Lys Ile Ser Ile Glu Gly Arg
 565 570 575
 Ser Ala Gly Gly Gln Val Met Gly Ala Val Thr Asn Glu Ala Pro Glu
 580 585 590
 Leu Trp Gly Ala Val Leu Ala Gly Val Pro Phe Val Asp Val Ile Asn
 595 600 605
 Thr Met Val Asp Glu Thr Leu Pro Leu Thr Pro Gly Glu Trp Pro Glu
 610 615 620
 Trp Gly Asn Pro Ile Thr Asp Lys Ala Ala Phe Asp Tyr Met Leu Ser
 625 630 635 640
 Tyr Ser Pro Tyr Asp Asn Val Thr Ala Lys Ala Tyr Pro Pro Met Leu
 645 650 655
 Val Ser Ala Gly Leu Asn Asp Pro Arg Val Thr Tyr Trp Glu Pro Ala
 660 665 670
 Lys Trp Val Ala Lys Leu Arg Ala Thr Arg Thr Asn Asp Ala Thr Leu
 675 680 685
 Leu Leu Arg Thr Asn Met Gly Ala Gly His Ala Gly Lys Ser Gly Arg
 690 695 700
 Trp Gly Ser Leu His Glu Asp Ala Glu Glu Phe Ala Phe Val Leu Thr
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 Gln Leu Gly Val Glu Lys 725

<210> 11
 <211> 1374
 <212> DNA
 <213> Unknown

<220>
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 gctttgcccg aagatctaca gcgattaatt cgcgcgaatg cgccggatac tgccggattt 180
 gaagccgttt gtgcacgctg tgtcaggctt tttgaacgcg ccaaagataa tattttgagt 240
 gatgcggcga tgaacaaaga cggttcgtat gtgctttcga cacttttgcg gctcgaatgct 300
 gacgaacggt ttacgggcaa gggcgtgacg atcgcgtttc tcgattcggg tttttatccg 360
 cacgtcgatc tgactacacc gaacaatcga attatcgggt accgcagctt gatgcatgca 420
 gaagcgcgatc tgacgacact ttttcaatcg gatgtagcga gctggcacgg aatgatgacc 480
 tcggtcgtcg cggcaggaaa cggctcgttt tccaacgggt tttatcgcgg aattgcgccc 540
 catgccaatg ttgtgttggt gaaactggca cgaacaggac gaatcaccga gcaaaatatt 600
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 gccgcgcttg accgtcccgc gtatatgctt cgcgacggga catcttttgc cgccgcgatc 1140
 gaaagcgtaa ttaccgcgtc ttacaaatac gcaaatccga atctgacacc gcagaaaatt 1200
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10336256.txt

aaacgaattt tgatcagttc ggcggaacgt cttccgcatt atgaagtcga tcggcaaggc 1320
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<210> 12
 <211> 457
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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 Arg Asp Glu Phe Val Pro Leu Val Ala Leu Pro Glu Asp Leu Gln Arg
 35 40 45
 Leu Ile Arg Ala Asn Ala Pro Asp Thr Ala Gly Phe Glu Ala Val Cys
 50 55 60
 Ala Arg Cys Val Arg Leu Phe Glu Arg Ala Lys Asp Asn Ile Leu Ser
 65 70 75 80
 Asp Ala Ala Met Asn Lys Asp Gly Ser Tyr Val Leu Ser Thr Pro Leu
 85 90 95
 Arg Leu Asp Ala Asp Glu Arg Phe Thr Gly Lys Gly Val Thr Ile Ala
 100 105 110
 Phe Leu Asp Ser Gly Phe Tyr Pro His Val Asp Leu Thr Thr Pro Asn
 115 120 125
 Asn Arg Ile Ile Gly Tyr Arg Ser Leu Met His Ala Glu Gly Asp Leu
 130 135 140
 Thr Thr Leu Phe Gln Ser Asp Val Ala Ser Trp His Gly Met Met Thr
 145 150 155 160
 Ser Val Val Ala Ala Gly Asn Gly Ser Leu Ser Asn Gly Phe Tyr Arg
 165 170 175
 Gly Ile Ala Pro Asp Ala Asn Val Val Leu Val Lys Leu Ala Arg Thr
 180 185 190
 Gly Arg Ile Thr Glu Gln Asn Ile Gln Asp Gly Leu Glu Trp Ile Leu
 195 200 205
 Ala Asn Arg Thr Lys Tyr Gly Ile Lys Val Val Asn Ile Ser Ala Gly
 210 215 220
 Gly Asp Phe Glu Gln Ser Tyr Leu His Asp Ala Leu Ser Gln Thr Val
 225 230 235 240
 Glu Glu Cys Val Ala Lys Gly Leu Thr Ile Val Cys Ala Ile Gly Asn
 245 250 255
 Ala Gly His Leu Pro Thr His Pro Val Phe Pro Pro Ala Ser Ser Pro
 260 265 270
 Ser Ala Ile Ala Val Gly Gly Leu Asp Asp His Asn Ser Ile Asn Arg
 275 280 285
 Ala Lys Arg Gly Met Tyr Arg Ser Ser Tyr Gly Pro Thr Leu Asp Gly
 290 295 300
 Phe Gln Lys Pro Glu Ile Ile Ala Ser Ser Ile Trp Val Pro Ala Pro
 305 310 315 320
 Ile Leu Pro Asn Thr Pro Thr Ala Lys Gln Val Asp Phe Leu Glu Thr
 325 330 335
 Leu Asp Lys Ala Ser Asp Glu Asp Leu His Arg Ile Ile Glu Glu Asn
 340 345 350
 Arg Gly Met Asp Gly Glu Leu Glu Ala Ala Leu Asp Arg Pro Ala Tyr
 355 360 365
 Met Leu Arg Gln Ile Ile Leu Leu Lys Leu Gln Arg Glu Ser Val Ile
 370 375 380
 Thr Arg His Tyr Lys Tyr Val Asp Gly Thr Ser Phe Ala Ala Pro Ile
 385 390 395 400
 Val Ser Ser Val Ile Ala Gln Met Leu Glu Ala Asn Pro Asn Leu Thr
 405 410 415
 Pro Gln Lys Ile Lys Arg Ile Leu Ile Ser Ser Ala Glu Arg Leu Pro
 420 425 430
 His Tyr Glu Val Asp Arg Gln Gly Trp Gly Val Ile Asp Pro Arg Lys
 435 440 445

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Ala Val Glu Met Ala Leu Ser Phe Val
450 455

<210> 13
 <211> 783
 <212> DNA
 <213> Bacteria

<400> 13
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 ggcaccccg cgcgccaggg cgagttcccg tggatggtcc ggctctccat gggctgcggc 180
 ggctcgctga tctcgccgca ggctcgtctc accgcccggc actgctcag cggctccggc 240
 aacaacacca gcatcaccgc caccgcccgt gtcgtcgacc tgcagagcag cagcgccatc 300
 aaggtccggt ccaccaaggt cctccaggcc cccggctaca acggcaaggg caaggactgg 360
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 agctcgtacg gcagcgacct cgtccccgcc gaggagatct gcgcccggcta cagccagggc 600
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 gcgtgggtcc aggtcggcat cgtgagctgg ggcgagggct gcgcccgcgc cggctacccg 720
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 taa 783

<210> 14
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 <212> PRT
 <213> Bacteria

<220>
 <221> SIGNAL
 <222> (1)...(33)

<400> 14
 Met Ser Gln Asn Arg Met Val Arg Ala Leu Gln Lys Leu Ala Ala Ala
 1 5 10 15
 Gly Ala Val Val Leu Ala Ala Val Ser Leu Gln Pro Thr Thr Ala Ser
 20 25 30
 Ala Ala Pro Ala Pro Val Val Gly Thr Arg Ala Ala Gln Gly Glu
 35 40 45
 Phe Pro Trp Met Val Arg Leu Ser Met Gly Cys Gly Gly Ser Leu Ile
 50 55 60
 Ser Pro Gln Val Val Leu Thr Ala Ala His Cys Val Ser Gly Ser Gly
 65 70 75 80
 Asn Asn Thr Ser Ile Thr Ala Thr Ala Gly Val Val Asp Leu Gln Ser
 85 90 95
 Ser Ser Ala Ile Lys Val Arg Ser Thr Lys Val Leu Gln Ala Pro Gly
 100 105 110
 Tyr Asn Gly Lys Gly Lys Asp Trp Ala Leu Ile Lys Leu Ala Ser Pro
 115 120 125
 Ile Thr Ser Leu Pro Asn Leu Lys Ile Ala Glu Thr Thr Ala Tyr Asn
 130 135 140
 Ser Gly Thr Phe Thr Val Ala Gly Trp Gly Ala Arg Glu Gly Gly
 145 150 155 160
 Gly Gln Gln Arg Tyr Leu Leu Lys Ala Asn Val Pro Phe Val Ser Asp
 165 170 175
 Ala Ser Cys Gln Ser Ser Tyr Gly Ser Asp Leu Val Pro Ala Glu Glu
 180 185 190
 Ile Cys Ala Gly Tyr Ser Gln Gly Gly Val Asp Thr Cys Gln Gly Asp
 195 200 205
 Ser Gly Gly Pro Met Phe Arg Lys Asp Asn Ala Gly Ala Trp Val Gln
 210 215 220
 Val Gly Ile Val Ser Trp Gly Glu Gly Cys Ala Arg Ala Gly Tyr Pro
 225 230 235 240
 Gly Val Tyr Thr Glu Val Ser Thr Phe Ala Ala Ala Ile Lys Ser Ala
 245 250 255
 Ala Ala Thr Leu
 260

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<210> 15
 <211> 900
 <212> DNA
 <213> Bacteria

<400> 15
 atgCGcacca cccccacgag aaccgtccgg ctgctcgccg tcgCGgcagg cctcgccgcc 60
 gccgcccgcg tCGccgcccc caccgcgagc gcgggcaccg ccgactccgc gcggagcacc 120
 cgcaccttcg acgcccgcgc cctctcgggc accggcgacg ccgtccgcgc cgcgacgtg 180
 gccgGCaccg cctggtacgc cgacacggcc accggcgagc tggtcgtcac cgcCGactcc 240
 accgtcaccC ccgCCgggat cgcgaagatc aagCGgcagg cgggggCGaa cgcgGacgcc 300
 atcCGggtcg agcggacccc gggcaagttc accaagctga tctccggcgg cgacgcgatc 360
 tacGCCacca gctggcgctg ctCGctgggt ttcaacgtcc gggacagtgc gggcaactac 420
 tacttcctga ccgCCggcca ctgcaccgac ggcgcgggca cctgggtactc caactcctcc 480
 cggaccaccg tcctcgGCac caccgcgggg tccagcttcc ccggcaacga ctacggtctg 540
 gtgcgctaca ccaactcctc cgtcaccaag tccggcacgg tcggcagcgt ggacatcacc 600
 agcGCCgcca acgCCaccgt cggcatgtcg gtcacccgcc gcggctccac caccggcatc 660
 cacagcggct ccgtgacggg cctgaacgcc accgtgaact acggcggcgg tgacatcgtc 720
 tccgggctga tccgtacgaa cgtgtgcgcc gagcccggcg actccggcgg tccgctctac 780
 tcgggcagcc gggccgtcgg cctcacctcg ggcggcagcg gcaactgtct cacgggcggc 840
 acgaccttct tccagcccgt gaccgagggc ctgagcgcgt acggggtcag cgtcttctag 900

<210> 16
 <211> 299
 <212> PRT
 <213> Bacteria

<220>
 <221> SIGNAL
 <222> (1)...(31)

<400> 16
 Met Arg Thr Thr Pro Thr Arg Thr Val Arg Leu Leu Ala Val Ala Ala
 1 5 10 15
 Gly Leu Ala Ala Ala Ala Leu Ala Ala Pro Thr Ala Ser Ala Gly
 20 25 30
 Thr Ala Asp Ser Ala Arg Ser Thr Arg Thr Phe Asp Ala Ala Ala Leu
 35 40 45
 Ser Ala Thr Gly Asp Ala Val Arg Ala Ala Asp Val Ala Gly Thr Ala
 50 55 60
 Trp Tyr Ala Asp Thr Ala Thr Gly Glu Leu Val Val Thr Ala Asp Ser
 65 70 75 80
 Thr Val Thr Pro Ala Gly Ile Ala Lys Ile Lys Arg Gln Ala Gly Ala
 85 90 95
 Asn Ala Asp Ala Ile Arg Val Glu Arg Thr Pro Gly Lys Phe Thr Lys
 100 105 110
 Leu Ile Ser Gly Gly Asp Ala Ile Tyr Ala Thr Ser Trp Arg Cys Ser
 115 120 125
 Leu Gly Phe Asn Val Arg Asp Ser Ala Gly Asn Tyr Tyr Phe Leu Thr
 130 135 140
 Ala Gly His Cys Thr Asp Gly Ala Gly Thr Trp Tyr Ser Asn Ser Ser
 145 150 155 160
 Arg Thr Thr Val Leu Gly Thr Thr Ala Gly Ser Ser Phe Pro Gly Asn
 165 170 175
 Asp Tyr Gly Leu Val Arg Tyr Thr Asn Ser Ser Val Thr Lys Ser Gly
 180 185 190
 Thr Val Gly Ser Val Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly
 195 200 205
 Met Ser Val Thr Arg Arg Gly Ser Thr Thr Gly Ile His Ser Gly Ser
 210 215 220
 Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Ile Val
 225 230 235 240
 Ser Gly Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly
 245 250 255
 Gly Pro Leu Tyr Ser Gly Ser Arg Ala Val Gly Leu Thr Ser Gly Gly
 260 265 270
 Ser Gly Asn Cys Ser Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Thr

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275 280 285
 Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Phe
 290 295

<210> 17
 <211> 1137
 <212> DNA
 <213> Bacteria

<400> 17
 gtgaaacgcc cgggtgtccat cgtattcccc gcgtatctcg agaagtacgc gcggctcctc 60
 gtagactaca gcgtcgaggt taagcgcggc gaccgtgtcg ttataaggac gtggcttgag 120
 gctctcccc tcgcaaggct cgtctaccgc gaggtgctga ggagggcgcg gcaccccgca 180
 ctatacctgg aggatgatat cctcgccgag atattctacc gcgaggctag cgacgagcag 240
 atcgatttcg ttgacgccct ccgccgcagc atatacaccg agttcgacgt cgtgataacc 300
 ctctttgccc cgagccactt gaagaatctt gtgagtatcc cgccggagaa gcaggctagg 360
 aggagcaagg ccctcgagcc ctacttcacg aggttcctcc aggaggccgc tgagggcaag 420
 aagaggtggg ttctcgccgc ctaccgcagc ctgcgcatgg ccaggaggc tggcatgacg 480
 cctatcgagt tcgaggagtt cgtggcaaga gcagtgaagg tcacggagga cgacccggtc 540
 gccgcgtgga ggaggcaagc cgagtaccag aggaggatag tcgacgagat cctctcgaag 600
 gctgatgagc ttgtcttcaa gggcccgggc atcgacctaa ccgtgaaggt cgggtggccgc 660
 cgctggatcg ttgacgacgg ccacgagaat atgccgggtg gcgaggtgtt caccggcccg 720
 gtcgaggata gcgtggaggg ctgtgtacgc ttcgacttcc cgagcgtcta tcgcggcggtg 780
 gaggttagagg gcgtcaagct gtgcttcaag agggcgaggg ttgtagagta tgacgccgtc 840
 aagggccgcg acttcctcgc taagatgctg agtgtggacg agggcgccaa gaggctagga 900
 gagctggcct tcgggtaccg ctatggcata accaggcgca cgcgagagat actcttcgac 960
 gagaagatag ggggtaccat ccacatggcg cttggaaacg gctaccggga gaccggctcg 1020
 agaaacaaga gcgccatcca ctgggacctg ataaaagaca tgagggaccc agaggcacgc 1080
 gtctatgccg atggcgagct tatctacaag gctggcaggt tcctactaga ggagtga 1137

<210> 18
 <211> 378
 <212> PRT
 <213> Bacteria

<400> 18
 Met Lys Arg Pro Val Ser Ile Val Phe Pro Ala Tyr Leu Glu Lys Tyr
 1 5 10 15
 Ala Arg Leu Leu Val Asp Tyr Ser Val Glu Val Lys Arg Gly Asp Arg
 20 25 30
 Val Val Ile Arg Thr Trp Leu Glu Ala Leu Pro Leu Ala Arg Leu Val
 35 40 45
 Tyr Arg Glu Val Leu Arg Arg Gly Ala His Pro Ala Leu Tyr Leu Glu
 50 55 60
 Asp Asp Ile Leu Ala Glu Ile Phe Tyr Arg Glu Ala Ser Asp Glu Gln
 65 70 75 80
 Ile Asp Phe Val Asp Ala Leu Arg Arg Ser Ile Tyr Thr Glu Phe Asp
 85 90 95
 Val Val Ile Thr Leu Phe Ala Pro Ser His Leu Lys Asn Leu Val Ser
 100 105 110
 Ile Pro Pro Glu Lys Gln Ala Arg Arg Ser Lys Ala Leu Glu Pro Tyr
 115 120 125
 Phe Thr Arg Phe Leu Gln Glu Ala Ala Glu Gly Lys Lys Arg Trp Val
 130 135 140
 Leu Ala Ala Tyr Pro Thr Leu Ala Met Ala Gln Glu Ala Gly Met Thr
 145 150 155 160
 Pro Ile Glu Phe Glu Phe Val Ala Arg Ala Val Lys Val Thr Glu
 165 170 175
 Asp Asp Pro Val Ala Ala Trp Arg Arg Gln Ala Glu Tyr Gln Arg Arg
 180 185 190
 Ile Val Asp Glu Ile Leu Ser Lys Ala Asp Glu Leu Val Phe Lys Gly
 195 200 205
 Pro Gly Ile Asp Leu Thr Val Lys Val Gly Gly Arg Arg Trp Ile Val
 210 215 220
 Asp Asp Gly His Glu Asn Met Pro Gly Gly Glu Val Phe Thr Gly Pro
 225 230 235 240
 Val Glu Asp Ser Val Glu Gly Cys Val Arg Phe Asp Phe Pro Ser Val
 245 250 255

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Tyr Arg Gly Val Glu Val Glu Gly Val Lys Leu Cys Phe Lys Arg Gly
 260 265 270
 Glu Val Val Glu Tyr Asp Ala Val Lys Gly Arg Asp Phe Leu Ala Lys
 275 280 285
 Met Leu Ser Val Asp Glu Gly Ala Lys Arg Leu Gly Glu Leu Ala Phe
 290 295 300
 Gly Leu Asn Tyr Gly Ile Thr Arg Ala Thr Arg Glu Ile Leu Phe Asp
 305 310 315 320
 Glu Lys Ile Gly Gly Thr Ile His Met Ala Leu Gly Asn Gly Tyr Pro
 325 330 335
 Glu Thr Gly Ser Arg Asn Lys Ser Ala Ile His Trp Asp Leu Ile Lys
 340 345 350
 Asp Met Arg Asp Pro Glu Ala Arg Val Tyr Ala Asp Gly Glu Leu Ile
 355 360 365
 Tyr Lys Ala Gly Arg Phe Leu Leu Glu Glu
 370 375

<210> 19

<211> 2298

<212> DNA

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 19

gtgaaactta	aacccttttc	gctccgactc	caggccaaga	cttggttggt	attcatactg	60
actctctgct	acagccttgc	ggcttiaccct	tcattctcaaa	acacagaagc	cttggcgcaa	120
attcaagata	agattgctca	aaatgacagc	actctagtct	tggtagaatt	acttctaccg	180
agcactgcgg	ccaatttgag	cggcggcaat	ctggcatctc	acactgaaca	gctcagaaat	240
attcagttga	gtgtattggg	tgacctaaact	accggagcca	gcaccaactc	aaacctgatc	300
aatgccactt	tatttgatta	cgtcaatggg	atggctctga	cagttgatgc	aaacctgctg	360
gatcagctgt	tgcagcacc	ttctgtgggc	cgcatttcgc	caaatgatgt	tagttatcca	420
atgctaacgg	atagcatgcc	cttgattggc	gctgatccca	caggcggctt	ttccggacac	480
ggcggctcaag	gtcaagcggg	agccattttg	gatacaggcg	ttgataaata	tcaccccgct	540
tttcaaggta	gagttatctc	agaagcctgt	tattctgcgt	ctgcttatac	tgatgactgg	600
ttgattcagt	ccttttctact	atgccctgga	ggggttgctg	aatcagtatt	gccaggctct	660
ggcatacact	gcgagaacca	ccgtgatggc	ggccacggta	cacacgtagc	gggcatagca	720
actggtcaag	cggtaaagcgt	caataatcaa	tctgtctttg	gtgttgctcc	gtcggccgac	780
ataatcgcca	ttcaggtatt	cacactccca	accagaccac	aggctggatt	gcaggccac	840
actttggata	ttcttaaagg	gttggagcgc	gtcatagcct	tgcacgacgc	aggcaccctt	900
atcgctgcgg	ctaatatgag	tttaggggtt	tcattatttc	aggactcatg	cgatgatcac	960
caacctctga	tgactcaagc	cattgagaac	ttgcgagtc	gtggcattgc	aacctatagtc	1020
gccagcggtg	actatgggtt	tagagaccgc	ataagctggc	cggcatgtat	atccagcgct	1080
atcagtggtg	gcagcacaa	gaaagatgat	gaagtatccg	attttagcaa	tcacacctct	1140
cttgtaaatt	tactagcgcc	tggcagtgaa	attcttgag	ccgtgccggg	taacgctttt	1200
gaggtttata	gcggtacatc	tatggccgca	ccccatgttg	ccggtgcctg	ggctgtgctt	1260
aaaggcgctt	acccagagtc	aagtgtggac	gacattttta	ctgcgctaga	cgctacaggt	1320
attcccgtat	tggtatacag	gcatggcgcc	attgatcatg	ccatacctcg	catacaggtt	1380
gaccaagcac	ttttggccct	aggcaccctt	aattacgatt	caacttatcc	aagcatgcac	1440
attcgcgcca	ctttcaacgc	ctgggacaac	gccagcatga	gacttgtaga	tgactttaca	1500
tggaagcaa	atcttggtact	gcaaccttag	aacggtgctg	ctcacctttt	caagtttgat	1560
gcatacggtg	attggcttag	aaattatggg	tccagtggcg	aagcaggagt	agcttcactt	1620
tacggcgctg	atcttgaaac	acagtgcacc	ggagaagtga	cggttaagggt	caacgatgcc	1680
aacctttcat	actctgtaga	aggtaggggc	tgtactgatt	ccaactggcg	ccgcactggt	1740
atcttcatct	atgggtcaaac	ccaagtaggg	caagacatgt	ttattcgtgg	cggaatagac	1800
cacggttacg	ccagcagtg	attgggcatt	aattgcacgc	aggaaaacat	gctttgcgcc	1860
atacctattc	gtacatttgaa	taaccttaac	agcacgacaa	acccctggaa	agtgaacgac	1920
caccacctgg	attggtatgg	tgctgagcct	gggcaaagta	gtagcgcgcc	aggcacacca	1980
tttgattgga	ccacaaacct	ctggccatcc	agctggggca	ccagaagaac	ggttgaagtt	2040
gatggttacg	gcgaaacacc	tctcaatcaa	tggggggatc	attactggat	gctggacggt	2100
gaaatggatt	gctccagagt	gggtgaatgg	tggtttgaag	taaaatcctt	tataacaaat	2160
gggcccggct	gggaaagcga	tgtgaatcaa	cccgacgccc	cttgggtatc	tggcaatcac	2220
tttgctcaat	gtggaacgct	taatgtcttt	aggcgcaatg	aagatcaacc	cgtatttggt	2280
ggtcagccaa	ttccgtga					2298

<210> 20

<211> 765

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<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(39)

<400> 20

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Met Lys Leu Lys Pro Phe Pro Leu Arg Leu Gln Ala Lys Thr Trp Leu
1      5      10      15
Leu Phe Ile Leu Thr Leu Cys Tyr Ser Leu Ala Ala Tyr Pro Ser Ser
20      25      30
Gln Asn Thr Glu Ala Leu Ala Gln Ile Gln Asp Lys Ile Ala Gln Asn
35      40      45
Asp Ser Thr Leu Val Leu Val Glu Leu Leu Leu Pro Ser Thr Ala Ala
50      55      60
Asn Leu Ser Gly Gly Asn Leu Ala Ser His Thr Glu Gln Leu Arg Asn
65      70      75      80
Ile Gln Leu Ser Val Leu Gly Asp Leu Thr Thr Gly Ala Ser Thr Asn
85      90      95
Ser Asn Leu Ile Asn Ala Thr Leu Phe Asp Tyr Val Asn Gly Met Ala
100      105      110
Leu Thr Val Asp Ala Asn Leu Leu Asp Gln Leu Leu Gln His Pro Ser
115      120      125
Val Gly Arg Ile Ser Pro Asn Asp Val Ser Tyr Pro Met Leu Thr Asp
130      135      140
Ser Met Pro Leu Ile Gly Ala Asp Pro Thr Gly Gly Phe Ser Gly His
145      150      155      160
Gly Gly Gln Gly Gln Ala Val Ala Ile Leu Asp Thr Gly Val Asp Lys
165      170      175
Tyr His Pro Ala Phe Gln Gly Arg Val Ile Ser Glu Ala Cys Tyr Ser
180      185      190
Ala Ser Ala Tyr Thr Asp Asp Trp Leu Ile Gln Ser Phe Ser Leu Cys
195      200      205
Pro Gly Gly Val Ala Glu Ser Val Leu Pro Gly Ser Gly Ile His Cys
210      215      220
Glu Asn His Arg Asp Cys Gly His Gly Thr His Val Ala Gly Ile Ala
225      230      235      240
Thr Gly Gln Ala Val Ser Val Asn Asn Gln Ser Val Phe Gly Val Ala
245      250      255
Pro Ser Ala Asp Ile Ile Ala Ile Gln Val Phe Thr Leu Pro Thr Arg
260      265      270
Pro Gln Ala Gly Leu Gln Ala His Thr Leu Asp Ile Leu Lys Gly Leu
275      280      285
Glu Arg Val Ile Ala Leu His Asp Ala Gly Thr Pro Ile Ala Ala Ala
290      295      300
Asn Met Ser Leu Gly Phe Ser Leu Phe Gln Asp Ser Cys Asp Asp His
305      310      315      320
Gln Pro Leu Met Thr Gln Ala Ile Glu Asn Leu Arg Ser Arg Gly Ile
325      330      335
Ala Thr Ile Val Ala Ser Gly Asn Tyr Gly Phe Arg Asp Arg Ile Ser
340      345      350
Trp Pro Ala Cys Ile Ser Ser Ala Ile ser Val Gly Ser Thr Thr Lys
355      360      365
Asp Asp Glu Val Ser Asp Phe Ser Asn His Thr Ser Leu Val Asn Leu
370      375      380
Leu Ala Pro Gly Ser Glu Ile Leu Ala Ala Val Pro Gly Asn Ala Phe
385      390      395      400
Glu Val Tyr Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Gly Ala
405      410      415
Trp Ala Val Leu Lys Gly Ala Tyr Pro Glu Ser Ser Val Asp Asp Ile
420      425      430
Leu Thr Ala Leu Asp Ala Thr Gly Ile Pro Val Leu Asp Thr Arg His
435      440      445
Gly Ala Ile Asp His Ala Ile Pro Arg Ile Gln Val Asp Gln Ala Leu
450      455      460

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Leu Ala Leu Gly Thr Pro Asn Tyr Asp Ser Thr Tyr Pro Ser Met His
 465 470 475 480
 Ile Arg Gly Thr Phe Asn Ala Trp Asp Asn Ala Ser Met Arg Leu Val
 485 490 495
 Asp Asp Phe Thr Trp Glu Ala Asn Leu Val Leu Gln Pro Ser Asn Gly
 500 505 510
 Ala Ala His Leu Phe Lys Phe Asp Ala Tyr Gly Asp Trp Leu Arg Asn
 515 520 525
 Tyr Gly Ser Ser Ala Glu Ala Gly Val Ala Ser Leu Tyr Gly Ala Asp
 530 535 540
 Leu Glu Thr Gln Cys Thr Gly Glu Val Thr Val Arg Phe Asn Asp Ala
 545 550 555 560
 Asn Leu Ser Tyr Ser Val Glu Gly Glu Gly Cys Thr Asp Ser Asn Trp
 565 570 575
 Arg Arg Thr Val Ile Phe Ile Tyr Gly Gln Thr Gln Val Gly Gln Asp
 580 585 590
 Met Phe Ile Arg Gly Gly Ile Asp His Gly Tyr Ala Ser Ser Val Leu
 595 600 605
 Gly Ile Asn Cys Thr Gln Glu Asn Met Leu Cys Ala Ile Pro Ile Arg
 610 615 620
 His Leu Asn Asn Leu Asn Ser Thr Thr Asn Pro Trp Lys Val Asn Asp
 625 630 635 640
 His His Leu Asp Trp Tyr Gly Ala Glu Pro Gly Gln Ser Ser Ser Ala
 645 650 655
 Ala Gly Thr Pro Phe Asp Trp Thr Thr Asn Leu Trp Pro Ser Ser Trp
 660 665 670
 Gly Thr Arg Arg Thr Val Glu Val Asp Gly Tyr Gly Glu Thr Pro Leu
 675 680 685
 Asn Gln Trp Gly Asp His Tyr Trp Met Leu Asp Val Glu Met Asp Cys
 690 695 700
 Ser Arg Thr Val Asn Gly Trp Phe Glu Val Lys Ser Phe Ile Thr Asn
 705 710 715 720
 Gly Pro Gly Trp Glu Ser Asp Val Asn Gln Pro Gly Arg Pro Trp Val
 725 730 735
 Ser Gly Asn His Phe Ala Gln Cys Gly Thr Leu Asn Val Phe Arg Arg
 740 745 750
 Asn Glu Asp Gln Pro Val Leu Val Gly Gln Pro Ile Pro
 755 760 765

<210> 21
 <211> 867
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 21
 atgaataaca taaaaaagat aataatgtta ctgttaacga tagcaaacgg tttatatatta 60
 agttctcaaa atatagattt tgacaaccaa tccaaattaa acataacctca attgcaactt 120
 cccaacgttc aaccggccat aggaaccgaa gaaaagggtt cgaaaatagt cggcggagtg 180
 acaacgacaa actcgggaatt tcctttcata gtttccttac aacattctta ctacggccat 240
 ttctgcgag gctcattaat agcaaaggat tgggttttaa ccgcggtca ctgcgtagac 300
 ggaataactc cttcttacat agtaacgggc ataagcaagc tcacggatac cgtcgggtcaa 360
 agatttactc cggttaaaat aataaaacat ccttcctgga attcccagac aatggactac 420
 gactacgctt taatcaaatt aagcggacaa tcctccgctc cgattataga attaaacacg 480
 ctggaattaa acgccggaac caatctaacg gtagcggggt ggggacttac caaagaaaac 540
 ggagacatct ccaatacgct tcaaaaagta actcttcgc tcgtatccaa aacaacctgc 600
 ttaaaagctt atcctaacgc cataaccgac agaatgatat gcgcgggtta cgccaccggc 660
 gggaaagact catgtcaggg agatagcggc ggtccttgg tatacaaaac ctcttcaaaa 720
 cgtatcttg tcggtgtggt tagctggggg gagggatgcg cgagagaagg gaaatatgga 780
 atttattcaa aggtaagcgc cgttaaaaac tggatagaaa acaccgtaaa aacgggaagt 840
 tcaagctcac ttatactcga ttattga 867

<210> 22
 <211> 288
 <212> PRT
 <213> Unknown

10336256.txt

<220>

<223> obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(22)

<400> 22

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Met Asn Asn Ile Lys Lys Ile Ile Met Leu Leu Leu Thr Ile Ala Asn
 1      5      10      15
Gly Leu Tyr Leu Ser Ser Gln Asn Ile Asp Phe Asp Asn Gln Ser Lys
 20      25      30
Leu Asn Ile Pro Gln Leu Gln Leu Pro Asn Val Gln Pro Ala Ile Gly
 35      40      45
Thr Glu Glu Lys Val Ser Lys Ile Val Gly Gly Val Thr Thr Thr Asn
 50      55      60
Ser Glu Phe Pro Phe Ile Val Ser Leu Gln His Ser Tyr Tyr Gly His
 65      70      75      80
Phe Cys Gly Gly Ser Leu Ile Ala Lys Asp Trp Val Leu Thr Ala Ala
 85      90      95
His Cys Val Asp Gly Ile Thr Pro Ser Tyr Ile Val Thr Gly Ile Ser
100      105      110
Lys Leu Thr Asp Thr Val Gly Gln Arg Phe Thr Pro Val Lys Ile Ile
115      120      125
Lys His Pro Ser Trp Asn Ser Gln Thr Met Asp Tyr Asp Tyr Ala Leu
130      135      140
Ile Lys Leu Ser Gly Gln Ser Ser Ala Pro Ile Ile Glu Leu Asn Thr
145      150      155      160
Leu Glu Leu Asn Ala Gly Thr Asn Leu Thr Val Ala Gly Trp Gly Leu
165      170      175
Thr Lys Glu Asn Gly Asp Ile Ser Asn Thr Leu Gln Lys Val Thr Leu
180      185      190
Pro Leu Val Ser Lys Thr Thr Cys Leu Lys Ala Tyr Pro Asn Ala Ile
195      200      205
Thr Asp Arg Met Ile Cys Ala Gly Tyr Ala Thr Gly Lys Asp Ser
210      215      220
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Tyr Lys Thr Ser Ser Lys
225      230      235      240
Ala Tyr Leu Val Gly Val Val Ser Trp Gly Glu Gly Cys Ala Arg Glu
245      250      255
Gly Lys Tyr Gly Ile Tyr Ser Lys Val Ser Ala Val Lys Asn Trp Ile
260      265      270
Glu Asn Thr Val Lys Thr Gly Ser Ser Ser Leu Ile Leu Asp Tyr
275      280      285

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<210> 23

<211> 1647

<212> DNA

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 23

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atgaatcggt cgcaagtga gttgctggcc gcgtcgctgc tgctggccct cagcctgccg      60
gccgcggcgg aagacatctc cggcaatacc cggttcgcacc tcagttcggg gcaggaaggc      120
gccacctatg accgcttcac cgtggtctac cgcaatggca gcacggagca cgccagcccc      180
gcccgcgcga tccaggcgct gtcggcgggc gccggcaagg cgagctttc cgacgcggga      240
acggggcgct cgcccaatac ccttcgcgcc ggcggccgcg cgctgggcct gaactacaag      300
cgcaagctcg ccagcggcgg cgacctggtc accacctcgc gccgcctgag cgcgtccgag      360
gcccgcaggt tcgtgcagca gatcgcggcc gatccggccg tcgagttcgt gcagccggac      420
tacctgcgcc acgcgtggg caagccggtc aaggtgcagc ccgagggcgc ggccaccttc      480
accacgccga atgaccagta ctacgccggc tatcagtggg attacctgcc cgccgacggc      540
gcagccttca acgacaacag cctgggcaag gccgtggcca actggggcgg cgccaacatc      600
cagaaggcat ggagcctggc cgacggcacc ggcacgtcga tcgccagcct cgataccggc      660
gtgaccaacc atccgacct ggacctgacc ctggccgacg ccggctacga cttcatcagg      720
accgcgctgg tgctggggcg ctccaccgac ggcgcggctg cgggcgggcg ggatctgggc      780
gactggacca ccggcagcaa gtacctggcc agcaacggcg gctgcgtgga ctccaccat      840

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ccggccgagg	acagcagctg	gcacggcact	catgtgttcg	gcaccgccgg	cggcgagaag	900
accaacaaca	gcaccggcat	ggtcgggtacc	gccttcggcg	ccaagggtgct	gccgggtccgc	960
gtgctgggcc	actgcggcgg	ctacgacagc	gacatcgccg	acgccatcac	ctgggcttcc	1020
ggcgggccacg	tggacggcgt	gccggacaac	acccatccgg	cgcaggtgat	cagcatgagc	1080
ctgggcgggca	gcggcacctg	cacctccagc	acggtgaccg	gtcgcgccat	cagtggcgcg	1140
atcagcccg	gcgcgaccgt	ggtcgtggcg	gccggcaaca	gcaacgcca	cgtgtccaac	1200
ttctcgccgg	ccagctgccc	cggcgtgatc	gcggtcgcgg	ccaccggcat	caccagccgc	1260
cgcgcgtact	actccaacta	cggcaagggc	atcaccttgg	ccgcgccggg	cggcggtcgtg	1320
tacgccaacg	acggctccag	cggttcgcag	gcgaccaccg	gcttcacatc	gtcgaccatc	1380
gactcgggca	ccaccacgcc	ggccgggttcc	acctacggcg	gcatggcggg	tacctcgag	1440
gccacgccc	acgtggccgg	cgcggtggcg	ctgatgcaga	gctaccgcct	ggcgctgggc	1500
aagtcgctgc	tgagctccgc	gcaggtgacg	tcgctgctga	agtccacggc	caccgtgccc	1560
cacgtggccg	ccagcggcag	caagccgatc	ggcgcgggca	tcctcaacgc	ctacgcccg	1620
gtgcaggccg	cgggcgcgca	gccctga				1647

<210> 24
 <211> 548
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(23)

<400> 24

Met	Asn	Arg	Ser	Gln	Val	Lys	Leu	Leu	Ala	Ala	Ser	Leu	Leu	Leu	Ala
1				5					10					15	
Leu	Ser	Leu	Pro	Ala	Ala	Ala	Glu	Asp	Ile	Ser	Gly	Asn	Thr	Arg	Phe
			20					25					30		
Asp	Leu	Ser	Ser	Val	Gln	Glu	Gly	Ala	Thr	Tyr	Asp	Arg	Phe	Ile	Val
		35					40					45			
Val	Tyr	Arg	Asn	Gly	Ser	Thr	Glu	His	Ala	Ser	Pro	Ala	Ala	Ala	Ile
	50					55					60				
Gln	Ala	Leu	Ser	Ala	Ala	Ala	Gly	Lys	Ala	Gln	Leu	Ser	Asp	Ala	Gly
65				70						75				80	
Thr	Gly	Ala	Ser	Pro	Asn	Thr	Leu	Arg	Ala	Gly	Gly	Arg	Ala	Leu	Gly
			85						90					95	
Leu	Asn	Tyr	Lys	Arg	Lys	Leu	Ala	Ser	Gly	Gly	Asp	Leu	Val	Thr	Thr
			100					105					110		
Ser	Arg	Arg	Leu	Ser	Ala	Ser	Glu	Ala	Arg	Gln	Phe	Val	Gln	Gln	Ile
		115					120					125			
Ala	Ala	Asp	Pro	Ala	Val	Glu	Phe	Val	Gln	Pro	Asp	Tyr	Leu	Arg	His
	130					135					140				
Ala	Leu	Gly	Lys	Pro	Val	Lys	Val	Gln	Pro	Glu	Gly	Ala	Ala	Thr	Phe
145				150						155				160	
Thr	Thr	Pro	Asn	Asp	Gln	Tyr	Tyr	Ala	Gly	Tyr	Gln	Trp	Asp	Tyr	Leu
			165						170				175		
Pro	Ala	Asp	Gly	Ala	Ala	Phe	Asn	Asp	Asn	Ser	Leu	Gly	Lys	Ala	Val
			180					185					190		
Ala	Asn	Trp	Gly	Gly	Ala	Asn	Ile	Gln	Lys	Ala	Trp	Ser	Leu	Ala	Asp
		195					200					205			
Gly	Thr	Gly	Ile	Val	Ile	Ala	Ser	Leu	Asp	Thr	Gly	Val	Thr	Asn	His
	210					215					220				
Pro	Asp	Leu	Asp	Leu	Thr	Leu	Ala	Asp	Ala	Gly	Tyr	Asp	Phe	Ile	Ser
225					230					235				240	
Thr	Ala	Leu	Val	Ser	Gly	Arg	Ser	Thr	Asp	Gly	Arg	Ala	Ser	Gly	Gly
			245						250					255	
Trp	Asp	Leu	Gly	Asp	Trp	Thr	Thr	Gly	Ser	Lys	Tyr	Leu	Ala	Ser	Asn
			260					265					270		
Gly	Gly	Cys	Val	Asp	Ser	Thr	His	Pro	Ala	Glu	Asp	Ser	Ser	Trp	His
		275					280					285			
Gly	Thr	His	Val	Phe	Gly	Thr	Ala	Gly	Gly	Glu	Lys	Thr	Asn	Asn	Ser
	290					295					300				
Thr	Gly	Met	Val	Gly	Thr	Ala	Phe	Gly	Ala	Lys	Val	Leu	Pro	Val	Arg
305					310					315					320
Val	Leu	Gly	His	Cys	Gly	Gly	Tyr	Asp	Ser	Asp	Ile	Ala	Asp	Ala	Ile

10336256.txt

```

      325      330      335
Thr Trp Ala Ser Gly Gly His Val Asp Gly Val Pro Asp Asn Thr His
      340      345      350
Pro Ala Gln Val Ile Ser Met Ser Leu Gly Gly Ser Gly Thr Cys Thr
      355      360      365
Ser Ser Thr Val Thr Gly Arg Ala Ile Ser Gly Ala Ile Ser Arg Gly
      370      375      380
Ala Thr Val Val Val Ala Ala Gly Asn Ser Asn Ala Asn Val Ser Asn
      385      390      395
Phe Ser Pro Ala Ser Cys Pro Gly Val Ile Ala Val Ala Ala Thr Gly
      400      405      410
Ile Thr Ser Arg Arg Ala Tyr Tyr Ser Asn Tyr Gly Lys Gly Ile Thr
      415      420      425
Leu Ala Ala Pro Gly Gly Gly Val Tyr Ala Asn Asp Gly Ser Ser Gly
      430      435      440
Ser Gln Ala Thr Thr Gly Phe Ile Trp Ser Thr Ile Asp Ser Gly Thr
      445      450      455
Thr Thr Pro Ala Gly Ser Thr Tyr Gly Gly Met Ala Gly Thr Ser Gln
      460      465      470
Ala Thr Pro His Val Ala Gly Ala Val Ala Leu Met Gln Ser Tyr Arg
      475      480      485
Leu Ala Leu Gly Lys Ser Leu Leu Ser Ser Ala Gln Val Thr Ser Leu
      490      495      500
Leu Lys Ser Thr Ala Thr Val Pro His Val Ala Ala Ser Gly Ser Lys
      505      510      515
Pro Ile Gly Ala Gly Ile Leu Asn Ala Tyr Ala Ala Val Gln Ala Ala
      520      525      530
Gly Ala Gln Pro
      535      540      545

```

<210> 25
 <211> 1323
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 25

atgagcagca	tcgcagtgtc	tccagcgccc	cagccgacag	gcaatatgct	ggttatgttc	60
catccggacc	ggaagcccag	ggatgtcgag	cggctggtgt	ccaatgtcgt	cggcgcggaag	120
gtcgtgcatt	cgcgcgattt	ccgggcccgat	acgcccgggca	tcgccgaagc	cttcgcggat	180
gccggtgcgc	tcaaccttga	ccgggtcggc	atcgcggtcg	tgaaggcgcc	ggaggacgac	240
ggcttctcgg	tgcccgccga	gacgcttcgc	aaccgcaagg	aggctcgtcga	ggtgctccg	300
gagttctgga	tgcacatgct	ggccgggttg	gacgatcgct	acgccgcctg	ggtgcgcgac	360
ggcctctccc	tgctggccga	ccaggcgctg	cgcggcgtcc	tgccgccgcc	tcccggcggc	420
atcgcgggcg	gaccgggcgt	tgcggtcgcc	tcccagctct	ctgcgacctg	ggggcttgcc	480
gccaccggcg	tcgatcgctc	gtcctatacg	ggcgctcgga	tcaaggctcg	ggtgctggac	540
accgggttcg	acttcaccca	tcccgacttc	gccgggcgca	cgctcgtgtc	aaaaagcttc	600
gtgccgggcg	aggacgtcca	ggatgtgcag	ggccacggca	cccatgtcat	cggcacggcc	660
tgccggccgc	tgctcgccgc	cgaacaggct	cgctacggcg	tcgcctacga	agccgagatc	720
tatgcgggca	aggttttgga	caacaacggc	tccggcgccg	aacgctgggt	gctcgccggc	780
atggaatggg	cgatcgagca	gaagtgcgag	gtcatatcca	tgctcgtcgg	ccgcgcgctg	840
cagccgggtg	aggcgccgga	cgattcttat	gagcgcgcg	gcgaatacgc	gctcgagaac	900
ggctcgtgta	tcatcgcggc	ggccggcaat	aacagctggc	ggcaatacaa	cgacatcaag	960
ccggtcggct	cgccggccaa	tgccccctcg	atcatggcg	tgccggcggt	cgacgccaag	1020
atgaaggctc	cgaacttctc	ctgcggcggc	gtcaatccgg	caggcggtga	ggtcaacatc	1080
gccgggcctg	gctgtcctcc	gtgccgatgc	cgcgcaaata	tgaccgcttc	tgaccgcttc	1140
tccggcacct	cgatggcgac	gccgcatgtc	gccggcatcg	ccgccctcct	cgccagtcg	1200
gacaagagcc	tgcgcgccaa	ggcgctgtgg	acggcgctgg	aacaaggcgc	gcgcaatatc	1260
gggcatcccc	cgcgcgacgt	gggcgcgggg	ctcgtgatgg	cgccgggaag	cgcctgtcga	1320
tag						1323

<210> 26
 <211> 440
 <212> PRT
 <213> Unknown

10336256.txt

<220>

<223> obtained from an environmental sample.

<400> 26

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Met Ser Ser Ile Ala Val Ser Pro Ala Pro Gln Pro Thr Gly Asn Met
 1      5      10      15
Leu Val Met Phe His Pro Asp Arg Lys Pro Arg Asp Val Glu Arg Leu
 20      25      30
Val Ser Asn Val Val Gly Ala Lys Val Val His Ser Arg Asp Phe Arg
 35      40      45
Ala Asp Thr Pro Gly Ile Ala Glu Ala Phe Ala Asp Ala Gly Ala Leu
 50      55      60
Asn Leu Asp Arg Leu Gly Ile Ala Val Val Lys Ala Pro Glu Asp Asp
 65      70      75      80
Gly Phe Ser Val Ala Ala Glu Thr Leu Arg Asn Arg Lys Glu Val Val
 85      90      95
Glu Val Arg Pro Glu Phe Trp Met His Met Leu Ala Gly Trp Asp Asp
 100      105      110
Arg Tyr Ala Ala Trp Val Arg Asp Gly Leu Ser Leu Leu Ala Asp Gln
 115      120      125
Ala Leu Arg Gly Val Leu Pro Pro Pro Gly Gly Ile Ala Ala Gly
 130      135      140
Pro Gly Val Ala Val Ala Ser Gln Leu Ser Ala Thr Trp Gly Leu Ala
 145      150      155      160
Ala Thr Gly Val Asp Arg Ser Ser Tyr Thr Gly Val Gly Ile Lys Val
 165      170      175
Ala Val Leu Asp Thr Gly Phe Asp Phe Thr His Pro Asp Phe Ala Gly
 180      185      190
Arg Ser Val Val Ser Lys Ser Phe Val Pro Gly Glu Asp Val Gln Asp
 195      200      205
Val Gln Gly His Gly Thr His Cys Ile Gly Thr Ala Cys Gly Pro Leu
 210      215      220
Ser Pro Ala Glu Gln Val Arg Tyr Gly Val Ala Tyr Glu Ala Glu Ile
 225      230      235      240
Tyr Ala Gly Lys Val Leu Gly Asn Asn Gly Ser Gly Ala Glu Arg Trp
 245      250      255
Val Leu Ala Gly Met Glu Trp Ala Ile Glu Gln Lys Cys Glu Val Ile
 260      265      270
Ser Met Ser Leu Gly Arg Ala Val Gln Pro Gly Glu Ala Pro Asp Ala
 275      280      285
Phe Tyr Glu Arg Ala Gly Glu Tyr Ala Leu Glu Asn Gly Ser Leu Ile
 290      295      300
Ile Ala Ala Ala Gly Asn Asn Ser Trp Arg Gln Tyr Asn Asp Ile Lys
 305      310      315      320
Pro Val Gly Ser Pro Ala Asn Ala Pro Ser Ile Met Ala Val Ala Ala
 325      330      335
Val Asp Ala Lys Met Lys Val Ala Asn Phe Ser Cys Gly Gly Val Asn
 340      345      350
Pro Ala Gly Gly Glu Val Asn Ile Ala Gly Pro Gly Val Asp Val Leu
 355      360      365
Ser Ser Val Pro Met Pro Arg Lys Tyr Asp Arg Phe Ser Gly Thr Ser
 370      375      380
Met Ala Thr Pro His Val Ala Gly Ile Ala Ala Leu Leu Ala Gln Ser
 385      390      395      400
Asp Lys Ser Leu Arg Gly Lys Ala Leu Trp Thr Ala Leu Glu Gln Gly
 405      410      415
Ala Arg Asn Ile Gly His Pro Ala Arg Asp Val Gly Ala Gly Leu Val
 420      425      430
Met Ala Pro Gly Ser Ala Cys Arg
 435      440

```

<210> 27

<211> 1893

<212> DNA

<213> Unknown

<220>

<223> obtained from an environmental sample.

10336256.txt

```

<400> 27
gtgatcaaga agcagaacct tcgcatcaat gtgttggcag ccgccgtgct gtcgctgacc 60
gggtgtggcc tggcacaggc cgccgacctg aaagcaaagt cgccgttgct cggcccgaag 120
acgcagcagg tggatggcat catcgtgaaa taccgcgctg gcagcggcgc agctgccgat 180
gcgaacgcca agctggccgt ggtcaactcg gccatcgccc gcgccgtgcc ggcagggtacc 240
aacgcggctg cgcgcagtgc cgcgctgcgc ccgcagggtg cccgcaagct gggcatcggt 300
gccgatctga tccgcctgca gggaggggac gcgcgcgccc aactggacaa ggtgctgggc 360
gaactgaagg ctgacccgac cgtcgaatat gcggtggccc acgccatcat gtatccgatc 420
gatgtgcgt cgtcgccgcg tgcggacgcc gtcgcgaagt ccgatgcgtc gccagcttc 480
gtgcccaacg atccgtacta ccagagccac aactggcact tccacaaccc ggtcgggtggc 540
gtgaacgcac cggccgcagt ggacgtctcg caggggcgagg gcatcggtgt ggccgtgctc 600
gataccggga tcctgcccgga gcacccggat ttcgcccgcg gcaccctgct ggagggtac 660
gacttcattca gccaggccag ccgctcgctg cgtgcccgcg atggccgcgt gccgggtgca 720
ctcgactacg gtgactggat gccaccgcgc aatgcctgct acgacggttc gccggtacgt 780
gacagcagct ggcacggtag ccatgtgacc ggcaccatcg ccgaggccac caacaacggc 840
ctgcataacc cgggcctggc ctacaaggcc aaggtgttgc cggtgccgct gctcggctac 900
tgcggtggca ccctgtcgga catcacccgac gccatcacct gggcctcggg cggtgccgtg 960
gccggcatcc ctgccaacca gaatccggcc gagatcatca acatgagcct gggcggctcc 1020
ggcagctgcg atccggccta ccaggcggcc atcaccggtg ccaccaaccg cggtagccctg 1080
gtggtgtgtg cagccggcaa cgactcgatg aatgtggcca acgcccgcgc ggccaactgc 1140
gatggcgtgg tctcggtcgg cgcgaccgac atcaccggcg ccatggccta ctactccaac 1200
ttcggtagcc gcatcgatct gtccggcccg ggcgggtggc tcaccgacgg caatccgaac 1260
ggctatgtct ggcaggcggg gtccagcagc aagacgtcgc cgccggcagc cggttccacc 1320
gaggggtaca cccttggcgg caaggccggc acgtcgatgg cggcaccgca tgtggctgcc 1380
gtcgcgcgcg tggtcagag cgcgctgatc gccgccaacc gcgaccgcgt cgcgcccggc 1440
ggcatgcgta ccctgctgaa ggaaacggca cgtccgttcc cggtcagcat tccgtccgac 1500
accccgatcg gtaccggcat cgtcgatgcc aaggccgcgc tggacaaggc cctggaagag 1560
ccatgcaccg agaactgcgg gccggtggcc aagccgctga ccaacaaggg ggccatcggc 1620
gggttgagtg gtgccgcggc cagcagcgct ctttacagct tcgaagccgc ggcaggcaag 1680
cagctcagcg tcatcaccta tgggtggcacc ggcaacgtgt cgggtctacct ggccaagggc 1740
cgcgagccga gtgccaccga caacgatgcg cgctcgaccc gtccgggcac ctcggaacgc 1800
gtcggggtga cggcaccgac tgccggcacc tactacatca aggtggtggg cgaggcggct 1860
tacagcgggtg tgagcattct cgccacgcag taa 1893

```

```

<210> 28
<211> 630
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample.

```

```

<221> SIGNAL
<222> (1)...(27)

```

```

<400> 28
Met Ile Lys Lys Gln Asn Leu Arg Ile Asn Val Leu Ala Ala Ala Val
1      5      10      15
Leu Ser Leu Thr Gly Val Gly Leu Ala Gln Ala Ala Asp Leu Lys Ala
20     25     30
Asn Ala Pro Leu Ser Gly Pro Lys Thr Gln Gln Val Asp Gly Ile Ile
35     40     45
Val Lys Tyr Arg Ala Gly Ser Ala Ala Ala Ala Asp Ala Asn Ala Lys
50     55     60
Leu Ala Val Val Asn Ser Ala Ile Ala Arg Ala Val Pro Ala Gly Thr
65     70     75     80
Asn Ala Ala Ala Arg Ser Ala Ala Leu Arg Pro Gln Val Ala Arg Lys
85     90     95
Leu Gly Ile Gly Ala Asp Leu Ile Arg Leu Gln Gly Gly Ile Ala Arg
100    105    110
Ala Glu Leu Asp Lys Val Leu Gly Glu Leu Lys Ala Asp Pro Thr Val
115    120    125
Glu Tyr Ala Val Ala Asp Ala Ile Met Tyr Pro Ile Asp Ala Ala Ser
130    135    140
Ser Pro Arg Ala Asp Ala Val Ala Lys Ser Asp Ala Ser Pro Ser Phe
145    150    155    160
Val Pro Asn Asp Pro Tyr Tyr Gln Ser His Asn Trp His Phe His Asn

```

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Pro	Val	Gly	Gly	Val	Asn	Ala	Pro	Ala	Ala	Trp	Asp	Val	Ser	Gln	Gly
Glu	Gly	Ile	Val	Val	Ala	Val	Leu	Asp	Thr	Gly	Ile	Leu	Pro	Glu	His
Pro	Asp	Phe	Ala	Ala	Gly	Thr	Leu	Leu	Glu	Gly	Tyr	Asp	Phe	Ile	Ser
Gln	Ala	Ser	Arg	Ser	Arg	Arg	Ala	Ala	Asp	Gly	Arg	Val	Pro	Gly	Ala
Leu	Asp	Tyr	Gly	Asp	Trp	Met	Pro	Thr	Ala	Asn	Ala	Cys	Tyr	Asp	Gly
Ser	Pro	Val	Arg	Asp	Ser	Ser	Trp	His	Gly	Thr	His	Val	Thr	Gly	Thr
Ile	Ala	Glu	Ala	Thr	Asn	Asn	Gly	Leu	His	Thr	Ala	Gly	Leu	Ala	Tyr
Lys	Ala	Lys	Val	Leu	Pro	Val	Arg	Val	Leu	Gly	Tyr	Cys	Gly	Gly	Thr
Leu	Ser	Asp	Ile	Thr	Asp	Ala	Ile	Thr	Trp	Ala	Ser	Gly	Gly	Ala	Val
Ala	Gly	Ile	Pro	Ala	Asn	Gln	Asn	Pro	Ala	Glu	Ile	Ile	Asn	Met	Ser
Leu	Gly	Gly	Ser	Gly	Ser	Cys	Asp	Pro	Ala	Tyr	Gln	Ala	Ala	Ile	Thr
Gly	Ala	Thr	Asn	Arg	Gly	Thr	Leu	Val	Val	Val	Ala	Ala	Gly	Asn	Asp
Ser	Met	Asn	Val	Ala	Asn	Ala	Arg	Pro	Ala	Asn	Cys	Asp	Gly	Val	Val
Ser	Val	Gly	Ala	Thr	Gly	Ile	Thr	Gly	Ala	Met	Ala	Tyr	Tyr	Ser	Asn
Phe	Gly	Thr	Arg	Ile	Asp	Leu	Ser	Gly	Pro	Gly	Gly	Gly	Val	Thr	Asp
Gly	Asn	Pro	Asn	Gly	Tyr	Val	Trp	Gln	Ala	Val	Ser	Ser	Ser	Lys	Thr
Ser	Pro	Pro	Ala	Ala	Gly	Ser	Thr	Glu	Gly	Tyr	Thr	Leu	Gly	Gly	Lys
Ala	Gly	Thr	Ser	Met	Ala	Ala	Pro	His	Val	Ala	Ala	Val	Ala	Ala	Leu
Val	Gln	Ser	Ala	Leu	Ile	Ala	Ala	Asn	Arg	Asp	Pro	Leu	Ala	Pro	Ala
Gly	Met	Arg	Thr	Leu	Lys	Glu	Thr	Ala	Arg	Pro	Phe	Pro	Val	Ser	
Ile	Pro	Ser	Ala	Thr	Pro	Ile	Gly	Thr	Gly	Ile	Val	Asp	Ala	Lys	Ala
Ala	Leu	Asp	Lys	Ala	Leu	Glu	Glu	Pro	Cys	Thr	Glu	Asn	Cys	Gly	Pro
Val	Ala	Lys	Pro	Leu	Thr	Asn	Lys	Val	Ala	Ile	Gly	Gly	Leu	Ser	Gly
Ala	Ala	Gly	Ser	Ser	Val	Leu	Tyr	Ser	Phe	Glu	Ala	Ala	Ala	Gly	Lys
Gln	Leu	Ser	Val	Ile	Thr	Tyr	Gly	Gly	Thr	Gly	Asn	Val	Ser	Val	Tyr
Leu	Ala	Lys	Gly	Arg	Glu	Pro	Ser	Ala	Thr	Asp	Asn	Asp	Ala	Arg	Ser
Thr	Arg	Pro	Gly	Thr	Ser	Glu	Thr	Val	Arg	Val	Thr	Ala	Pro	Thr	Ala
Gly	Thr	Tyr	Tyr	Ile	Lys	Val	Val	Gly	Glu	Ala	Ala	Tyr	Ser	Gly	Val
Ser	Ile	Leu	Ala	Thr	Gln										

<210> 29
 <211> 1506
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

10336256.txt

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<400> 29
atgCGTACgt cgcttcgggt ttcccttgcc agtgccatca ccctgggtcct ggccagcgcc 60
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tacagcagtt tcatcgtcaa gtaccgggac ggacgcagca agcgcgtctc cgccgacacc 180
gcccaggacg cgctgaagaa ggcgcctcggc gcccagcagc gcagcaagcg ttcgatcggc 240
agtgcgcccgc cagcggccgc gtccgtgacc catcaacgcc gcatgggaggc cggcgccgac 300
gtgggtcacca cggacaagcc actggaccgt ccggaggccg agatcctgat gcagcgcatc 360
gccgacgatc cggacgtcga gtatgtgcag ccgaactaca tgatgagtgc attcgctacg 420
ccgaacgacc cgcgctacgg cgagcagtgg cactacagca atccgaccag tggcgcgcgc 480
ctgccaggcg catgggatcg ctctaccggc cagggtgtgg tgggtggccgt ggtcgattcg 540
ggctacctca acaacaacga cctgcaggcc aatctgttgc cgggttacga catgatctcg 600
tcaacccgtc cgttcagtga ctggcagtgc atcatcgggg gcatgaatcc cggctgtggg 660
ggctccgacg atggtgacgg acgcgacgcc gatgcattcg atgcctcggg cattgcacac 720
ggcaccacac tcgcccgaac ggtcgctgcg gtgaccaaca accagatcgg cgtggccggc 780
gtggcctaca acgcaaaagt cgtaccgggtg cgcgtactgg gaaaccaggg caatgggtggc 840
tccgcccgata tcatcgacgg catgctctgg agtgccggta tcaacgtgcc caacgtcccg 900
gccaatgcc aacccggccga ggtcatcaat ctgagcctgg gtggccgccc cgcctgctcg 960
ccggccgagc aggatgcaat cgacgacatc acggcccagg gcacgatcgt ggtgggtcgcc 1020
gccggcaaca gcaatcttga tgtgtccgag ttcgccccgg cgaactgcaa gggcgatgc 1080
gcggttgctg ccaacgatca gggcggtcgt cgcgcgttct actccaacta tgggtgcaggc 1140
atccacatca ccgcaccggg tggcgagacc tggctcgtgcc gtgcgtcggg ggggtgagttc 1200
ctgccgctgg ccacgcccgc gagccaggcc aactgcgcac ccacccgcca gcatccggcg 1260
cagggcattcc tgtccaccgt gggtaaacaac gccttcgact tcatgtccgg cacctcgatg 1320
gcggcgcccc acgtcgtcgg catcgtcgcg ctgatgcagg cgggtggcgcc ggtgccgaag 1380
accaccgacc aggtcaagga catcctgcgt cgaaccgcgc acccgatcgc agcggcgaac 1440
tggccggcg gttgcggacc gggcattgtc gacgctgcag aagcggtgaa ggccgccagc 1500
aactga 1506

```

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<210> 30
<211> 501
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample.

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<221> SIGNAL
<222> (1)...(24)

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<400> 30
Met Arg Thr Ser Leu Arg Val Ser Leu Ala Ser Ala Ile Thr Leu Val
1 5 10 15
Leu Ala Ser Ala Pro Ala Phe Ala Gln Pro Thr Glu Arg Val Trp Thr
20 25 30
Arg Gly Met Ala Ser Asn Glu Gln Tyr Ser Ser Phe Ile Val Lys Tyr
35 40 45
Arg Asp Gly Ser Ser Lys Arg Val Ser Ala Asp Thr Ala Gln Asp Ala
50 55 60
Leu Lys Lys Arg Leu Gly Ala Gln Gln Arg Ser Lys Arg Ser Ile Gly
65 70 75 80
Ser Ala Pro Pro Ala Ala Ala Ser Val Thr His Gln Arg Arg Met Gly
85 90 95
Gly Gly Ala Asp Val Val Thr Thr Asp Lys Pro Leu Asp Arg Pro Glu
100 105 110
Ala Glu Ile Leu Met Gln Arg Ile Ala Asp Asp Pro Asp Val Glu Tyr
115 120 125
Val Gln Pro Asn Tyr Met Met Ser Ala Phe Ala Thr Pro Asn Asp Pro
130 135 140
Arg Tyr Gly Glu Gln Trp His Tyr Ser Asn Pro Thr Ser Gly Ala Arg
145 150 155 160
Leu Pro Gly Ala Trp Asp Arg Ser Thr Gly Gln Gly Val Val Val Ala
165 170 175
Val Val Asp Ser Gly Tyr Leu Asn Asn Asn Asp Leu Gln Ala Asn Leu
180 185 190
Leu Pro Gly Tyr Asp Met Ile Ser Ser Thr Arg Pro Phe Ser Asp Trp
195 200 205
Gln Cys Ile Ile Gly Gly Met Asn Pro Gly Cys Gly Gly Ser Asp Asp
210 215 220

```

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Gly Asp Gly Arg Asp Ala Asp Ala Phe Asp Ala Ser Gly Ile Ala His
 225 230 235 240
 Gly Thr His Val Ala Gly Thr Val Ala Val Thr Asn Asn Gln Ile
 245 250 255
 Gly Val Ala Gly Val Ala Tyr Asn Ala Lys Val Val Pro Val Arg Val
 260 265 270
 Leu Gly Asn Gln Gly Asn Gly Gly Ser Ala Asp Ile Ile Asp Gly Met
 275 280 285
 Leu Trp Ser Ala Gly Ile Asn Val Pro Asn Val Pro Ala Asn Ala Asn
 290 295 300
 Pro Ala Glu Val Ile Asn Leu Ser Leu Gly Gly Arg Arg Ala Cys Ser
 305 310 315 320
 Pro Ala Glu Gln Asp Ala Ile Asp Asp Ile Thr Ala Gln Gly Thr Ile
 325 330 335
 Val Val Val Ala Ala Gly Asn Ser Asn Leu Asp Val Ser Glu Phe Ala
 340 345 350
 Pro Ala Asn Cys Lys Gly Val Ile Ala Val Ala Ala Asn Asp Gln Gly
 355 360 365
 Gly Arg Arg Ala Phe Tyr Ser Asn Tyr Gly Ala Gly Ile His Ile Thr
 370 375 380
 Ala Pro Gly Gly Glu Thr Trp Ser Cys Arg Ala Ser Val Gly Glu Phe
 385 390 395 400
 Leu Pro Leu Ala Thr Pro Pro Ser Gln Ala Asn Cys Ala Pro Thr Arg
 405 410 415
 Gln His Pro Ala Gln Gly Ile Leu Ser Thr Val Gly Asn Asn Ala Phe
 420 425 430
 Asp Phe Met Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Gly Ile
 435 440 445
 Val Ala Leu Met Gln Ala Val Ala Pro Val Pro Lys Thr Thr Asp Gln
 450 455 460
 Val Lys Asp Ile Leu Arg Arg Thr Ala His Pro Ile Ala Ala Ala Asn
 465 470 475 480
 Cys Pro Gly Gly Cys Gly Pro Gly Ile Val Asp Ala Ala Glu Ala Val
 485 490 495
 Lys Ala Ala Ser Asn
 500

<210> 31
 <211> 1929
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 31
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 gccagcctcg gcgatcagca gatcttccgc cgcttcgtcg tgcagtaccg cgacggcacg 180
 cgcgagaaga ccgaccgcaa tgccggcgctc gccacgttca gccgcgcgtt gtcgcgctcg 240
 ggcctgtcga agagccgcg gcgcgacgcc aagcacgtgc gtacgctcgc caacggccac 300
 cagctgtcga agctctcgc cgccctcgat cgcgcggaag ccgaggccct gctgcgccag 360
 ctcaaggccg acccgaacgt ggtctcggtg cgccccgatc gcctgcgcca gatcgcgcgc 420
 ctgccaacg tgcagccggc ctacgtgccc aacgatccgc tgttccagga ataccagtgg 480
 cacatgcgtg cgccggacgg cggcgcgacc ttcgacggcg gcccccaacc cggcggcatc 540
 aacgcgcccg cgccctggga cctcgccgac ggcaacggca tcaccatcgc cgtgctcgac 600
 accggcatca cgcgcgcatc tgacgtcgat accctgatgg ccgatgccgg ctacgacttc 660
 atcagcgacg ccttcgtctc cggcgcgac accgacgacc gcgtgcccgg cggctgggac 720
 ctgggcgact ggaccatcgg ctatccgggc gcggaaacct gcatccagcg ctacagctcc 780
 tggcacggcg cccacgtcgc cggcaccgcc ggcgcgagc tgacggacaa cggcgtaggc 840
 ctgaccggcg tcgcctacaa cgccaacgtc gtgcccgtcc gcgtgctcgg ccactgcggc 900
 ggctacgaca ccgacatcgc cgacgcgac gtctggggcg cggcgggcga ggtggaaggc 960
 atgccgtcga acgagaacct ggcgacgtg atcaacctga gcctggggcg ctcgggcgcc 1020
 tgcaccgact acgaggccga tgcgatcgcg caggccaacg ccctggggcg cgtggctcgtg 1080
 gtcgcccggc gcaaccagaa cgccaatacc tcgggctatt cgccgggcaa ctgcccgggc 1140
 gtgatcacgg tggcgtcgaa cggcgtcgac agccgcctcg cctactactc caactacggc 1200
 gacggcatcg agatcgccgc gcccgggcgc ggcgctcagc ccaacgacgg cagcggcgcc 1260
 gcgcagatct acgacggcct cgtctggcag gcggtcaacc ccagcgacac cgagccgatg 1320

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ccggccgacg	agatcgcgcc	cgacggctcc	aacggcggct	acggcggatc	ggccggtact	1380
tcgcaggcgg	cgccgcacgt	ggccggcggtg	atcgcgctga	tcgagggcgc	gcgcctggat	1440
gcgggcatgc	cgctgtcac	tccggaggag	gtgctggacg	tgctgcagtc	gacggtgacg	1500
ccgttcgcgg	tcgcgccctc	gacctcgcag	ccgatcggcc	cgggcatcgt	gaacgcggcc	1560
gccgccgtgg	ccaaggcgat	cgagccgccc	tcgagggtcg	actgcgcgcc	ggatgccacg	1620
ccgatcgtca	acggcgctcg	gctcaccggc	ctgaccggca	ccgcgggcag	cgaaacgctc	1680
tacagcatca	ccgtgccgga	gggcgcgcgc	ggtccgctca	gcatcagcac	caccggcggc	1740
agcggcgacg	tgaacctgct	ggtgagcttc	gaggccgagc	ccaccgacgc	ggacgcggac	1800
ttccgctcgg	cgcgccggg	caacaacgag	acggtgcgca	tcaacgcgcc	gcaggcaggc	1860
acctactaca	tcaagctggt	cggcgcccgc	gcctacagca	acgtgcgtct	gctggtccgt	1920
cacaactga						1929

<210> 32
 <211> 642
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(26)

<400> 32

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			20					25					30		
Ala	Thr	Asp	Thr	Ala	Ala	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Gln	Gln	Ile
		35					40					45			
Phe	Arg	Arg	Phe	Val	Val	Gln	Tyr	Arg	Asp	Gly	Thr	Arg	Glu	Lys	Thr
	50					55					60				
Asp	Arg	Asn	Ala	Gly	Val	Ala	Thr	Phe	Ser	Arg	Ala	Leu	Ser	Arg	Ser
	65				70					75					80
Gly	Leu	Ser	Lys	Ser	Arg	Ala	Ala	Asp	Ala	Lys	His	Val	Arg	Thr	Leu
				85					90					95	
Ala	Asn	Gly	His	Gln	Leu	Leu	Lys	Leu	Ser	Arg	Gly	Leu	Asp	Arg	Ala
			100					105					110		
Glu	Ala	Glu	Ala	Leu	Leu	Arg	Gln	Leu	Lys	Ala	Asp	Pro	Asn	Val	Val
		115					120					125			
Ser	Val	Arg	Pro	Asp	Arg	Leu	Arg	Gln	Ile	Ala	Arg	Leu	Pro	Asn	Val
	130					135					140				
Gln	Pro	Ala	Tyr	Val	Pro	Asn	Asp	Pro	Leu	Phe	Gln	Glu	Tyr	Gln	Trp
	145				150					155					160
His	Met	Arg	Ala	Pro	Asp	Gly	Gly	Ala	Thr	Phe	Asp	Gly	Gly	Pro	Asn
				165					170					175	
Arg	Gly	Gly	Ile	Asn	Ala	Pro	Ala	Ala	Trp	Asp	Leu	Ala	Asp	Gly	Asn
			180					185					190		
Gly	Ile	Thr	Ile	Ala	Val	Leu	Asp	Thr	Gly	Ile	Ser	Ala	His	Pro	Asp
		195					200					205			
Val	Asp	Thr	Ser	Met	Ala	Asp	Ala	Gly	Tyr	Asp	Phe	Ile	Ser	Asp	Ala
	210					215					220				
Phe	Val	Ser	Gly	Arg	Asp	Thr	Asp	Asp	Arg	Val	Pro	Gly	Gly	Trp	Asp
	225				230					235					240
Leu	Gly	Asp	Trp	Thr	Ile	Gly	Tyr	Pro	Gly	Ala	Glu	Thr	Cys	Ile	Gln
			245						250					255	
Arg	Tyr	Ser	Ser	Trp	His	Gly	Thr	His	Val	Ala	Gly	Thr	Ala	Gly	Ala
			260					265					270		
Gln	Leu	Thr	Asp	Asn	Gly	Val	Gly	Leu	Thr	Gly	Val	Ala	Tyr	Asn	Ala
		275					280					285			
Asn	Val	Val	Pro	Ile	Arg	Val	Leu	Gly	His	Cys	Gly	Gly	Tyr	Asp	Thr
	290					295					300				
Asp	Ile	Ala	Asp	Ala	Ile	Val	Trp	Ala	Ala	Gly	Gly	Glu	Val	Glu	Gly
	305				310					315					320
Met	Pro	Leu	Asn	Glu	Asn	Pro	Ala	His	Val	Ile	Asn	Leu	Ser	Leu	Gly
			325						330					335	
Gly	Ser	Gly	Ala	Cys	Thr	Asp	Tyr	Glu	Ala	Asp	Ala	Ile	Ala	Gln	Ala
			340					345					350		

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Asn	Ala	Leu	Gly	Ala	Val	Val	Val	Val	Ala	Ala	Gly	Asn	Gln	Asn	Ala
355		355					360					365			
Asn	Thr	Ser	Gly	Tyr	Ser	Pro	Gly	Asn	Cys	Pro	Gly	Val	Ile	Thr	Val
370						375					380				
Ala	Ser	Asn	Gly	Val	Thr	Ser	Arg	Arg	Ala	Tyr	Tyr	Ser	Asn	Tyr	Gly
385					390					395					400
Asp	Gly	Ile	Glu	Ile	Ala	Ala	Pro	Gly	Gly	Gly	Val	Tyr	Ala	Asn	Asp
			405						410					415	
Gly	Ser	Gly	Gly	Ala	Gln	Ile	Tyr	Asp	Gly	Phe	Val	Trp	Gln	Ala	Val
			420					425					430		
Asn	Pro	Ser	Asp	Thr	Glu	Pro	Met	Pro	Ala	Asp	Glu	Ile	Ala	Pro	Asp
		435					440					445			
Gly	Ser	Asn	Gly	Gly	Tyr	Gly	Gly	Ser	Ala	Gly	Thr	Ser	Gln	Ala	Ala
450						455					460				
Pro	His	Val	Ala	Gly	Val	Ile	Ala	Leu	Met	Gln	Gly	Ala	Arg	Leu	Asp
465					470					475					480
Ala	Gly	Met	Pro	Leu	Leu	Thr	Pro	Glu	Glu	Val	Leu	Asp	Val	Leu	Gln
				485					490					495	
Ser	Thr	Val	Thr	Pro	Phe	Ala	Val	Ala	Pro	Ser	Thr	Ser	Gln	Pro	Ile
			500					505					510		
Gly	Pro	Gly	Ile	Val	Asn	Ala	Ala	Ala	Val	Ala	Lys	Ala	Ile	Glu	
		515					520				525				
Pro	Pro	Cys	Glu	Val	Asp	Cys	Ala	Pro	Asp	Ala	Thr	Pro	Ile	Val	Asn
530						535					540				
Gly	Val	Ala	Leu	Thr	Gly	Leu	Thr	Gly	Thr	Ala	Gly	Ser	Glu	Thr	Leu
545					550					555					560
Tyr	Ser	Ile	Thr	Val	Pro	Glu	Gly	Ala	Arg	Gly	Pro	Leu	Ser	Ile	Ser
				565					570					575	
Thr	Thr	Gly	Gly	Ser	Gly	Asp	Val	Asn	Leu	Leu	Val	Ser	Phe	Glu	Ala
			580					585					590		
Glu	Pro	Thr	Asp	Ala	Asp	Ala	Asp	Phe	Arg	Ser	Ala	Arg	Pro	Gly	Asn
		595					600					605			
Asn	Glu	Thr	Val	Arg	Ile	Asn	Ala	Pro	Gln	Ala	Gly	Thr	Tyr	Tyr	Ile
610						615					620				
Lys	Leu	Val	Gly	Ala	Arg	Ala	Tyr	Ser	Asn	Val	Arg	Leu	Leu	Val	Arg
625					630					635					640
His	Asn														

<210> 33
 <211> 981
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 33

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tttgggtccct	ctggcgggccc	gcgccccgac	gacatcgtcc	agggcccgat	cggcgactgc	180
tacttcctcg	cggcgctcgc	ctccttcgcg	cagcagcagc	cccagctgat	ccgcaacgcg	240
atcgcttctg	atgccaacac	cgaaaacttc	aacgtgacgc	tgacacaagga	tgcgcaaccc	300
tggaatccgt	tcaatcgcca	cgagaagggtg	accgtccggg	tcacgcagca	ggaaatcgac	360
agccatgtca	tgaacgacaa	gggcgcccag	ctgggcaacg	acggcgcgcg	gtggccgggtg	420
gtcatggaga	tcgcgcgcgc	caagatgctc	gacagcaatc	cgaagaacgg	cttggacgaa	480
ggctacaatg	cactcgagca	tcagacgcgg	ttcggcttgc	ttcagggcgg	catgccgtca	540
tcggccatgg	agaccatctc	cggccaaccc	ggcgacacgg	catacacgac	gccgctcggc	600
atcttcggag	acgcgacgca	aggacccttg	cagccgtggc	tctcgctcgt	ctcgcccggg	660
caggcggttag	cgccggaggc	ggcaaaccat	cactatagcc	aggtcaaagc	cgcgctggag	720
gacggacggc	ccgtgacgct	gggtaccggc	ttgtccagcc	cgcaggacgg	cctcgttcgc	780
gggcacgcct	atcagggtcga	ggatatccag	cgcaacgccg	acggcagcgt	taacgtcacg	840
gttcgcaatc	catggggaac	caatcagggt	gtcggcgaag	gcaccaatcc	ggccgaccgc	900
cgtgtcacca	tcaggatggg	agccgcgggc	ctgtcgctgt	tcgcaatcgg	ttcaagcgcg	960
caggagacca	gcgccggata	g				981

<210> 34
 <211> 326

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<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 34

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Met Ile Pro Pro Ile Gly Gly Lys Ser Asp Pro Ile Asp Thr Ser Ser
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20
Gln Gln Tyr Asn Ala Ser Gly Leu Phe Gly Pro Ser Gly Gly Pro Arg
35      40      45
Pro Asp Asp Ile Val Gln Gly Pro Ile Gly Asp Cys Tyr Phe Leu Ala
50      55      60
Ala Leu Ala Ser Phe Ala Gln Gln Gln Pro Gln Leu Ile Arg Asn Ala
65      70      75      80
Ile Ala Phe Asp Ala Asn Thr Gly Asn Phe Asn Val Thr Leu His Lys
85      90      95
Asp Ala Gln Pro Trp Asn Pro Phe Asn Arg His Glu Lys Val Thr Val
100      105      110
Arg Val Thr Gln Gln Glu Ile Asp Ser His Val Met Asn Asp Lys Gly
115      120      125
Ala Arg Leu Gly Asn Asp Gly Ala Arg Trp Pro Val Val Met Glu Ile
130      135      140
Ala Arg Ala Lys Met Leu Asp Ser Asn Pro Lys Asn Gly Leu Asp Glu
145      150      155      160
Gly Tyr Asn Ala Leu Glu His Gln Thr Pro Phe Gly Leu Leu Gln Gly
165      170      175
Gly Met Pro Ser Ala Met Glu Thr Ile Ser Gly Gln Pro Gly Asp
180      185      190
Thr Ala Tyr Thr Thr Pro Leu Gly Ile Phe Gly Asp Ala Thr Gln Gly
195      200      205
Pro Leu Gln Pro Trp Leu Ser Leu Val Ser Pro Gly Gln Ala Leu Ala
210      215      220
Pro Glu Ala Ala Asn His Tyr Ser Gln Val Lys Ala Ala Leu Glu
225      230      235      240
Asp Gly Arg Pro Val Thr Leu Gly Thr Gly Leu Ser Ser Pro Gln Asp
245      250      255
Gly Leu Val Arg Gly His Ala Tyr Gln Val Glu Asp Ile Gln Arg Asn
260      265      270
Ala Asp Gly Ser Val Asn Val Thr Val Arg Asn Pro Trp Gly Thr Asn
275      280      285
Gln Gly Val Gly Glu Gly Thr Asn Pro Ala Asp Pro Arg Val Thr Ile
290      295      300
Arg Met Gly Ala Ala Gly Leu Ser Leu Phe Ala Ile Gly Ser Ser Ala
305      310      315      320
Gln Glu Thr Ser Ala Gly
325

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<210> 35

<211> 1854

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 35

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gccgtcgggtg ccgtccacgc cgcggggttg ccgaccggtg aaccggtgct ccaggccagc 120
accgccgagc cgggcaccca gcgcatcatc gtcaagtacc gtgccggcac cgctgcggcg 180
ggcgaccggt cggccaagct gtccaccgtg cagtccgcgc tgaccgcgcg cagcctgtcc 240
ggtggcacta cccgcgccag cgcgctcggc ccgcaggctc tgcgcaggct gggcgctcgg 300
gccgacctga tccgcctgca ggggcgccctg gcgcctgccg aactgcagcg cgtgctgaag 360
gaactgaagg ccgatccgct cgtgcagtag gccgaggccg atgtgaagct gcgccgtacc 420
gagctgcgtg ccggtgacgt gcagccggcg ctggcgccga atgatcccta ctaccagcag 480
taccagtggc acctgcacaa cgccaccggc ggcacacacg caccgtcggc gtgggatgta 540

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tcgcagggcg	aaggcgtggt	ggtggcggta	ctcgacaccg	gcatcctgcc	gcagcacccg	600
gacctgggtcg	gcaacctgct	ggaaggctac	gacttcatca	gcgatgccga	gacgtcgcgc	660
cgtgccacca	acgaccgcgt	gccggggcgcg	caggactatg	gtgactgggt	cgagaacgac	720
aacgagtgtct	acaccggctc	cgtcgccgag	gacagctcct	ggcacgggtac	ccatgtggcc	780
ggtaccgtgg	ccgagcagac	caacaacggg	gtcggcatgg	ccggtgtcgc	gcacaaggcc	840
aaggtgtctgc	cgggtccgcgt	gctcggcaag	tgcggtggct	acctttccga	tatagccgac	900
gccatcacct	gggcctcccg	cggcacgggtg	gccggcggtac	ccgccaatgc	caaccgggcc	960
gaagtcatca	acatgagcct	cggcggcagc	ggcagctgcg	acgggacctta	ccaggaagcg	1020
atcaatggcg	cgatctcgcg	tggcaccacg	gtggctcgtg	cggccggcaa	cgagaccgac	1080
aacgcctcca	aataccgtcc	agccagttgc	gacggcgtgg	tgaccgtcgg	cgccaccgcg	1140
attaccggcg	gcatcaccta	ctactccaac	tacggcaccc	gcgtggacct	gtccgggtccg	1200
ggtggtgggtg	gcagcgtcga	tggcaatccc	ggcggctacg	tctggcagtc	cggttccgat	1260
gcggccacca	cgcgggagtc	gggcagctac	agctacatgg	gcatgggcgg	cacgtcgtatg	1320
gcctcgccgc	acgtgggtgc	cgtcgctgca	ctggtgcaga	gcgcgctgat	gcgcaagggc	1380
aaggatccgc	tggcccccgc	cgcgatgcgc	accctgctga	aggaaaccgc	gcgtccgttc	1440
ccggtcagca	tcccgaaccg	cactccgatc	ggcaccggca	tcgtcgatgc	caaggcggcg	1500
ctggccaagg	cgctggaaga	gccgtgcacc	gagaactgtg	gaccgggtgg	gacgccgctg	1560
accaacaagg	ccgccgtggg	ggggctgaac	ggcacggccg	gcagcagccg	cctgtacagc	1620
ttcgaggcag	ccgctggcaa	gcagctcagc	gtgatcacct	acggtggcac	cggaacagtg	1680
tcggtctaca	tcgcccaggg	tcgcgagccg	agcggcagcg	acaacgatgg	caagtcgacc	1740
cgtcccggca	cgtccgaaac	ggtacgggtg	aacaagccgg	tggcaggcac	ctactacatc	1800
aaggtagtgg	gcgaagcggc	ctacaacggc	gtgagcatcc	tcgccacgca	gtaa	1854

<210> 36

<211> 617

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(27)

<400> 36

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			20					25					30		
Arg	Glu	Pro	Val	Arg	Gln	Ala	Ser	Thr	Ala	Glu	Pro	Gly	Thr	Gln	Arg
			35				40						45		
Ile	Ile	Val	Lys	Tyr	Arg	Ala	Gly	Thr	Ala	Ala	Ala	Gly	Asp	Arg	Ser
	50					55					60				
Ala	Lys	Leu	Ser	Thr	Val	Gln	Ser	Ala	Leu	Thr	Arg	Ala	Ser	Leu	Ser
65					70					75				80	
Gly	Gly	Thr	Thr	Arg	Ala	Ser	Ala	Leu	Gly	Pro	Gln	Val	Val	Arg	Arg
				85				90						95	
Leu	Gly	Val	Gly	Ala	Asp	Leu	Ile	Arg	Leu	Gln	Gly	Arg	Leu	Ala	Pro
			100					105					110		
Ala	Glu	Leu	Gln	Arg	Val	Leu	Lys	Glu	Leu	Lys	Ala	Asp	Pro	Ser	Val
			115				120					125			
Gln	Tyr	Ala	Glu	Ala	Asp	Val	Lys	Leu	Arg	Arg	Thr	Glu	Leu	Arg	Ala
	130					135					140				
Gly	Asp	Val	Gln	Pro	Ala	Leu	Ala	Pro	Asn	Asp	Pro	Tyr	Tyr	Gln	Gln
145					150					155				160	
Tyr	Gln	Trp	His	Leu	His	Asn	Ala	Thr	Gly	Gly	Ile	Asn	Ala	Pro	Ser
			165					170						175	
Ala	Trp	Asp	Val	Ser	Gln	Gly	Glu	Gly	Val	Val	Val	Ala	Val	Leu	Asp
			180					185					190		
Thr	Gly	Ile	Leu	Pro	Gln	His	Pro	Asp	Leu	Val	Gly	Asn	Leu	Leu	Glu
	195					200						205			
Gly	Tyr	Asp	Phe	Ile	Ser	Asp	Ala	Glu	Thr	Ser	Arg	Arg	Ala	Thr	Asn
	210					215					220				
Asp	Arg	Val	Pro	Gly	Ala	Gln	Asp	Tyr	Gly	Asp	Trp	Val	Glu	Asn	Asp
225					230					235				240	
Asn	Glu	Cys	Tyr	Thr	Gly	Ser	Val	Ala	Glu	Asp	Ser	Ser	Trp	His	Gly
			245						250					255	
Thr	His	Val	Ala	Gly	Thr	Val	Ala	Glu	Gln	Thr	Asn	Asn	Gly	Val	Gly

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Met Ala Gly Val Ala His Lys Ala Lys Val Leu Pro Val Arg Val Leu
 260 265 270
 Gly Lys 275 Gly Gly Tyr Leu 280 Ser Asp Ile Ala Asp 285 Ile Thr Trp
 290 Cys Gly Gly Thr Val 295 Ala Gly Val Pro Ala 300 Asn Ala Asn Pro Ala
 305 Ala Ser Gly Gly Thr Val 310 Ala Gly Gly Ser Gly 315 Ser Cys Asp Gly Thr
 Glu Val Ile Asn Met 325 Ser Leu Gly Gly 330 Ser Arg Gly Thr Thr Val Val
 Tyr Gln Glu Ala Ile Asn Gly Ala Ile Ser Arg Gly Thr Thr Val Val
 340 345 350
 Val Ala Ala Gly Asn Glu Thr Asp Asn Ala Ser Lys Tyr Arg Pro Ala
 355 360 365
 Ser Cys Asp Gly Val Val Thr Val Gly Ala Thr Arg Ile Thr Gly Gly
 370 375 380
 Ile Thr Tyr Tyr Ser Asn Tyr Gly Thr Arg Val Asp Leu Ser Gly Pro
 385 390 395 400
 Gly Gly Gly Gly Ser Val Asp Gly Asn Pro Gly Gly Tyr Val Trp Gln
 405 410 415
 Ser Gly Ser Asp Ala Ala Thr Thr Pro Glu Ser Gly Ser Tyr Ser Tyr
 420 425 430
 Met Gly Met Gly Gly Thr Ser Met Ala Ser Pro His Val Ala Ala Val
 435 440 445
 Ala Ala Leu Val Gln Ser Ala Leu Ile Ala Lys Gly Lys Asp Pro Leu
 450 455 460
 Ala Pro Ala Ala Met Arg Thr Leu Leu Lys Glu Thr Ala Arg Pro Phe
 465 470 475 480
 Pro Val Ser Ile Pro Thr Ala Thr Pro Ile Gly Thr Gly Ile Val Asp
 485 490 495
 Ala Lys Ala Ala Leu Ala Lys Ala Leu Glu Glu Pro Cys Thr Glu Asn
 500 505 510
 Cys Gly Pro Val Ala Thr Pro Leu Thr Asn Lys Ala Ala Val Gly Gly
 515 520 525
 Leu Asn Gly Thr Ala Gly Ser Ser Arg Leu Tyr Ser Phe Glu Ala Ala
 530 535 540
 Ala Gly Lys Gln Leu Ser Val Ile Thr Tyr Gly Gly Thr Gly Asn Val
 545 550 555 560
 Ser Val Tyr Ile Ala Gln Gly Arg Glu Pro Ser Ala Ser Asp Asn Asp
 565 570 575
 Gly Lys Ser Thr Arg Pro Gly Thr Ser Glu Thr Val Arg Val Asn Lys
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 595 600 605
 Asn Gly Val Ser Ile Leu Ala Thr Gln
 610 615

<210> 37
 <211> 3582
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 37
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 accgatgtcc tgcagcgta ccagcagcag cgcgcagagc agtcgcgtcg gttcgcgctg 180
 gacctgcaca gcgcttcgct ggcggcgacc tttgttgctc cgatcggcgc caacgaccag 240
 accgtttcct tcacggggcc gcgcaccagc gccgaggccg ccggcccatc tctgggcaag 300
 ccgggtgatg tggaaagctg gcatagcgat gagttcaatg ccgactgggg tctggccgcg 360
 atgggggccc attacgcgta tgcgcgcggc ctaccgggtc agggcggtcg cttgggcgtg 420
 ttcgattcgg gctctgccct tgcccacgac gaattcgccg gacgcaacac ctccagcatc 480
 tccatcggca acggcggtg cgccgaccgc agcatcggtg cggcggaagg cgcctgcggc 540
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 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(37)

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 Val Pro Ala Leu Ala Ser Pro Thr Asp Val Leu Gln Arg Tyr Gln
 35 40 45
 Gln Gln Arg Ala Glu Gln Ser Val Ala Phe Ala Arg Asp Leu His Ser
 50 55 60

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Thr	Val	Ser	Phe	Thr	Gly	Pro	Arg	Thr	Ser	Ala	Glu	Ala	Ala	Gly	Pro
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Ile	Leu	Gly	Lys	Pro	Gly	Asp	Val	Glu	Ser	Trp	His	Ser	Asp	Glu	Phe
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Asn	Ala	Asp	Trp	Gly	Leu	Ala	Ala	Met	Gly	Ala	Asp	Tyr	Ala	Tyr	Ala
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Arg	Gly	Leu	Thr	Gly	Gln	Gly	Val	Arg	Leu	Gly	Val	Phe	Asp	Ser	Gly
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Ser	Ala	Leu	Ala	His	Asp	Glu	Phe	Ala	Gly	Arg	Asn	Thr	Ser	Ser	Ile
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Ser	Ile	Gly	Asn	Gly	Gly	Cys	Ala	Asp	Pro	Ser	Ile	Val	Ala	Gly	Glu
				165					170					175	
Gly	Ala	Cys	Gly	Ser	Thr	Arg	Gly	Asp	Gln	Pro	Gly	Tyr	Asn	Tyr	Tyr
			180					185					190		
Gly	Leu	Gly	Pro	Gly	Val	Pro	Pro	Ala	Leu	Ala	Asp	Arg	Leu	Ile	Ala
		195					200					205			
Ala	Gly	Gln	Pro	Tyr	Gly	Phe	Ser	Tyr	Ala	Asp	His	Gly	Thr	His	Val
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Leu	Gly	Thr	Val	Gly	Ala	Asn	Arg	Asp	Gly	Thr	Gly	Met	His	Gly	Val
225					230					235					240
Ala	Phe	Gly	Ala	Asn	Leu	Thr	Ala	Ala	Arg	Val	Phe	Gly	Asp	Thr	Tyr
				245					250					255	
Tyr	Glu	Trp	Arg	Leu	Asp	Pro	Asp	Asn	Phe	Tyr	Arg	Pro	Arg	Ala	Leu
			260					265					270		
Tyr	Arg	Thr	Asp	Pro	Asp	Asp	Ala	Ala	Thr	Leu	Asp	Met	Tyr	Ala	Gln
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Ala	Glu	Ala	Gln	Gly	Val	Arg	Val	Leu	Asn	His	Ser	Trp	Gly	Ile	Ser
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Thr	Arg	His	Ala	Thr	Val	Ala	Ser	Leu	Asp	Ala	Gln	Tyr	Ala	Ala	Ile
305					310					315					320
Gly	Ala	Asp	Tyr	Gly	Val	Tyr	Gly	Ser	Ile	Tyr	Gly	Asp	Thr	Glu	Gly
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Ala	Pro	Gly	Ser	Lys	Leu	Ile	Gln	Val	Trp	Ser	Ala	Gly	Asn	Ser	Ala
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Ile	Glu	Pro	Tyr	Trp	Leu	Ala	Val	Ala	Asn	Val	Arg	Leu	Pro	Thr	Ala
	370					375					380				
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Ser	Ala	Asn	Trp	Cys	Leu	Ser	Ala	Pro	Gly	Thr	Asn	Ile	Ala	Ser	Thr
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Ile	Val	Ala	Gly	Glu	Ile	Asn	Gly	Arg	Met	Glu	Leu	Thr	Glu	Asp	Tyr
			420					425					430		
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Lys	Thr	Gly	Thr	Ser	Met	Ala	Ala	Pro	His	Ile	Thr	Gly	Ala	Leu	Gly
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Val	Leu	Leu	Thr	Thr	Ala	Arg	Asp	Leu	Gly	Ala	Pro	Gly	Val	Asp	Ala
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Gly	Arg	Leu	Val	Asp	Ser	Ser	Leu	Thr	Ser	Ala	Gly	Ala	Thr	Arg	Val
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Thr	Val	Ser	Phe	Asn	Gly	Val	Gln	Gln	Asp	Gly	Ala	Thr	Val	Val	Gly
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Ala	Lys	Gly	Thr	Leu	Lys	Gly	Val	Gly	Thr	Leu	Gly	Ser	Thr	Arg	Val
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Glu	Gly	Ile	Ile	Ala	Pro	Gly	Asn	Ser	Ile	Gly	Thr	Leu	Thr	Val	Asn
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Gly	Asp	Tyr	Val	Gln	Thr	Ala	Thr	Gly	Ile	Tyr	Gln	Ala	Glu	Leu	Ala
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785					790					795					800
Ala	Thr	Thr	Asp	Phe	Ser	Ala	Phe	Ser	Pro	Phe	Leu	Lys	Phe	Ser	Leu
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Gly	Tyr	Ser	Ala	Asn	Gly	Leu	Arg	Ile	Asp	Val	Ala	Arg	Gly	Asn	Ala
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Leu	His	Ala	Ala	Thr	Pro	Met	Ala	Leu	Val	Glu	Ser	Ser	Arg	Tyr	Leu
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Arg	Asp	Ala	Ala	Leu	Ser	Arg	Ala	Val	Gly	Val	Arg	Ser	Pro	Gly	Ala
			900					905					910		
Ala	Asp	Glu	Ala	Ala	Gly	Gly	Ala	Trp	Val	Gln	Ala	Ile	Gly	Gly	Ser
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Asn	Gly	Leu	Leu	Val	Gly	Ala	Asp	His	Val	Phe	Gly	Gly	Gly	Trp	Gln
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Val	Gly	Gly	Leu	Val	Gly	Thr	Gly	Arg	Thr	Asp	Ile	Lys	Gln	Ala	Ala
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Ser	Arg	His	Asp	Val	Asp	Ser	Lys	Arg	Gln	Leu	Thr	Phe	Ala	Gly	Tyr
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Ile	Glu	Gly	Ala	Tyr	Arg	Phe	Gly	Gly	Arg	Glu	Ala	Gly	Leu	Glu	Pro
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Tyr	Leu	Gln	Phe	Ala	Arg	Val	Glu	Val	Asp	Val	Asp	Gly	Ile	Thr	Glu
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Gln	Gly	Gly	Ala	Ala	Ala	Leu	His	Gly	Gln	Val	Ala	Asp	Thr	Arg	Thr
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Arg	Ala	Ser	Gly	Asp	Arg	Ser	Gln	Val	Ala	Asp	Leu	Ala	Trp	Thr	Gly
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Gly	Asn	Ser	Phe	Ala	Val	Ser	Gly	Ala	Ala	Ile	Ala	Asp	Asn	Ala	Val
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 Glu Leu Gly Tyr Asn Gly Thr Phe Gly Asp Asp Ala Arg Asp Arg Ser
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 gtgctgacgg cgaccgcgac ggcgcttggc gaaacccggg acttcgatca tgattacggc 1320
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 <211> 461
 <212> PRT
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<220>
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 35 40 45
 Leu Asp Glu Leu Ser Val Pro Val Pro Met Phe Ala Gln Gly Asn Glu
 50 55 60
 Gly Asp Arg Thr Ile Leu Ser Arg Phe Ala Ala Phe Ala Ala Pro Thr
 65 70 75 80
 Pro Asn Pro Glu Thr Ala Arg Ala Val Val Leu Pro Val Glu Val
 85 90 95
 Asp Arg Ala Arg Leu Glu Glu Leu Glu His Arg Pro Gly Val Thr Val
 100 105 110
 Trp Pro Asn Ser Glu Leu Ser Leu Phe Asn Thr Gly Asn Glu Asp Pro
 115 120 125
 Ile Asp Leu Ala Trp Ser Lys Gly Gly Leu Asp Cys Arg Pro Phe Arg
 130 135 140

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145 150 155 160
Val Trp Leu Glu Gly Tyr Arg Gly Gln Asn Ile Ile Val Gly Ile Ile
165 170 175
Asp Glu Gly Ile Ser Gly Glu His Tyr Pro Val Val Gly Gly Phe Ser
180 185 190
Arg Pro Asn Ala Arg Arg Pro Gly Thr Ala Pro Ile Thr Ser His Gly
195 200 205
Ser Met Cys Ala Ala Asp Val Leu Ile Ala Ala Pro Ala Arg Leu
210 215 220
Tyr Asp Tyr Pro Phe Leu Gly Val Pro Asn Ser Gly Gly Ala Leu Gln
225 230 235
Met Phe Gln Ala Val Leu Asp Gln Arg Arg Leu Asp Gly Thr Pro His
240 245 250 255
Leu Thr Asn Asn Ser Tyr Gly Phe Val Gly Val Pro Asp Pro Arg Gln
260 265 270
Trp Pro Asn His Glu Val His Asn Ile Asn His Pro Leu His Arg Lys
275 280 285
Val Arg Glu Val Val Ala Ala Gly Val Ala Cys Phe Phe Ala Ala Gly
290 295 300
Asn Cys Gly Ala Asp Cys Pro Ser Gly Asn Cys His Pro Ser Gly Ile
305 310 315 320
Gly Ala Gly Lys Ser Ile His Ala Ser Asn Ser Leu Ala Glu Val Val
325 330 335
Thr Val Ala Ala Val Asn Ser Arg His Glu Arg Ile Gly Tyr Ser Ser
340 345 350
Gln Gly Pro Gly Met Phe Glu Pro Arg Lys Pro Asp Leu Ala Ser Tyr
355 360 365
Ser His Ile Phe Ala Asn Phe Gly Pro Gly Arg Pro Ala Gly Thr Gly
370 375 380
Ser Gln Pro Phe Asp Asn Gly Thr Ser Ala Ala Thr Pro Val Ala Ala
385 390 395 400
Gly Val Ala Ala Leu Leu Leu Ser Ala Phe Pro Asp Val Asp Pro Asp
405 410 415
Arg Leu Lys Arg Val Leu Thr Ala Thr Ala Thr Arg Leu Gly Glu Thr
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Ala Tyr Arg Ser Leu Arg Arg Ala Ser Gly Ala Ile Ser
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 <211> 1281
 <212> DNA
 <213> Unknown

<220>
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agcagcatcc	gttcggcctg	gcacaccagc	aacaccgcag	ccaacaccat	cagtgggtacc	1080

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```

tcgatggccg ctccgcacgt tgctggcgta gccgccttgt tcctggccaa caacccgaac 1140
gccaccccg cccaggttga aaacgcgacg tacagcaacg gtagcaccgg caagctcagc 1200
ggcctgaatg gttcgcccaa cctgctggtc tactcgcgct tcggcggcgg cggcggccccg 1260
gatccagatc gaggcggatg a 1281

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<210> 42
 <211> 426
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(22)

<400> 42
 Met Ser Trp Lys Thr Leu Ser Thr Ser Leu Thr Gly Ala Ala Val Leu
 1 5 10 15
 Ala Leu Ser Ser Phe Ala Ala Ser Asp Ala Ala Ala Asn Asn Arg Ser
 20 25 30
 Asn Ser Glu Thr Arg Ala Gln Thr Ser Ala Asp Phe Arg His Ala Glu
 35 40 45
 Arg Pro Val Glu Gly Arg Tyr Ile Val Val Leu Lys Asp Glu Val Ala
 50 55 60
 Arg Leu Ala His Glu Asn Gly Ser Ala Arg Ala Asn Leu Pro Glu Val
 65 70 75 80
 Ala Gln Val Ala Gln Ala Met Ala Arg Gly His Gly Ala Gln Leu Glu
 85 90 95
 Arg Ser Phe Thr His Ala Leu Arg Gly Phe Val Val Glu Ala Asp Asp
 100 105 110
 Arg Ala Leu Ala Arg Leu Leu Leu Asp Glu Arg Val Ala Phe Ile Glu
 115 120 125
 Glu Asp Gly Ile Val Ser Ile Ser Gln Thr Thr Gln Pro Asn Ala Thr
 130 135 140
 Trp Gly Leu Asp Arg Ile Asp Gln Arg Asp Arg Pro Leu Asp Gly Asn
 145 150 155 160
 Tyr Ile Tyr Asp Thr Thr Ala Ser Asn Val Tyr Thr Tyr Ile Val Asp
 165 170 175
 Thr Gly Val Arg Thr Asn His Asn Asp Phe Gly Gly Arg Val Leu Ser
 180 185 190
 Gly Phe Thr Ser Ile Asn Asp Gly Asn Gly Thr Asn Asp Cys Asn Gly
 195 200 205
 His Gly Thr His Val Ala Gly Thr Val Ala Gly Ser Thr Trp Gly Val
 210 215 220
 Ala Lys Ala Ala Arg Ile Val Pro Val Arg Val Leu Gly Cys Gln Gly
 225 230 235 240
 Asn Gly Thr Asn Ala Gly Val Ile Ala Gly Met Asp Trp Ile Ala Ala
 245 250 255
 Asn His Val Lys Pro Ala Val Ala Asn Met Ser Leu Gly Gly Gly Ala
 260 265 270
 Ser Thr Ala Thr Asp Asn Ala Val Thr Asn Met Arg Asn Ala Gly Val
 275 280 285
 Thr Val Val Val Ala Ala Gly Asn Glu Asn Gln Asn Ala Cys Asn Val
 290 295 300
 Ser Pro Ala Arg Ser Gly Asn Ala Ile Thr Val Gly Ser Thr Thr Ser
 305 310 315 320
 Thr Asp Ala Arg Ser Asn Phe Ser Asn Trp Gly Asn Cys Val Asp Ile
 325 330 335
 Phe Ala Pro Gly Ser Ser Ile Arg Ser Ala Trp His Thr Ser Asn Thr
 340 345 350
 Ala Ala Asn Thr Ile Ser Gly Thr Ser Met Ala Ala Pro His Val Ala
 355 360 365
 Gly Val Ala Ala Leu Phe Leu Ala Asn Asn Pro Asn Ala Thr Pro Ala
 370 375 380
 Gln Val Glu Asn Ala Ile Tyr Ser Asn Gly Ser Thr Gly Lys Leu Ser
 385 390 395 400
 Gly Leu Asn Gly Ser Pro Asn Leu Leu Val Tyr Ser Arg Phe Gly Gly

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405 410 415
 Gly Gly Gly Pro Asp Pro Asp Arg Gly Gly
 420 425

<210> 43
 <211> 1881
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 43
 atgaacaaga catccatcag cgtggccctg gccgcggttc tggccggcgc gctcggcgcg 60
 caggtcgccg atgctgcccg tacccccgcc aagatcgtgc cgcgcacgca tgtggcgccg 120
 ccggccgagg ccgctgccga ccgtatcgtc gtgcgctacg cgcaagcgcg catcgccagc 180
 accgatcgca ccggcaagct gcaggtcgcg accgcgcga tccgccgcgc cgggctcgag 240
 cgtccggtcg cctccggccg cgcggccaag gcgctgccgg cgttgcaagg cggccatctg 300
 cgcacgaccg cggctcggtt cgacgtgtc cggctgtcgc ggccgctgcc cgcgcgcgac 360
 ttgcaggcgc tggtagccga actggccgcc gatccggcgg tggcgtcggt gcacgtggat 420
 cggcgcatgc ggcgaccgg tgtggacaag cgcaccgtca cggcgcagt caccctcaac 480
 gacgagttct tcgccagcca ccagtggcac ctgcagggt cggccggcgc gatcaacgtt 540
 gccaacgcct gggaccgctc gaccgggtgcc ggcacgtggt tcgcggtgct cgacaccggc 600
 atcctggccg agcaccggga cttcgcgcac aacatcctgc ccggctacga cttcatcacc 660
 gatcctttcg tgtcccggcg cgagaccgcc gaccgtgtgc ccggcgact ggaccacggc 720
 gactggaaac ccgtggcggg cgagtgttac agcggctcgc cggtgatcga cagcacctgg 780
 catggcacc atgtggccgg cacggctgcc gaggcgacc acaacggcat cggtggtgct 840
 ggcgtcgcc acgacgcga ggtgttgccg gtgcgcgtgc tcggccgctg cgggggctat 900
 gactctgaca tcgccgatgc gatcgtctgg gcctcgggcg gcgcggtcga gggcgtgccg 960
 gaaaacgtgc acccggtga ggtcatcaat ctacgcctcg gcggacaagg cacgtgcgag 1020
 gcgatgaccc aggcggcgat cgacagtgc gtcgcgcgcg gcagcgtggt cgtggtcgcg 1080
 gccggcaact acaacgacga tgcccagcgc tattcgccag ccaactgcaa gaacgtgatc 1140
 acggctcggcg ccaaccgcat caacagcggg cgcgcgtact actccaact cggtgcggtg 1200
 gtcgacgttt ttggccccgg cgggtggcggc gagttcgaca ccggcaatgg cggctggaat 1260
 ggctacgtgc tgcagaccgg ttacgacggc aagaccacgc gcacctccgg gcagtacctc 1320
 tacaccgggc tgatgggcac ctcgatggcg gccccgcagt tgtcgggcat cgccgcgctg 1380
 gtgcagagcg cgtggtcgc ccaggaccgt ccgccgctga cgccggccga gatggagctc 1440
 ctgctcaagc gcaccgcgcg tccgttcaat gtgccgcgcg cgccaatac gccgatcggc 1500
 gtgggcatcg ttgatgcgac ccgcgcgtg gagaaggcgc tggagacccc ctgcgatccg 1560
 gccaccgaga cctgcgagct cggcacccag ctgttcaatg gcgccgacgt cactggcctg 1620
 gcctccaacg gcgagggcgc gctgttccgc ttcgaggccc aggccggctg cacgttgacg 1680
 ctgatgacgc tggccggccg cggcgacgtc actctgcac cgcgctatgg cgcaccgccg 1740
 acctcgacc actacgagtt ccgctcggcg cgtgcgggca gcaacatcga gacgatccgc 1800
 atcaccgcgc ccaaggccgg cacgtactac ctgcagttga gcggcagcta cacaggcctg 1860
 actgtcgtcg cccgtcagta g 1881

<210> 44
 <211> 626
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(25)

<400> 44
 Met Asn Lys Thr Ser Ile Ser Val Ala Leu Ala Ala Val Leu Ala Gly
 1 5 10 15
 Ala Leu Gly Ala Gln Val Ala Asp Ala Arg Thr Pro Ala Lys Ile
 20 25 30
 Val Pro Arg Ile Asp Val Ala Pro Pro Ala Glu Ala Ala Ser Asp Arg
 35 40 45
 Ile Val Val Arg Tyr Ala Gln Ala Arg Ile Ala Ser Thr Asp Arg Thr
 50 55 60
 Gly Lys Leu Gln Val Ala Thr Ala Ala Ile Arg Arg Ala Gly Leu Glu
 65 70 75 80

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Arg Pro Val Ala Ser Gly Arg Ala Ala Lys Ala Leu Pro Ala Leu Gln
 Val Gly His Leu 85 Arg Thr Thr Ala Val 90 Gly Phe Asp Val Leu 95 Arg Leu
 Ser Arg Pro 100 Leu Pro Ala Arg Asp Leu 105 Gln Ala Leu Val 110 Thr Glu Leu
 Ala Ala 115 Asp Pro Ala Val Ala Ser Val His Val 125 Arg Arg Met Arg
 Ala 130 Thr Gly Val Asp Lys 135 Arg Thr Val Thr Pro 140 Gln Phe Thr Pro Asn
 145 Asp Glu Phe Phe Ala 150 Ser His Gln Trp His 155 Leu Gln Gly Ser Ala 160 Gly
 Ala Ile Asn Val 165 Ala Asn Ala Trp Asp 170 Arg Ser Thr Gly Ala 175 Ile
 Val Val Ala 180 Val Leu Asp Thr Gly 185 Ile Leu Ala Glu His 190 Pro Asp Phe
 Ala 195 Asn Ile Leu Pro Gly 200 Tyr Asp Phe Ile Thr 205 Asp Pro Phe Val
 Ser 210 Arg Arg Glu Thr Ala 215 Asp Arg Val Pro Gly 220 Ala Leu Asp His Gly
 225 Asp Trp Asn Pro Val 230 Ala Gly Glu Cys Tyr 235 Ser Gly Ser Pro Val 240 Ile
 Asp Ser Thr Trp 245 His Gly Thr His Val 250 Ala Gly Thr Val Ala 255 Glu Ala
 Thr His Asn 260 Gly Ile Gly Gly Ala 265 Gly Val Ala Tyr Asp 270 Ala Gln Val
 Leu 275 Val Arg Val Leu Gly 280 Arg Cys Gly Gly Tyr 285 Asp Ser Asp Ile
 Ala 290 Asp Ala Ile Val Trp 295 Ala Ser Gly Gly Ala 300 Val Glu Gly Val Pro
 305 Glu Asn Val His Pro 310 Ala Glu Val Ile Asn 315 Leu Ser Leu Gly Gly 320 Gln
 Gly Thr Cys Glu 325 Ala Met Thr Gln Ala 330 Ala Ile Asp Ser Ala 335 Val Ala
 Arg Gly Ser 340 Val Val Val Val Ala 345 Gly Asn Tyr Asn 350 Asp Asp Ala
 Gln Arg Tyr Ser Pro Ala Asn 355 Cys Lys Asn Val Ile Thr Val Gly Ala
 360 Asn Arg Ile Asn Ser Gly 365 Arg Ala Tyr Tyr Ser Asn Phe Gly Ala Val
 370 Val Asp Val Ser Gly 375 Pro Gly Gly Gly Gly Glu Phe Asp Thr Gly Asn
 385 Gly Gly Trp Asn 390 Gly Tyr Val Leu Gln 400 Thr Gly Tyr Asp Gly Lys Thr
 Thr Pro Thr Ser Gly Gln Tyr Leu 410 Tyr Thr Gly Leu Met 415 Gly Thr Ser
 Met Ala 420 Pro His Val Ser 425 Gly Ile Ala Ala Leu 430 Val Gln Ser Ala
 435 Leu Val Ala Gln Asp Arg Pro Pro Leu Thr Pro 440 Ala Glu Met Glu Leu
 445 Leu Leu Lys Arg Thr 450 Ala Arg Pro Phe Asn 455 Val Pro Pro Pro Ala Asn
 Thr Pro Ile Gly Val Gly Ile Val Asp 460 Ala Thr Arg Ala Leu 465 Glu Lys
 Ala Leu Glu Thr Pro Cys Asp Pro 470 Ala Thr Glu Thr Cys 475 Glu Leu Gly
 Thr Gln 480 Leu Phe Asn Gly Ala 485 Asp Val Thr Gly Leu 490 Ala Ser Asn Gly
 Glu 495 Gly Ala Leu Phe Arg Phe Glu Ala Gln Ala Gly Arg Thr Leu Thr
 500 Leu Met Thr Leu Ala 505 Gly Arg Gly Asp Val Thr Leu His Ala Arg Tyr
 510 Gly Ala Pro Pro Thr Ser Thr Asp Tyr 515 Glu Phe Arg Ser Ala Arg Ala
 520 Gly ser Asn 525 Ile Glu Thr Ile Arg 525 Ile Thr Ala Pro Lys 530 Ala Gly Thr
 Tyr Tyr 535 Leu Gln Leu Ser Gly 540 Ser Tyr Thr Gly Leu 545 Thr Val Val Ala
 550 610 615 620

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Arg Gln
625

<210> 45
 <211> 1875
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 45
 atgcaacgctc gttcagtcct gaccgctgcg gtcagcaccg ccctcgtgtg cgcattcgggt 60
 gccacgctcgg tcctcgtctc cgagctgctc ttccgagaga acccgatcga gggccaatac 120
 atcgtcgtcc tcaaggagga cgcggccacg ctccgaggcg agacctcgat cgcgtccaac 180
 cgtcccaacg tggccaatgc cgcgcgcaac ctggcccgcg cccaccgcgc cgaggctcgc 240
 cacacctaca accgcgccct gcgcggcttc gtggcccgcg ccgacgagcg tgccctggcc 300
 cgctgctgc aggaacccggc cgtggcctac gtcgaggagg acggcatcgt ctccatcggc 360
 gccacccaga ccggcgccac ctggggcatc gaccgcatcg accagcgcg cctgcccgtg 420
 aaccagacct acgtctacga caccaccgca tccaacgtcc acgtctacat cgtcgacacc 480
 ggcattccgtt cggcgacaa cgacttcggc ggccgcgtcg gttccggcta caccgccatc 540
 aacgacggcc agggcacaa cgactgcaac ggccacgga cccatgtcgc ctccaccgcc 600
 gccggtgcca cctacggcgt ggccaaggcc gccgcctct atccgggtgcg cgtgctcggc 660
 tgccaggggca acggctccaa ttccggcggtg atcgccggca tggactgggt cgccagcaac 720
 caggtcaagc cggccgtggc caacatgagc ctggggcgcg gcgcctcgca ggccaccgat 780
 gatgccgtga cgcgcatgcg caacgccggc gtcaccgtcg tgggtggccgc gggcaacgac 840
 aacgccaacg cctgcaacta ctgcggcgcg cgtgcagcct cggcgatcac cgtgggctcg 900
 accaccaaca ccgacgcacg ctccagcttc tccaacttcg gcacctgctg gaacatcttc 960
 gcgcggggct ccaacatcac cgccgcctgg cacaccagca acaccgcgac caacaccatc 1020
 agcggcacct cgtggtgctc gccgcacgtc gccggcggtg ccgcgctgtg gctggccaac 1080
 aacccaacg ccaccccggc ccaggctcag caggcgtgtg acaacaacgc cagcccaac 1140
 aaggtgacca atgccggcac cggctcggcc aaccgcctgc tgtactcgcg ctggggcgcg 1200
 ggcaccaacc cggatcccga tccggatccg acgcccggca gcctgaccaa cggcgtgccg 1260
 gtcaccggcc tctccggcgc agccggctcc gagcgtcgt acaccatgac cgtcccggcc 1320
 ggccccaaca acctgtcgtt cgccatcagc ggccgacg gtcggtacct caacggcaac 1440
 cgcttcgggtt cggcgccgac caccacgacc caacgtgcag gccggcacgt accacgtgct ggtccgtggc 1500
 aacgagacct gcaacatcag acagcggcgt gagcctggt ggcaacttca cccggcctc cggcggtggc 1560
 tacagccagt acagcggcgt caagtacacc ggctccctca gcggcacccg ccaggcccag 1620
 gcgcccgtga ccggctgcac ctaccagtc acccgctccg gcacgcaccg cggctggctg 1680
 gtccagccca acggcaccta ctaccagtc acccgctccg gctggaacgg cagcagctgg 1740
 cgtggcccgt ccaacgccga cttcgacctg gagctgtacc agcaacgagg agatcagcta caacggcacg 1800
 gcccgcggtg ccagctcgac cggcggcacc agcaacgagg agatcagcta caacggcacg 1860
 gctggctact actactggcg catcgtgtcc tacagcggca gcggcagcta cgacttctac 1875
 ctgaccggcc cgtga

<210> 46
 <211> 624
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(26)

<400> 46
 Met Gln Arg Arg Ser Val Leu Thr Ala Ala Val Ser Thr Ala Leu Val
 1 5 10 15
 Cys Ala Phe Gly Ala Thr Ser Val Leu Ala Ser Glu Leu Arg Phe Ala
 20 25 30
 Glu Asn Pro Ile Glu Gly Gln Tyr Ile Val Val Leu Lys Glu Asp Ala
 35 40 45
 Ala Thr Leu Glu Gly Glu Thr Ser Ile Ala Ser Asn Arg Pro Asn Val
 50 55 60
 Ala Asn Ala Ala Arg Asn Leu Ala Arg Ala His Arg Ala Glu Val Arg
 65 70 75 80
 His Thr Tyr Asn Arg Ala Leu Arg Gly Phe Val Ala Arg Ala Asp Glu

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Arg	Ala	Leu	Ala	Arg	Leu	Leu	Gln	Asp	Pro	Ala	Val	Ala	Tyr	Val	Glu
Glu	Asp	Gly	Ile	Val	Ser	Ile	Gly	Ala	Thr	Gln	Thr	Gly	Ala	Thr	Trp
Gly	Ile	Asp	Arg	Ile	Asp	Gln	Arg	Asp	Leu	Pro	Leu	Asn	Gln	Thr	Tyr
Val	Tyr	Asp	Thr	Thr	Ala	Ser	Asn	Val	His	Val	Tyr	Ile	Val	Asp	Thr
Gly	Ile	Arg	Ser	Ala	His	Asn	Asp	Phe	Gly	Gly	Arg	Val	Gly	Ser	Gly
Tyr	Thr	Ala	Ile	Asn	Asp	Gly	Gln	Gly	Thr	Asn	Asp	Cys	Asn	Gly	His
Gly	Thr	His	Val	Ala	Ser	Thr	Ala	Ala	Gly	Ala	Thr	Tyr	Gly	Val	Ala
Lys	Ala	Ala	Arg	Leu	Tyr	Pro	Val	Arg	Val	Leu	Gly	Cys	Gln	Gly	Asn
Gly	Ser	Asn	Ser	Gly	Val	Ile	Ala	Gly	Met	Asp	Trp	Val	Ala	Ser	Asn
His	Val	Lys	Pro	Ala	Val	Ala	Asn	Met	Ser	Leu	Gly	Gly	Gly	Ala	Ser
Gln	Ala	Thr	Asp	Asp	Ala	Val	Thr	Arg	Met	Arg	Asn	Ala	Gly	Val	Thr
Val	Val	Val	Ala	Ala	Gly	Asn	Asp	Asn	Ala	Asn	Ala	Cys	Asn	Tyr	Ser
Pro	Ala	Arg	Ala	Ala	Ser	Ala	Ile	Thr	Val	Gly	Ser	Thr	Thr	Asn	Thr
Asp	Ala	Arg	Ser	Ser	Phe	Ser	Asn	Phe	Gly	Thr	Cys	Val	Asn	Ile	Phe
Ala	Pro	Gly	Ser	Asn	Ile	Thr	Ala	Ala	Trp	His	Thr	Ser	Asn	Thr	Ala
Thr	Asn	Thr	Ile	Ser	Gly	Thr	Ser	Met	Ala	Ser	Pro	His	Val	Ala	Gly
Val	Ala	Ala	Leu	Trp	Leu	Ala	Asn	Asn	Pro	Asn	Ala	Thr	Pro	Ala	Gln
Val	Glu	Gln	Ala	Leu	Tyr	Asn	Asn	Ala	Thr	Pro	Asn	Lys	Val	Thr	Asn
Ala	Gly	Thr	Gly	Ser	Ala	Asn	Arg	Leu	Leu	Tyr	Ser	Arg	Trp	Gly	Gly
Gly	Thr	Asn	Pro	Asp	Pro	Asp	Pro	Asp	Pro	Thr	Pro	Gly	Ser	Leu	Thr
Asn	Gly	Val	Pro	Val	Thr	Gly	Leu	Ser	Gly	Ala	Ala	Gly	Ser	Glu	Arg
Arg	Tyr	Thr	Met	Thr	Val	Pro	Ala	Gly	Ala	Thr	Asn	Leu	Ser	Phe	Ala
Ile	Ser	Gly	Gly	Ser	Gly	Asp	Ala	Asp	Leu	Tyr	Val	Arg	Phe	Gly	Ser
Ala	Pro	Thr	Thr	Thr	Thr	Tyr	Asp	Cys	Arg	Pro	Tyr	Leu	Asn	Gly	Asn
Asn	Glu	Thr	Cys	Asn	Ile	Ser	Asn	Val	Gln	Ala	Gly	Thr	Tyr	His	Val
Leu	Val	Arg	Gly	Tyr	Ser	Gln	Tyr	Ser	Gly	Val	Ser	Leu	Val	Gly	Asn
Phe	Thr	Pro	Ala	Ser	Gly	Gly	Gly	Ala	Pro	Cys	Thr	Gly	Cys	Thr	Lys
Tyr	Thr	Gly	Ser	Leu	Ser	Gly	Thr	Gly	Gln	Ala	Gln	Val	Gln	Pro	Asn
Gly	Thr	Tyr	Tyr	Gln	Ser	Thr	Arg	Ser	Gly	Thr	His	Arg	Gly	Trp	Leu
Arg	Gly	Pro	Ser	Asn	Ala	Asp	Phe	Asp	Leu	Glu	Leu	Tyr	Arg	Trp	Asn
Gly	Ser	Ser	Trp	Ala	Arg	Val	Ala	Ser	Ser	Thr	Gly	Gly	Thr	Ser	Asn
Glu	Glu	Ile	Ser	Tyr	Asn	Gly	Thr	Ala	Gly	Tyr	Tyr	Tyr	Trp	Arg	Ile
Val	Ser	Tyr	Ser	Gly	Ser	Gly	Ser	Tyr	Asp	Phe	Tyr	Leu	Thr	Arg	Pro

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<210> 47
 <211> 1506
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 47
 atgctgtacgt cgcttcgggt ttcccttgcc agtgccatca ccctggctcct ggccagcgcc 60
 cccgccttcg cccaacccac cgaacgggta tggacgcgag gcatggccag caacgagcag 120
 tacagcagtt tcacgtcaa gtaccgggac ggcagcagca agcgcgtctc cgccgacacc 180
 gcccaaggacg cgctgaagaa gcgcctcggc gtccagcagc gcagcaagcg ttcgatcggc 240
 agtgcgcccgc cggcgggccgc gtccgtgacc catcaacgcc gcatggggcg cgccgcccgc 300
 gtgggtcacca cggacaagcc actggaccgt ccggaggccg agatcctgat gcagcgcatc 360
 gccgacgatc ctgacgtcga gtatgtgcag ccgaactaca tgatgagtgat attcgccacg 420
 ccgaacgacc cgcgctacgg cgagcagtgg cactacagca actcgaccag tggcgcgcg 480
 ctgcccggcg cgtgggatcg ctccaccggc cagggcggtg tggttgcggg ggtcgattcg 540
 ggctatctca acaacaacga cctgcaggcg aacctgctgc cgggttacga catgatctcg 600
 tcaacccgctc cgttcagtga ctggcagtgat atcatcgggg gcatgaatcc cggctgtggg 660
 ggctccgacg atggtgacgg acgcgacgac gatgcattcg atgcctcggg cattgcacac 720
 ggacccacg tcgcccgaac ggtcgtgctg gtgaccaaca accagattgg cgtggccggc 780
 gtggcctaca acgcgaaagt cgtaccgggt cgcgtactgg gaaaccaggg caatggtggc 840
 tccgcccgata tcacgtacgg catgctctgg agtgccggta tcaacgtgcc caacgtcccg 900
 gccaatgcc aacccggccga ggtcatcaat ctgagcctgg gtggccgccc cgccctgctcg 960
 ccggcccagc aggatgcaat cgacgacatc acggcccagg gcacgatcgt ggtggtcgcc 1020
 gccggcaaca gcaatcttga tgtgtccgag ttccgcccgg cgaactgcaa gggcgtgatc 1080
 gcggttgctg ccaacgatca gggcggtcgt cgcgcgttct actccaacta tgggtgcaggc 1140
 atccacatca ccgcaccggg tggcgagacc tggctgtgcc gtgcgtcggg gggtgagttc 1200
 ctgcccgttg ccacgcccgc gagccaggcc aactgcgcac ccacccgcca gcatccggcg 1260
 cagggcatcc tgtccaccgt ggttaacaac gccttcggct tcatgtccgg cacctcgatg 1320
 gcggcgccctc acgtcgtcgg catcgtcgcg ctgatgcagg cgggtggcgcc ggtgccgaag 1380
 accactgacc aggtcaagga catcctgctg cgaaccgcgc acccgatcgc agcggcgaac 1440
 tgcccgggag gttgcggacc gggcattgtc gacgctgcag aagcggtgaa ggccgcccagc 1500
 aactga 1506

<210> 48
 <211> 501
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(24)

<400> 48
 Met Arg Thr Ser Leu Arg Val Ser Leu Ala Ser Ala Ile Thr Leu Val
 1 5 10 15
 Leu Ala Ser Ala Pro Ala Phe Ala Gln Pro Thr Glu Arg Val Trp Thr
 20 25 30
 Arg Gly Met Ala Ser Asn Glu Gln Tyr Ser Ser Phe Ile Val Lys Tyr
 35 40 45
 Arg Asp Gly Ser Ser Lys Arg Val Ser Ala Asp Thr Ala Gln Asp Ala
 50 55 60
 Leu Lys Lys Arg Leu Gly Val Gln Gln Arg Ser Lys Arg Ser Ile Gly
 65 70 75 80
 Ser Ala Pro Pro Ala Ala Ala Ser Val Thr His Gln Arg Arg Met Gly
 85 90 95
 Gly Gly Ala Asp Val Val Thr Thr Asp Lys Pro Leu Asp Arg Pro Glu
 100 105 110
 Ala Glu Ile Leu Met Gln Arg Ile Ala Asp Asp Pro Asp Val Glu Tyr
 115 120 125
 Val Gln Pro Asn Tyr Met Met Ser Ala Phe Ala Thr Pro Asn Asp Pro
 130 135 140
 Arg Tyr Gly Glu Gln Trp His Tyr Ser Asn Ser Thr Ser Gly Ala Arg
 145 150 155 160

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Leu Pro Gly Ala Trp Asp Arg Ser Thr Gly Gln Gly Val Val Val Ala
 Val Val Asp Ser 165 Gly Tyr Leu Asn Asn 170 Asp Leu Gln Ala 175 Asn Leu
 Leu Pro Gly Tyr Asp Met Ile Ser Ser Thr Arg Pro Phe 190 Ser Asp Trp
 Gln Cys 195 Ile Ile Gly Gly Met 200 Asn Pro Gly Cys Gly 205 Ser Asp Asp
 Gly Asp Gly Arg Asp Ala 215 Asn Phe Asp Ala 220 Ser Gly Ile Ala His
 225 Gly Thr His Val Ala 230 Gly Thr Val Ala Val Thr Asn Asn Gln Ile
 Gly Val Ala Gly 245 Val Ala Tyr Asn Ala 250 Lys Val Val Pro Val Arg Val
 Leu Gly Asn 260 Gln Gly Asn Gly Gly Ser Ala Asp Ile Ile Asp Gly Met
 Leu Trp 275 Ser Ala Gly Ile Asn 280 Val Pro Asn Val Pro Ala Asn Ala Asn
 Pro Ala Glu Val Ile Asn 295 Leu Ser Leu Gly Gly Arg Arg Ala Cys Ser
 305 Pro Ala Glu Gln Asp 310 Ala Ile Asp Asp Ile Thr Ala Gln Gly Thr Ile
 Val Val Val Ala Ala Gly Asn Ser Asn Leu Asp Val Ser Glu Phe Ala
 Pro Ala Asn 340 Cys Lys Gly Val Ile Ala Val Ala Ala Asn Asp Gln Gly
 Gly Arg Arg Ala Phe Tyr Ser Asn Tyr Gly Ala Gly 365 Ile His Ile Thr
 Ala Pro Gly Gly Glu Thr Trp Ser Cys Arg Ala Ser Val Gly Glu Phe
 385 Leu Pro Leu Ala Thr 405 Pro Ser Gln Ala Asn Cys Ala Pro Thr Arg
 Gln His Pro Ala 420 Gln Gly Ile Leu Ser Thr Val Gly Asn Asn Ala Phe
 Gly Phe Met 435 Ser Gly Thr Ser Met 440 Ala Ala Pro His Val Ala Gly Ile
 Val Ala Leu Met Gln Ala Val Ala Pro Val Pro Lys Thr Thr Asp Gln
 450 Val Lys Asp Ile Leu Arg 470 Thr Ala His Pro Ile Ala Ala Ala Asn
 465 Cys Pro Gly Gly Cys 485 Gly Pro Gly Ile Val Asp Ala Ala Glu Ala Val
 Lys Ala Ala Ser Asn 500

<210> 49

<211> 1545

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 49

atgaaaaaca	tgatgaaaaa	aatgacaact	atactggcgg	ttacatctgc	tggttgTTTT	60
gcactaagcc	tgacatcggt	agcggtagca	gaagggtataa	aaaaagcaga	gccggcagca	120
gagcgtgaac	ttagcctggt	tgacctggca	gaagataaaa	ccaaccgtta	cattattaaa	180
tttaaagagc	cggctcgca	gatgagtgca	accggcacag	agcagcgcg	tgagttctcg	240
gtacaacgtg	cacagcaagt	gctgcaaaaa	gccaacgtta	acgcactgtc	acatttaaaa	300
tcagtgcattg	ccagtgtagc	cgagctgact	cctaaacagc	tgaagttact	gcaggcta	360
cctgacgttg	aatacattga	agaagatcat	aaacgttacc	tgatggatgt	gatcacgcct	420
atggcacaaa	ccacacctta	tggtattacc	atggtgcagg	ctaatacagg	aagtgatggc	480
agtgtctggca	atacaaaagt	gtgctgtatt	gataccggtt	ggacttcagg	ccatgaagat	540
ttacaaaact	cgggcgtgac	gggatattct	ttttccggcc	acggtaactg	gtatcaggac	600
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tctggcaact	ggaccacagc	ttcaaatctg	atcacggcta	ttcagtcctg	taaagatgcc	780
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cgtgatacgt	cttacgggtg	gggtattgtc	aaagccaaag	ctgcacatga	ttacttaacc	1260
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aacctgtcag	caaccagtgg	ccagtgggta	agaggcagtt	accagatccc	ttcaggtgta	1380
tcaacggtaa	ctttccagat	atccggcggt	agcggtgatg	ccgatctata	tggttaactat	1440
ggtagtgaac	cgagcacaa	aacctataac	tgccggcctt	acctgaatgg	taacaatgaa	1500
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<210> 50

<211> 515

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(30)

<400> 50

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			20					25					30		
Ile	Lys	Lys	Ala	Glu	Pro	Ala	Ala	Glu	Arg	Glu	Leu	Ser	Leu	Val	Asp
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Leu	Ala	Glu	Asp	Lys	Thr	Asn	Arg	Tyr	Ile	Ile	Lys	Phe	Lys	Glu	Pro
	50					55					60				
Val	Ala	Gln	Met	Ser	Ala	Thr	Gly	Thr	Glu	Gln	Arg	Ala	Glu	Phe	Ser
65					70					75					80
Val	Gln	Arg	Ala	Gln	Gln	Val	Leu	Gln	Lys	Ala	Asn	Val	Asn	Ala	Leu
			85						90					95	
Ser	His	Leu	Lys	Ser	Val	His	Ala	Ser	Val	Ala	Glu	Leu	Thr	Pro	Lys
			100					105					110		
Gln	Leu	Lys	Leu	Leu	Gln	Ala	Asn	Pro	Asp	Val	Glu	Tyr	Ile	Glu	Glu
		115					120					125			
Asp	His	Lys	Arg	Tyr	Leu	Met	Asp	Val	Ile	Thr	Pro	Met	Ala	Gln	Thr
	130					135					140				
Thr	Pro	Tyr	Gly	Ile	Thr	Met	Val	Gln	Ala	Asn	Gln	Val	Ser	Asp	Gly
145					150					155					160
Ser	Ala	Gly	Asn	Thr	Lys	Val	Cys	Val	Ile	Asp	Thr	Gly	Trp	Thr	Ser
			165						170					175	
Gly	His	Glu	Asp	Leu	Gln	Asn	Ser	Gly	Val	Thr	Gly	Tyr	Ser	Phe	Ser
		180						185					190		
Gly	His	Gly	Asn	Trp	Tyr	Gln	Asp	Gly	Asn	Gly	His	Gly	Thr	His	Val
		195					200					205			
Ala	Gly	Thr	Met	Val	Ala	Leu	Asn	Asn	Asn	Ser	Gly	Val	Val	Gly	Val
	210					215					220				
Ile	Gly	Ser	Gly	Gln	Ala	Gly	Val	His	Ile	Val	Lys	Ile	Phe	Asn	Asn
225					230					235					240
Ser	Gly	Asn	Trp	Thr	Ala	Ser	Asn	Leu	Ile	Thr	Ala	Ile	Gln	Ser	
			245					250					255		
Cys	Lys	Asp	Ala	Gly	Ala	Lys	Val	Val	Asn	Met	Ser	Leu	Gly	Gly	Ser
		260						265					270		
Ser	Ser	Asn	Gln	Thr	Glu	Asn	Thr	Ala	Met	Thr	Asn	Phe	Tyr	Asn	Gly
		275					280					285			
Gly	Met	Leu	Leu	Val	Ala	Ala	Gly	Asn	Ala	Gly	Asn	Thr	Ser	Phe	
	290					295				300					
Ser	Tyr	Pro	Ala	Ser	Tyr	Asn	Ala	Val	Val	Ser	Val	Ala	Ala	Val	Asn
305					310					315					320
Ser	Ser	Gly	Ala	Leu	Ala	Ser	Phe	Ser	Gln	Arg	Asn	Ser	Gln	Val	Glu
			325						330					335	
Ile	Ser	Gly	Pro	Gly	Val	Asn	Val	Asn	Ser	Thr	Trp	Asn	Asn	Gly	Gly

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Tyr Asn Ser 340 Ile Ser Gly Thr Ser 345 Met Ala Ser Pro His 350 Val Ala Gly
 Val Ala 355 Leu Val Trp Ser 360 His Pro Gln Cys 365 Thr Ala Ala Gln
 Ile Arg Asn Ala Leu Asn Ala Thr Ala Glu Asp Arg Gly Ala Val Gly
 385 Arg Asp Thr Ser Tyr 390 Gly Trp Gly Ile Val Lys Ala Lys Ala Ala His
 Asp Tyr Leu Thr Asn Asn Gly Cys Gly Gly Gly Gly Ser Asn 415 Pro
 Pro Thr Gly 420 Ala Thr Phe Pro Asn Leu Ser Ala Thr Ser Gly Gln
 Trp Leu Arg Gly Ser Tyr Gln Ile Pro Ser Gly Val 445 Thr Val Thr
 Phe Gln Ile Ser Gly Gly Ser Gly Asp Ala Asp 460 Leu Tyr Val Asn Tyr
 465 Gly Thr Glu Pro Ser 470 Thr Thr Tyr Asn Cys Arg Pro Tyr Leu Asn
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<210> 51

<211> 2874

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 51

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gtctcctccc	agccgggcat	gcgccatggc	agcctgttca	accagctggc	gatgcacctg	1980
gtcgaagccgg	cgtcgggcag	cggtgcgggc	agcgtgctgtg	ctggacgcag	ccacggcatc	2040
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agccacacca tcggtggcat cgtggtcggt gccgataccc gcgtggccga tgaccgcgtg 2160
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ggtgtgacca gccgtgccag cgagcggctg tccatcatgg ccgattatgt gggtgagcgc 2820
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<210> 52
 <211> 957
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(27)

<400> 52

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20      25      30
Gln Asp Asp Arg Val Phe Leu Ser Gly Gly Val Thr Val Ala Asp Val
35      40      45
Val Ala Leu Pro Ala Leu Leu Ala Lys Ala Gln Ala Glu Gly Arg Pro
50      55      60
Ile Arg Glu Val Val Leu Arg Thr Ser Asn Gly Ala Leu Ile Ala
65      70      75      80
Gly Glu Trp Leu Gln Ala Val Ile Arg Thr Gln Gly Leu Asp Thr Ile
85      90      95
Val Ser Gly His Cys Ile Ser Ser Cys Ser Ile Met Gln Ser Gly Gly
100     105     110
Val Asn Arg Tyr Leu Gly Gly Asp Leu Pro Leu Val Asp Ser Val Gln
115     120     125
Ile His Ala Ala Ser Ser Gly Arg Ile Thr Tyr Ala Pro Ser Ala
130     135     140
Arg Met Thr Gln Ile Tyr Thr Gly Asn Tyr Gly Gly Met Asp Ala
145     150     155     160
Gly Leu Leu His Lys Ala Met Tyr Glu Val Val Gln Pro Asn Gly Leu
165     170     175
Leu Val Phe Arg Asp Pro Ala Arg Thr Thr Gly Thr Ser Val Thr Phe
180     185     190
Asp Pro Asp Gly Ser Gly Ser Lys Leu Glu Ser Phe Pro Gly Gln Asp
195     200     205
Ile Arg Ser Asn Ser Ile Ile Asn Thr Ala Gly Tyr Arg Asp Pro Gly
210     215     220
Asp Thr Leu Arg Val Thr Ser Asn Val Ser Gly Asp Ile Asn Pro Gly
225     230     235     240
Tyr Leu Arg Thr Ala Arg Gln Leu Gln Ala Phe Val Asp Asp Asp Phe
245     250     255
Ala Arg Trp Asn Thr Asp Trp Ala Ser Thr Tyr Ile Asn Tyr Ala Val
260     265     270
Ser Leu Tyr Asn Phe Ser Thr Arg Gly Ala Asn Gly Ile Gly Ala Gln
275     280     285
Ser Leu Gln Gln Leu Leu Ala Asp Pro Asp Leu Gln Asp Glu Leu Arg
290     295     300
Gly Gln Leu Arg Leu Ala Asp Leu Asp Ala Ser Thr Leu Ala Asn Ser
305     310     315     320
Ala Gly Val Ile Arg Val Ser Asn Gly Ala Thr Trp Arg Thr Ala Glu
325     330     335

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Thr	Thr	Gly	Ala	Asp	Phe	Ile	Leu	Val	Asp	Asn	Gly	Thr	Ile	Ala	Leu
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		355					360					365			
Ile	Val	Val	Gly	Arg	Gly	Asp	Ile	Ala	Ser	Val	Gly	Thr	Asp	Ser	Asp
	370					375					380				
Ala	Leu	Leu	Asp	Gly	Thr	Gly	Pro	Ser	Tyr	Arg	Glu	Asp	Gly	Phe	Asn
385					390					395					400
Arg	Leu	Arg	Val	Phe	Gly	Thr	Leu	Met	Pro	Arg	Gly	Gly	Asp	Leu	Val
				405					410					415	
Thr	His	Gly	Tyr	Val	Asn	Ile	Met	Pro	Gly	Gly	Gln	Val	Leu	Phe	Asp
			420					425					430		
Val	Thr	Glu	Thr	Gly	Gly	Thr	Gly	Ser	Gly	Arg	Leu	Arg	Val	Gly	Ser
		435					440					445			
Phe	Tyr	Asp	Gly	Gly	Ala	Glu	Glu	Gly	Ala	Leu	Val	Ile	Ala	Gln	Gly
	450					455					460				
Ala	His	Leu	Ala	Leu	Asn	Val	Ala	Gln	Gly	Phe	Tyr	Ala	Gly	Ala	Tyr
465					470					475					480
Arg	Arg	Asp	Leu	Val	Glu	Gly	Pro	Ile	Tyr	Gln	Gly	Gly	Phe	Gln	Asp
				485					490					495	
Val	Val	Arg	Leu	Gly	Asp	Ala	Gly	Tyr	Ser	Ala	Ser	Ile	Thr	Ala	Gly
			500					505					510		
Glu	Val	Phe	Arg	Pro	Arg	His	Asn	Ser	Leu	Leu	Ser	Phe	Asn	Val	Lys
		515					520					525			
Gln	Thr	Ala	Asp	Gly	Leu	Trp	Leu	Thr	Ala	Asn	Pro	Gly	Phe	Asp	Gln
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Leu	Gly	Leu	Phe	Ala	Asn	Gly	Thr	Ser	Gly	Asp	Gly	Leu	Gly	Arg	Ala
545					550					555					
Leu	Ala	Thr	Ala	Ser	Asp	Arg	Gln	Asp	Lys	Gly	Leu	Arg	Ser	Leu	Leu
				565					570					575	
Gly	Ala	Leu	Gln	Phe	Ala	Asp	Arg	Asp	Val	Ile	Ala	Gln	Gln	Ala	Gly
			580					585					590		
Ala	Leu	Arg	Gly	Asp	Ala	His	Ala	Ser	Leu	Arg	Leu	Ala	Asp	Thr	Ala
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Leu	Val	Gly	Ser	Ile	Gly	Asn	Val	Val	Gln	Gln	His	Gln	Ser	Ala	Met
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Arg	Ser	Gly	Gly	Asp	Ala	Asp	Gly	Leu	Ala	Ser	Gln	Val	Ala	Gln	Ser
625					630					635					640
Val	Ser	Ser	Gln	Pro	Gly	Met	Arg	His	Gly	Ser	Leu	Phe	Asn	Gln	Leu
				645					650					655	
Ala	Met	His	Leu	Val	Glu	Pro	Ala	Ser	Gly	Ser	Val	Ala	Gly	Ser	Ala
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Asp	Ala	Gly	Arg	Ser	His	Gly	Ile	Trp	Ala	Arg	Gly	Phe	Ala	Ser	His
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705					710					715					720
Thr	Leu	Gly	Val	Ser	Val	Ala	Ala	Ala	Asp	Met	Ser	Thr	Lys	Ala	Ser
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Asp	Gly	Ser	Gly	Phe	Thr	Gly	Asp	Val	Arg	Ala	Leu	Asp	Val	Gly	Gly
			740					745					750		
Tyr	Leu	Asp	Ala	Thr	Tyr	Ala	Arg	Gly	Tyr	Leu	Ser	Ala	Ala	Val	Arg
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Tyr	Thr	Asp	Leu	Arg	His	Asp	Thr	Arg	Arg	Ser	Ile	Asn	Gly	Ile	Asp
	770					775					780				
Gly	Leu	Gln	Gln	Pro	Leu	Arg	Ala	Lys	Tyr	Ser	Asn	Asp	Ala	Ile	Ser
785					790					795					800
Ala	Arg	Val	Glu	His	Ala	Phe	Ser	Phe	Thr	Thr	Ala	Lys	Gly	Leu	Val
				805					810					815	
Ile	Gln	Pro	Leu	Leu	Pro	Val	Val	Asp	Tyr	Ala	Arg	Thr	Ser	Ala	Thr
			820					825					830		
Arg	Phe	Asn	Glu	Gly	Gln	Gly	Ala	Gly	Ala	Leu	Val	Gly	Arg	Ser	Gly
		835					840					845			
Ser	Leu	Glu	Ser	Ile	Arg	Val	Gly	Ala	Gly	Leu	Gln	Leu	Phe	Lys	Thr
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Phe	Glu	Gly	Asn	Asn	Gly	Glu	Arg	Ile	Thr	Pro	Arg	Ala	Arg	Val	Val
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 Ala Ala Ala Pro Asp Leu Val Phe Gly Ala Ser Ser Gln Ala Val Gly
 900 905 910
 Glu Gln Val Leu Ala Trp Asn Leu Gly Val Thr Ser Arg Ala Ser Glu
 915 920 925
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<210> 53
 <211> 2580
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 53
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 aagggcgcg ccgccacgac gacgcgcacg gtcaccgtga agatgcccga caccggcaat 2220
 cctgaccccc ctggcgacac ctggagcgta ccggtgtgag ccgacgcaga caccgcttg 2280
 ctcggtcagg cgtgtggacg gatgggactg acggccaaga aggtggaatc ccgctacctc 2340
 atgggtctgg tgcccgcgg cactccccgc ctgaccgtca cgtcgggtgg cgggagcgg 2400
 gacgccaacc tgtacgtcag ccactacggc tggccgagcc cgcagaacca cgtggcgcg 2460
 tcgaccaact cgggcaagg cgaacaggtg gtggtcgagt ggcggcatc gggctggaac 2520
 tacgtcgcgc tgcacggagt caaggacttc gcgaactgta gcgcggtcgc ccactactga 2580

<210> 54
 <211> 859
 <212> PRT
 <213> Unknown

10336256.txt

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(32)

<400> 54

Met	Thr	Gln	Arg	Met	Met	Gln	Arg	Gly	Ala	Thr	Met	Leu	Leu	Ser	Ile
1				5					10					15	
Ala	Val	Cys	Ala	Gly	Leu	Ala	Leu	Thr	Ala	Pro	Thr	Thr	Ala	Phe	Ala
		20						25					30		
Ser	Thr	Pro	Ala	Thr	Ala	Pro	Thr	His	Asp	Asp	Ser	Glu	Ala	Ala	Pro
		35					40					45			
Ser	Tyr	Ile	Ser	Gly	Leu	Val	Asp	Pro	Gln	Ser	Glu	Glu	Glu	Val	Ser
	50				55						60				
Ala	Thr	Pro	Pro	Ile	Ser	Ala	Asn	Thr	Asp	Ala	Leu	His	Thr	Val	Val
	65				70					75					80
Gly	Glu	Ala	Asp	Ala	Glu	Pro	Glu	Arg	Pro	Ser	Met	Gln	Thr	Arg	Ala
			85						90					95	
Thr	Ala	Lys	Ser	Ile	Ala	Ala	Val	Cys	Thr	Ala	Ala	Asp	Phe	Ala	Gln
			100					105					110		
Ala	Ser	Gly	Glu	Ala	Leu	Val	Thr	Leu	Ile	Lys	Gly	Ser	Thr	Thr	Asp
		115					120					125			
Cys	Val	Asn	Thr	Leu	Phe	Ser	Val	Lys	Gly	Ser	Gln	Ala	Ala	Ser	Ile
	130					135					140				
Phe	Thr	Glu	Ala	Lys	Met	Val	Thr	Ala	Ala	Asn	Gly	Leu	Arg	Ala	Val
	145				150					155					160
Ala	Gln	Ser	Tyr	Thr	Gly	Asp	Asn	Ser	Gly	Ser	Ala	Ala	Gln	Leu	Val
				165					170					175	
Leu	Phe	Leu	Arg	Ala	Gly	Tyr	Tyr	Val	Gln	Trp	Tyr	Asp	Ser	Ser	Val
			180					185					190		
Pro	Ala	Phe	Gly	Thr	Ala	Leu	Arg	Ser	Ala	Val	Ser	Ala	Ala	Leu	Asp
		195					200					205			
Glu	Phe	Phe	Asn	Ser	Pro	Arg	Ser	Lys	Asp	Val	Thr	Asp	Ala	Asn	Gly
	210					215					220				
Glu	Thr	Leu	Ser	Glu	Ala	Val	Thr	Leu	Ile	Asp	Ser	Ala	Glu	Leu	Asn
	225				230					235					240
Asp	Arg	Tyr	Ile	His	Val	Val	Lys	Arg	Leu	Leu	Thr	Asp	Tyr	Asn	Ala
				245					250					255	
Gly	Tyr	Asn	Ser	Ser	Trp	Trp	Met	Met	Asn	Ala	Val	Asn	Gly	Thr	Phe
			260					265					270		
Thr	Val	Leu	Phe	Arg	Gly	His	Gln	Val	Pro	Ala	Phe	Val	Gln	Lys	Val
		275					280					285			
Ala	Ser	Asp	Thr	Ser	Leu	Leu	Thr	Thr	Leu	Arg	Asp	Phe	Ala	Leu	Gly
	290					295					300				
His	Thr	Asp	Leu	Leu	Ala	Gly	Glu	Asn	Ala	Tyr	Leu	Val	Thr	Asn	Ala
	305				310					315					320
Gly	Arg	Glu	Leu	Gly	Arg	Phe	Leu	Gly	Asp	Ala	Pro	Ile	Lys	Ala	Ala
				325					330					335	
Val	Lys	Pro	Met	Val	Lys	Ala	Val	Leu	Asp	Gln	Thr	Ser	Leu	Asp	Gly
			340					345					350		
Pro	Thr	Ser	Gly	Leu	Trp	Val	Ala	Leu	Ala	Glu	Met	Ala	Asp	Trp	Tyr
		355					360					365			
Asp	Lys	Thr	Asp	Cys	Ser	Tyr	Tyr	Gly	Thr	Cys	Asn	Leu	Gln	Glu	Arg
	370					375					380				
Ile	Glu	Ala	Lys	Val	Leu	Pro	Thr	Thr	His	Val	Cys	Ser	Pro	Ser	Ile
	385				390					395					400
Thr	Ile	Arg	Ala	Gln	Asp	Met	Asn	Ala	Glu	Gln	Leu	Thr	Ala	Ser	Cys
				405					410					415	
Ala	Ser	Leu	Asn	Ala	Gln	Asp	Ala	Tyr	Phe	His	Ala	Val	Ala	Lys	Asp
			420					425					430		
Pro	Gly	Pro	Val	Pro	Gly	Asp	Val	Asn	Thr	Lys	Ile	Glu	Val	Val	Val
		435					440					445			
Phe	Asp	Ser	Ser	Thr	Glu	Tyr	Gln	Ala	Tyr	Ala	Gly	Thr	Leu	Phe	Gly
	450					455					460				
Ile	Asp	Thr	Asn	Asn	Gly	Gly	Met	Tyr	Leu	Glu	Gly	Asp	Pro	Thr	Lys
	465				470					475					480

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Thr Asn Asn Lys Ala Arg Phe Ile Ala Tyr Glu Ala Glu Trp Leu Arg
 485 490 495
 Pro Glu Phe Ala Ile Trp Asn Leu Asn His Glu Tyr Thr His Tyr Leu
 500 505 510
 Asp Gly Arg Phe Asn Met His Gly Asp Phe Thr Glu Asn Ile Ser Thr
 515 520 525
 Pro Thr Ile Trp Trp Val Glu Gly Phe Ala Glu Tyr Ile Ser Tyr His
 530 535 540
 Tyr Arg Gln Met Pro Tyr Thr Ala Ala Gln Gln Leu Ala Ala Thr Gly
 545 550 555 560
 Gln Tyr Lys Leu Ser Gln Leu Phe Asp Thr Thr Tyr Asp His Asp Thr
 565 570 575
 Asp Arg Ile Tyr Arg Trp Gly Tyr Leu Ala Val Ser Phe Met Leu Asn
 580 585 590
 Lys His Pro Ile Glu Met Gln Ala Val Leu Gly Asn Tyr Arg Ser Gly
 595 600 605
 Asn Trp Asn Ala Ala Arg Ser Tyr Leu Lys Asn Ser Ile Gly Thr Thr
 610 615 620
 Tyr Asp Ala Glu Phe Thr Ala Phe Leu Ala Glu Cys Ala Gln Gly Asn
 625 630 635 640
 Cys Ser Ala Asp Leu Gly Gly Gly Gly Glu Pro Pro Arg Asn Gln Ala
 645 650 655
 Pro Thr Ala Ala Phe Thr Val Ala Thr Asn Gly Leu Thr Ala Thr Phe
 660 665 670
 Thr Asp Gly Ser Ser Asp Pro Asp Gly Gln Ile Ala Ser Arg Ala Trp
 675 680 685
 Asp Phe Gly Asn Gly Arg Thr Ser Thr Glu Lys Asn Pro Ser Val Thr
 690 695 700
 Tyr Ala Gln Ala Gly Ser Phe Thr Val Ala Leu Thr Val Lys Asp Asp
 705 710 715 720
 Lys Gly Ala Thr Ala Thr Thr Arg Thr Val Thr Val Lys Met Pro
 725 730 735
 Asp Thr Gly Asn Pro Asp Pro Gly Gly Asp Thr Trp Ser Val Pro Val
 740 745 750
 Cys Ala Asp Ala Asp Thr Arg Leu Leu Gly Gln Ala Cys Gly Arg Met
 755 760 765
 Gly Leu Thr Ala Lys Lys Gly Glu Ser Arg Tyr Leu Met Val Trp Val
 770 775 780
 Pro Ala Gly Thr Pro Arg Leu Thr Val Thr Ser Gly Gly Gly Ser Gly
 785 790 795 800
 Asp Ala Asn Leu Tyr Val Ser His Tyr Gly Trp Pro Ser Pro Gln Asn
 805 810 815
 His Val Ala Arg Ser Thr Asn Ser Gly Asn Gly Glu Gln Val Val Val
 820 825 830
 Glu Trp Pro Ala Ser Gly Trp Asn Tyr Val Ala Leu His Gly Val Lys
 835 840 845
 Asp Phe Ala Asn Val Ser Ala Val Ala His Tyr
 850 855

<210> 55

<211> 2022

<212> DNA

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 55

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ttt	tc	cgcca	tcg	gtt	tcgc	ggg	cg	agg	cg	aac	atcc	atc	tcg	atg	cgct	cac	cg	aggg	120
atc	ccg	tacg	acc	gctt	cat	cg	tca	agtt	cgc	gat	ggca	gcc	cct	gag	ca	tgt	gaat	gcc	180
ggc	gc	acgcg	agc	agg	cgct	ggt	cg	cgcc	gct	cg	cggt	cag	ggc	ctg	ca	gct	cg	gccat	240
ctg	cg	tcggc	tgg	ccat	cg	tg	ccg	ac	ctg	gtc	ga	agt	gt	cg	acca	agct	gcc	ggca	300
gcg	gc	cgagg	cct	tgat	gcg	cg	cg	ctgg	ca	cg	aat	ccga	ac	gtc	gaata	cg	tcg	agccg	360
gac	gc	gatca	tg	cg	ctcg	gct	ca	cgcc	g	aac	gata	ccc	g	ctac	cccc	ga	ccag	tgg	420
tact	tc	gagg	cc	acc	ggtg	cg	ca	atct	t	ccc	cg	gctt	ggg	aca	agg	c	cac	cg	480
ggc	gt	ggtcg	tc	gc	ggtg	ct	gc	ac	ccgg	c	agc	ac	gatt	c	ac	agc	gat	ct	540
acc	gt	cgccg	gct	ac	gactt	cat	cag	cag	c	tcg	ac	gac	g	cg	cg	ac	g	gtc	600

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gatgccaaacc	ctcgcgacga	aggcgattgg	gtcagcgcca	acgagtgcgg	ctacacccat	660
ccggcacaga	actcgagctg	gcatggcacc	cacgtcgccg	gcaccatcgg	cgcggtcacc	720
aacaacgcca	agggcggtgg	cggcgtggcc	ttcggcgcca	aggtgcagca	tgtgcgcgtg	780
ctcggccggg	gtggcggtgc	gttgctcgac	atcgccgatg	cgatcgtgtg	ggcctcgggt	840
ggcagtgtca	gcgggtgtgcc	cgccaatgcc	acgcccggcg	aggtgatcaa	catgagcctg	900
gggggacagc	gcagctgcgg	ttcgacctat	caggccgcga	tcgattcggc	agtgaaccgc	960
ggcagcgtgg	tcgtggctcg	tgccggcaac	gacaacgtca	acgtgtccaa	cgcgctccg	1020
gccaactgca	acaacgtgat	cgcggtggcg	gccaccgatc	gcaacggcgc	acgtgccagt	1080
ttctccaact	acggcagcct	gatcgacgtc	tcggcgccag	gtgtgggtat	ctggtcgacg	1140
ctcaattcgg	gtaccaccac	gccgggcagc	gagagctacg	ccgcctacaa	cggcacctcg	1200
atggcgacac	cgcacgtggc	cggcacatcg	gcgctgatgc	aaagcgtatc	ggccaagacc	1260
ccggccagg	tggagcagat	tctcaaggac	acggcgcgct	cgctgccggg	tgcctgctcc	1320
ggcggttgcg	gggcccggcat	cgctcgacgc	ctggcgccgg	tgaatgccgc	gatcggcggg	1380
ggcgcgcgca	acgtgctgca	gaacgggtgtc	accgtgaccg	gcctggctgc	cagcaccggc	1440
aacgcgctca	actacacgat	ggaggtgccc	gccggtgcc	ccaacctgca	gttcgcgatc	1500
agcggtggca	ccggcgatgc	tgatctctac	gtcaagttcg	gcagcgacac	gaccgacagc	1560
agctacgact	ggcgctcccta	caagtcgggc	aatgccgaga	gctgcagctt	cgccacgccc	1620
gccgcccggga	cctggcacgt	gcgctggaag	gcctattcga	ccttttcggg	ggtcagcctg	1680
accggcagtt	acactccgcc	gagcagcgcg	ccgtgcagcg	actgcaccaa	gtacagcggc	1740
tcgctttccg	gcagcggcag	cgcacagatc	cagcccagcg	gcagctacta	ccagtcgacc	1800
atctccggca	cgcaccaggg	ctggctcaag	ggctccggctg	gtaccgactt	cgatctggag	1860
ttgtaccgct	ggaacggcag	cagctggagt	cggtcgcgcg	gtgcccgcgac	cagcggctcg	1920
gaggaaacgc	tcagctacag	cggcgcggcc	ggctattact	actggcggat	cggtgtctat	1980
acgggcagcg	gcagctacga	cttctggctc	aagcggccct	ga		2022

<210> 56

<211> 673

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(27)

<400> 56

Met	Arg	Lys	Ser	Asn	Arg	Thr	Leu	Arg	Leu	Gln	Ser	Leu	Ala	Ala	Ala
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Thr	Leu	Phe	Ala	Phe	Ser	Ala	Ile	Gly	Phe	Ala	Gly	Glu	Ala	Asn	Ile
		20						25				30			
His	Leu	Asp	Ala	Leu	Thr	Glu	Gly	Ile	Pro	Tyr	Asp	Arg	Phe	Ile	Val
		35					40				45				
Lys	Phe	Arg	Asp	Gly	Ser	Pro	Glu	His	Val	Asn	Ala	Gly	Ala	Arg	Glu
	50					55				60					
Gln	Ala	Leu	Val	Ala	Ala	Ala	Arg	Gly	Gln	Gly	Leu	Gln	Leu	Gly	His
65				70				75						80	
Leu	Arg	Arg	Leu	Ala	Ile	Gly	Ala	Asp	Leu	Val	Glu	Val	Ser	Thr	Lys
			85					90					95		
Leu	Pro	Ala	Lys	Ala	Ala	Glu	Ala	Leu	Met	Arg	Ala	Leu	Ala	Arg	Asn
			100					105				110			
Pro	Asn	Val	Glu	Tyr	Val	Glu	Pro	Asp	Ala	Ile	Met	Arg	Ser	Leu	Leu
		115					120					125			
Thr	Pro	Asn	Asp	Thr	Arg	Tyr	Pro	Asp	Gln	Trp	His	Tyr	Phe	Glu	Ala
	130					135					140				
Thr	Gly	Gly	Ala	Asn	Leu	Pro	Ala	Ala	Trp	Asp	Lys	Ala	Thr	Gly	Ser
145				150						155					160
Gly	Val	Val	Val	Ala	Val	Leu	Asp	Thr	Gly	Ser	Thr	Ile	His	Ser	Asp
			165					170						175	
Leu	Asp	Ala	Asn	Thr	Val	Ala	Gly	Tyr	Asp	Phe	Ile	Ser	Ser	Ser	Thr
			180					185					190		
Thr	Ala	Arg	Asp	Gly	Asn	Gly	Arg	Asp	Ala	Asn	Pro	Arg	Asp	Glu	Gly
		195					200					205			
Asp	Trp	Val	Ser	Ala	Asn	Glu	Cys	Gly	Tyr	Thr	His	Pro	Ala	Gln	Asn
	210					215					220				
Ser	Ser	Trp	His	Gly	Thr	His	Val	Ala	Gly	Thr	Ile	Gly	Ala	Val	Thr
225					230					235					240
Asn	Asn	Ala	Lys	Gly	Val	Ala	Gly	Val	Ala	Phe	Gly	Ala	Lys	Val	Gln

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His Val Arg Val 245 Leu Gly Arg Cys Gly 250 Gly Ala Leu Ser Asp 255 Ile Ala
 Asp Ala Ile Val 260 Trp Ala Ser Gly 265 Gly Ser Val Ser Gly 270 Val Pro Ala
 Asn Ala 275 Thr Pro Ala Glu Val 280 Ile Asn Met Ser Leu 285 Gly Gly Ser Gly
 Ser 290 Cys Gly Ser Thr Tyr 295 Gln Ala Ala Ile Asp 300 Ser Ala Val Asn Arg
 305 Gly Ser Val Val 310 Val Ala Ala Gly Asn 315 Asp Asn Val Asn Val Ser
 Asn Ala Arg Pro 325 Ala Asn Cys Asn 330 Val Ile Ala Val Ala Thr
 Asp Arg Asn 340 Gly Ala Arg Ala Ser 345 Phe Ser Asn Tyr Gly 350 Ser Leu Ile
 Asp Val 355 Ser Ala Pro Gly Val 360 Gly Ile Trp Ser Thr 365 Leu Asn Ser Gly
 Thr 370 Thr Thr Pro Gly Ser 375 Glu Ser Tyr Ala Ala 380 Tyr Asn Gly Thr Ser
 385 Met Ala Thr Pro His 390 Val Ala Gly Ile Val 395 Ala Leu Met Gln Ser Val
 Ser Ala Lys Thr 405 Pro Ala Gln Val Glu 410 Gln Ile Leu Lys Asp 415 Thr Ala
 Arg Pro Leu 420 Pro Gly Ala Cys Ser 425 Gly Gly Cys Gly Ala Gly Ile Val
 Asp Ala 435 Leu Ala Ala Val Asn 440 Ala Ala Ile Gly Gly 445 Gly Gly Asn
 Val 450 Leu Gln Asn Gly Val 455 Thr Val Thr Gly Leu Ala Ala Ser Thr Gly
 465 Asn Ala Leu Asn Tyr 470 Thr Met Glu Val Pro 475 Ala Gly Ala Thr Asn Leu
 Gln Phe Ala Ile 485 Ser Gly Gly Thr Gly 490 Asp Ala Asp Leu Tyr Val Lys
 Phe Gly Ser 500 Ala Pro Thr Asp 505 Ser Tyr Asp Cys Arg 510 Pro Tyr Lys
 Ser Gly Asn Ala Glu Ser 515 Cys Ser Phe Ala Thr Pro 525 Ala Ala Gly Thr
 Trp 530 His Val Arg Val Lys 535 Ala Tyr Ser Thr Phe 540 Ser Gly Val Ser Leu
 545 Thr Gly Ser Tyr Thr 550 Pro Pro Ser Ser Ala 555 Pro Cys Ser Asp Cys Thr
 Lys Tyr Ser Gly 560 Ser Leu Ser Gly Ser 565 Gly Ser Ala Gln Ile Gln Pro
 Asp Gly Ser 570 Tyr Tyr Gln Ser Thr 575 Ile Ser Gly Thr His 580 Gln Gly Trp
 Leu Lys 585 Gly Pro Ala Gly Thr 590 Asp Phe Asp Leu Glu 595 Leu Tyr Arg Trp
 Asn 600 Gly Ser Ser Trp Ser 605 Arg Val Ala Arg Ala 610 Thr Ser Gly Ser
 625 Glu Glu Thr Leu Ser 630 Tyr Ser Gly Ala Ala 635 Gly Tyr Tyr Tyr Trp Arg
 Ile Val Ser Tyr 645 Thr Gly Ser Gly Ser 650 Tyr Asp Phe Trp Leu 655 Lys Arg
 Pro 660

<210> 57
 <211> 1293
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 57

gtggcaccgg	tgacgacgac	ctaccgtacg	gccgccctgc	tcgccgcggg	caccctcacc	60
gccctcctcg	cggcccccgg	ccaggcctcc	gccgccggcc	ccacgagcgg	cccggccggc	120
gtgccccgcc	ccgcgggacc	cgctcctggac	ggcagcggcg	agtgcacctt	cccgatgaag	180

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aagcagatcg	agggcacccc	ctggccgctc	cagcgggtcc	tcctcgacga	gctgtggcag	240
gacaccaagg	gcaagggcgt	ccgggtcgcg	gtcatcgaca	cgggcgtcga	cgacgtcaac	300
ccgcagctga	agcaggccgt	cgacgccaag	gcgggcaagg	actacctcaa	gcccgcacaag	360
aagaacccgg	gcttcggcga	cgagctgcgc	ggcaagaccg	acggcaccgt	cgacgaggtc	420
ggccacggca	ccaaggtcgc	cgggatcatc	gccgcccggc	cccggcccgg	caccggcttc	480
gtcggcctcg	cgcccagggc	gacgatcatc	ccgatccggc	agaacgacga	gaagaacagc	540
ggcaagtccg	acacgatggc	cgaggccatc	aagtggggccg	tcgccaaggg	cgcccacgtc	600
atcaacatct	cgcaggacac	caccagccg	ctggacgccg	actcgccgat	ggccaaggcg	660
atcgccctcg	cgctgtccaa	gcagatcgtc	gtggtcgcct	ccgccggcaa	cgacggcatg	720
gacggctccc	tgaagaagac	ctatccggcc	gcgttccccg	gcgtcctcgc	cgtcgcctcc	780
tccgaccgga	acaacgagcg	ggccgcgttc	tcccagtcgg	gcaccttcgt	gggcgtcgcc	840
gcccccgggc	tcgacgtcgt	ctccaccgtg	cccggcgggc	gccagtgctg	cgacaacggc	900
accagcttct	cgcggccgta	cgtcggcggc	gtcgcggccc	tgctgcgcgc	caagtacccg	960
gagtggaccg	cggcgagat	cgtcacccgg	atcgagcaga	ccgccgtccg	ccccgtcaag	1020
gggcgggaca	accacgtggg	ctggggcggtg	gtcgacccgg	tgcgggcgct	cgccgacacc	1080
cccggcacgc	cgccctcctc	gcccacggcc	gacccggggc	cgcccaagcc	gccggctccc	1140
gagccggccc	gactggcgct	gtcggagagc	cctcaggagc	gctccgaacg	gctcgccacc	1200
tacacgttgg	ggatcgggtg	cgtcctgggtg	gccgtggctg	ccggaaccgc	catcgtgatc	1260
cgcgacagcc	gccgcccggag	ggaggcccg	tga			1293

<210> 58
 <211> 430
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(31)

<400> 58

Met	Ala	Pro	Val	Thr	Thr	Thr	Tyr	Arg	Thr	Ala	Ala	Leu	Leu	Ala	Ala
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Gly	Thr	Leu	Thr	Ala	Leu	Leu	Ala	Ala	Pro	Gly	Gln	Ala	Ser	Ala	Ala
			20					25					30		
Gly	Pro	Thr	Ser	Gly	Pro	Ala	Gly	Val	Pro	Arg	Pro	Ala	Gly	Pro	Val
		35					40					45			
Leu	Asp	Gly	Ser	Gly	Glu	Cys	Thr	Phe	Pro	Met	Lys	Lys	Gln	Ile	Glu
	50					55					60				
Gly	Thr	Pro	Trp	Pro	Leu	Gln	Arg	Val	Leu	Leu	Asp	Glu	Leu	Trp	Gln
	65				70					75					80
Asp	Thr	Lys	Gly	Lys	Gly	Val	Arg	Val	Ala	Val	Ile	Asp	Thr	Gly	Val
				85					90					95	
Asp	Asp	Val	Asn	Pro	Gln	Leu	Lys	Gln	Ala	Val	Asp	Ala	Lys	Ala	Gly
			100					105					110		
Lys	Asp	Tyr	Leu	Lys	Pro	Asp	Lys	Lys	Asn	Pro	Gly	Phe	Gly	Asp	Glu
		115					120					125			
Leu	Arg	Gly	Lys	Thr	Asp	Gly	Thr	Val	Asp	Glu	Val	Gly	His	Gly	Thr
	130					135					140				
Lys	Val	Ala	Gly	Ile	Ile	Ala	Ala	Arg	Pro	Arg	Pro	Gly	Thr	Gly	Phe
	145				150					155					160
Val	Gly	Leu	Ala	Pro	Glu	Ala	Thr	Ile	Ile	Pro	Ile	Arg	Gln	Asn	Asp
				165					170					175	
Glu	Lys	Asn	Ser	Gly	Lys	Ser	Asp	Thr	Met	Ala	Glu	Ala	Ile	Lys	Trp
			180					185						190	
Ala	Val	Ala	Lys	Gly	Ala	His	Val	Ile	Asn	Ile	Ser	Gln	Asp	Thr	Thr
		195					200						205		
Gln	Pro	Leu	Asp	Ala	Asp	Ser	Pro	Met	Ala	Lys	Ala	Ile	Ala	Leu	Ala
	210					215					220				
Leu	Ser	Lys	Gln	Ile	Val	Val	Val	Ala	Ser	Ala	Gly	Asn	Asp	Gly	Met
	225				230					235					240
Asp	Gly	Ser	Leu	Lys	Lys	Thr	Tyr	Pro	Ala	Ala	Phe	Pro	Gly	Val	Leu
				245					250					255	
Ala	Val	Ala	Ser	Ser	Asp	Arg	Asn	Asn	Glu	Arg	Ala	Ala	Phe	Ser	Gln
			260					265					270		
ser	Gly	Thr	Phe	Val	Gly	Val	Ala	Ala	Pro	Gly	Val	Asp	Val	Val	Ser
		275					280					285			

10336256.txt

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Thr Val Pro Gly Gly Gly Gln Cys Val Asp Asn Gly Thr Ser Phe Ser
290 295 300
Ala Pro Tyr Val Ala Gly Val Ala Ala Leu Leu Arg Ala Lys Tyr Pro
305 310 315
Glu Trp Thr Ala Ala Gln Ile Val Thr Arg Ile Glu Gln Thr Ala Val
325 330 335
Arg Pro Val Lys Gly Arg Asp Asn His Val Gly Trp Gly Val Val Asp
340 345 350
Pro Val Arg Ala Leu Ala Asp Thr Pro Gly Thr Pro Pro Ser Ser Pro
355 360 365
Thr Pro Asp Pro Gly Pro Pro Lys Pro Pro Ala Pro Glu Pro Ala Arg
370 375 380
Leu Ala Leu Ser Glu Thr Pro Gln Glu Arg Ser Glu Arg Leu Ala Thr
385 390 395
Tyr Thr Leu Gly Ile Gly Val Val Leu Val Ala Val Val Ala Gly Thr
400 405 410 415
Ala Ile Val Ile Arg Asp Ser Arg Arg Arg Glu Ala Arg
420 425 430

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<210> 59
 <211> 1203
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

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<400> 59
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accaccgagg acatctcccg cgatggggcg gcggtggcct cgggcgagaa cctcgaaatg      180
gtcggctacg acgtcaacca gtacgaggcg ccgatactga tggccgcct cactaacgag      240
gagatcgccg agctgaagaa gaacaaggac gtcgcccggg tggaggacga cggcgagatg      300
tacgcccttg agatcaaggc gcccgaaggc tggggctcca gccaggggct cggcatccag      360
ggcatctccc gcgataccgg gatccagtcg gaccatcccg atctcgtcca gaacctgaaa      420
gtctacatcc tcgataccgg gatccagtcg gaccatcccg atctcgtcca gaacctgaaa      480
gcgggcaaga gcttcgtgac caacgagagc tcgaccgagg acttccacgg ccacggcacc      540
cactgcgccc gcaccgtcgc cgccgccttc aacaacttcg gcgtcgtcgg cgtcgccccg      600
ttcgccctatc tctacccggt gaaggttctc tcggcgaccg gcagcgcca gtggagctgg      660
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ggcgtcctgc tcgtcgccgc cgccggcaac aacggccctg gcaacaacac ggtcggcttc      840
ccggcggaagt acccccacgt catggccgtg tcggcggtcg acagcaacga ccagatcgcc      900
agcttctcga gccgtgggcc ggaggtcgag atccgcggcg ccggcggtga ggtgctctcg      960
accatccgca actccggcta cggccggatg agcggcacct cgatggcctg cccgcacgctc      1020
gccggcgccg ccgcgctcgc ctggggctcg caccgcggcc acaacaacaa gcagatccgc      1080
tggctgctca acgtctttgc ggacaaggtc ggcgaccagg acccgagca ctacggcaac      1140
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<210> 60
 <211> 400
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

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<400> 60
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20 25 30
Ile Ser Ser Arg Leu Arg Phe Leu Thr Thr Glu Asp Ile Ser Arg Asp
35 40 45
Gly Arg Ala Val Ala Ser Gly Glu Asn Leu Glu Met Val Gly Tyr Asp
50 55 60
Val Asn Gln Tyr Glu Ala Pro Ile Leu Met Ala Arg Leu Thr Asn Glu

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	Val	Leu	Ser	Gln	Thr	Ile	Pro	Thr	Gly	Ile	Ser	Gln	Ile	Lys	Ala	Pro
	Glu	Ala	Trp	Gly	Ser	Ser	Gln	Gly	Leu	Gly	Ile	Gln	Val	Tyr	Ile	Leu
	Asp	Thr	Gly	Ile	Gln	Ser	Asp	His	Pro	Asp	Leu	Val	Gln	Asn	Leu	Lys
	Ala	Gly	Lys	Ser	Phe	Val	Thr	Asn	Glu	Ser	Ser	Thr	Glu	Asp	Phe	His
	Gly	His	Gly	Thr	His	Cys	Ala	Gly	Thr	Val	Ala	Ala	Ala	Phe	Asn	Asn
	Phe	Gly	Val	Val	Gly	Val	Ala	Pro	Phe	Ala	Tyr	Leu	Tyr	Pro	Val	Lys
	Val	Leu	Ser	Ala	Thr	Gly	Ser	Gly	Gln	Trp	Ser	Trp	Leu	Ile	Ala	Gly
	Leu	Asp	Trp	Val	Ala	Ser	Lys	Lys	Gly	His	Arg	Ile	Ala	Ser	Met	Ser
	Leu	Gly	Gly	Gly	Gly	Ala	Pro	Gln	Ala	Leu	Ala	Asp	Met	Cys	Glu	Ala
	Val	Tyr	Asn	Lys	Gly	Val	Leu	Leu	Val	Ala	Ala	Ala	Gly	Asn	Asn	Gly
	Pro	Gly	Asn	Thr	Val	Gly	Phe	Pro	Ala	Lys	Tyr	Pro	His	Val	Met	
	Ala	Val	Ser	Ala	Val	Asp	Ser	Asn	Asp	Gln	Ile	Ala	Ser	Phe	Ser	Ser
	Arg	Gly	Pro	Glu	Val	Glu	Ile	Ala	Ala	Pro	Gly	Val	Gln	Val	Leu	Ser
	Thr	Ile	Arg	Asn	Ser	Gly	Tyr	Gly	Arg	Met	Ser	Gly	Thr	Ser	Met	Ala
	Cys	Pro	His	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ala	Trp	Gly	Ser	His	Arg
	Gly	His	Asn	Asn	Lys	Gln	Ile	Arg	Trp	Leu	Leu	Asn	Val	Phe	Ala	Asp
	Lys	Val	Gly	Asp	Gln	Asp	Pro	Gln	His	Tyr	Gly	Asn	Gly	Arg	Val	Asn
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<210> 61
 <211> 1824
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 61

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gcgcaaggcg	cgggcatgct	cgaccagacc	gatcgccctga	tcgtcaagta	caagggcgaa	180
tccgcaccga	gcgccaaggg	cctgacccgc	gccgcccgcct	acgtgccgat	ggccgcatcg	240
cgcaaggccg	tggtcgacca	ggtcggccgc	aagcacagcc	tgacgggtcca	ggaactgcac	300
gcgatcggtg	ccggcgcccgc	cgctgtcaag	ctgaaccgca	aggtctcggg	ggccgaggcc	360
gccaagctcg	ccgccgaact	ggcagccagc	gatgtctcga	tcgagtacgc	cgagccggac	420
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atccgcgtgg	ccgtgatcga	caccggctac	cgcccgcacg	tcgacctgca	gggcccagatc	600
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ggcggcggcg	cttgcgacac	caccacccag	accgcaatca	acggcgcccc	ctcgcgcccc	1020

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accgtggtcgc	tggtcgcggc	cggcaacgag	aaccagaacg	ccagcaacag	cagccccggcc	1080
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<210> 62
 <211> 607
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(40)

<400> 62

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			20					25					30		
Ala	Gly	Ala	Ala	Thr	Ala	Ser	Ala	Ala	Gln	Gly	Ala	Gly	Met	Leu	Asp
			35					40					45		
Gln	Thr	Asp	Arg	Leu	Ile	Val	Lys	Tyr	Lys	Gly	Glu	Ser	Ala	Pro	Ser
						55					60				
Ala	Lys	Gly	Leu	Thr	Arg	Ala	Ala	Ala	Tyr	Val	Pro	Met	Ala	Ala	Ser
65					70					75					80
Arg	Lys	Ala	Val	Val	Asp	Gln	Val	Gly	Arg	Lys	His	Ser	Leu	Thr	Val
				85					90					95	
Gln	Glu	Leu	His	Ala	Ile	Gly	Thr	Gly	Ala	Arg	Val	Leu	Lys	Leu	Asn
			100					105					110		
Arg	Lys	Val	Ser	Val	Ala	Glu	Ala	Ala	Lys	Leu	Ala	Ala	Glu	Leu	Ala
			115					120					125		
Ala	Ser	Asp	Ala	Ser	Val	Glu	Tyr	Ala	Glu	Pro	Asp	Arg	Ile	Met	Lys
			130			135					140				
Pro	Met	Phe	Thr	Pro	Asn	Asp	Thr	Tyr	Tyr	Asn	Gln	Gln	Trp	Asp	Tyr
145					150					155					160
Phe	Asp	Ala	Val	Gly	Gly	Met	Asn	Met	Pro	Ala	Ala	Trp	Asp	Lys	Ser
				165					170					175	
Thr	Gly	Thr	Gly	Ile	Arg	Val	Ala	Val	Ile	Asp	Thr	Gly	Tyr	Arg	Pro
			180					185					190		
His	Val	Asp	Leu	Gln	Gly	Gln	Ile	Leu	Ala	Gly	Tyr	Asp	Phe	Ile	Ile
			195				200					205			
Asp	Thr	Ala	Ile	Ser	Asn	Asp	Gly	Asn	Gly	Arg	Asp	Ser	Asp	Ala	Ser
			210			215					220				
Asp	Pro	Gly	Asp	Trp	Thr	Val	Ala	Gly	Gln	Cys	Gly	Thr	Gly	Ser	Ala
225					230					235					240
Ala	Ser	Asn	Ser	Ser	Trp	His	Gly	Thr	His	Val	Ala	Gly	Thr	Ile	Ala
				245					250					255	
Ala	Leu	Thr	Asn	Asn	Gly	Met	Gly	Val	Ala	Gly	Val	Ala	Tyr	Asn	Ala
			260					265					270		
Lys	Val	Val	Pro	Val	Arg	Val	Leu	Gly	Gln	Cys	Gly	Gly	Tyr	Thr	Ser
			275				280					285			
Asp	Ile	Ala	Asp	Gly	Ile	Ile	Trp	Ala	Ser	Gly	Gly	Thr	Val	Ser	Gly
			290			295					300				
Val	Thr	Asn	Ile	Ala	Ala	Arg	Ala	Gln	Val	Ile	Asn	Met	Ser	Leu	Gly
305					310					315					320
Gly	Gly	Gly	Ala	Cys	Asp	Thr	Thr	Thr	Gln	Thr	Ala	Ile	Asn	Gly	Ala

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Arg	Ser	Arg	Gly	325	Thr	Val	Val	Val	Val	330	Ala	Ala	Gly	Asn	Glu	335	Asn	Gln
Asn	Ala	Ser	340	Asn	Ser	Ser	Pro	Ala	345	Asn	Cys	Ser	Gly	Val	350	Ile	Thr	Val
Ala	Ala	355	Thr	Asn	Lys	Ser	Gly	360	Gly	Lys	Ala	Ser	Tyr	365	Ser	Asn	Tyr	Gly
Thr	370	Ile	Val	Asp	Val	Ala	375	Ala	Pro	Gly	Gly	Asp	380	Ser	Gly	Ala	Ala	Ile
385	Leu	Ser	Thr	Leu	Asn	390	Ala	Gly	Thr	Thr	Thr	Pro	395	Gly	Ala	Asp	Asn	Tyr
Val	Gly	Tyr	Met	405	Gly	Thr	Ser	Met	410	Ala	Thr	Pro	415	His	Val	Ala	Gly	Val
Val	Ala	Leu	Met	420	Leu	Ala	Lys	Asn	425	Pro	Asn	Leu	430	Thr	Pro	Asp	Glu	Val
Glu	Ala	Lys	Leu	435	Lys	Ser	Ser	Ala	440	Arg	Ala	Phe	445	Pro	Ala	Ala	Cys	Ser
Gly	450	Cys	Gly	Ala	Gly	Ile	Val	Asp	455	Ala	Ser	Ala	460	Ala	Ile	Asp	Ala	Ala
465	Val	Gly	Thr	Gly	470	Gly	Thr	Thr	475	Met	Ser	Glu	480	Thr	Glu	Ser	Asn	Asn
Thr	Ile	Ser	Thr	485	Ala	Asn	Ala	Val	490	Ser	Thr	Ser	495	Gly	Thr	Thr	Val	Asn
Gly	Asn	Met	Gly	500	Ser	Thr	Thr	Asp	505	Ser	Asp	Tyr	510	Phe	Ser	Val	Gln	Leu
Pro	Ala	Gly	Lys	515	Thr	Leu	Thr	520	Ser	Thr	Leu	Thr	525	Pro	Asn	Ala	Thr	Ser
Asp	530	Tyr	Asp	Leu	Tyr	Ile	Tyr	535	Asn	Ser	Ala	Gly	540	Thr	Gln	Ile	Thr	Ser
545	Ser	Thr	Asn	Gly	550	Gly	Ser	Val	555	Asp	Ser	Ala	560	Ser	Val	Ile	Asn	Asn
Gly	Thr	Thr	Thr	565	Thr	Thr	Ala	Tyr	570	Val	Arg	Val	575	Lys	Tyr	Tyr	Ser	Gly
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<210> 63

<211> 1869

<212> DNA

<213> Archea

<400> 63

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gagaagaagg	agaccgagat	atgggtggcc	gatatccaga	ccctgagcgc	caagaaagtc	300
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atagtcttcg	ttcacggcgg	gccgaagggc	atgtacggac	accgcttcgt	ctacgagatg	1200
cagctgatgg	cgagcaaggg	ctactacgtc	gtcttcgtga	acccgcgcgg	cagcgacggc	1260
tatagcgaag	acttcgcgct	ccgcgtcctg	gagaggactg	gcttgaggga	ctttgaggac	1320
ataatgaacg	gcatacgagga	gttcttcaag	ctcgaaccgc	aggccgacag	ggagcgcggt	1380
ggaataacgg	gcataagcta	cggcggcttc	atgaccaact	gggccttgac	tcagagcgac	1440
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tcggacatag	ggctctggta	cgacgtcgag	gtcatcgggc	caaatccgtt	agagaacgag	1560

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gggaactga						1869

<210> 64
 <211> 622
 <212> PRT
 <213> Archea

<400> 64

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			20					25					30		
Lys	Ala	Asn	Met	Lys	Asp	Asn	Lys	Tyr	Glu	Ser	Thr	Val	Val	Val	Glu
		35					40					45			
Asp	Leu	Glu	Thr	Gly	Ser	Arg	Arg	Phe	Ile	Glu	Asn	Ala	Ser	Met	Pro
	50					55					60				
Arg	Ile	Ser	Pro	Asp	Gly	Arg	Lys	Leu	Ala	Phe	Thr	Cys	Phe	Asn	Glu
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Glu	Lys	Lys	Glu	Thr	Glu	Ile	Trp	Val	Ala	Asp	Ile	Gln	Thr	Leu	Ser
				85					90					95	
Ala	Lys	Lys	Val	Leu	Ser	Thr	Lys	Asn	Val	Arg	Ser	Met	Gln	Trp	Asn
			100					105					110		
Asp	Asp	Ser	Arg	Arg	Leu	Leu	Val	Val	Gly	Phe	Lys	Arg	Arg	Asp	Asp
		115					120					125			
Glu	Asp	Phe	Val	Phe	Asp	Asp	Val	Pro	Val	Trp	Val	Phe	Asp	Asn	Met
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Gly	Phe	Phe	Asp	Gly	Glu	Lys	Thr	Thr	Phe	Trp	Val	Leu	Asp	Thr	Glu
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Ala	Glu	Glu	Ile	Ile	Glu	Gln	Phe	Glu	Lys	Pro	Arg	Phe	Ser	Ser	Gly
				165					170					175	
Leu	Trp	His	Gly	Asp	Ala	Ile	Val	Val	Asn	Val	Pro	His	Arg	Glu	Gly
			180					185					190		
Ser	Lys	Pro	Ala	Leu	Phe	Lys	Phe	Tyr	Asp	Ile	Val	Leu	Trp	Lys	Asp
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Ile	Ser	Glu	His	Asp	Trp	Leu	Tyr	Leu	Trp	Asp	Gly	Glu	Leu	Lys	Pro
				245					250					255	
Ile	Tyr	Glu	Gly	Pro	Leu	Asp	Val	Trp	Glu	Ala	Lys	Leu	Thr	Glu	Gly
			260					265					270		
Lys	Val	Tyr	Phe	Leu	Thr	Pro	Asp	Ala	Gly	Arg	Val	Asn	Leu	Trp	Leu
		275					280					285			
Trp	Asp	Gly	Lys	Ala	Glu	Arg	Val	Val	Thr	Gly	Asp	His	Trp	Ile	Tyr
	290					295					300				
Gly	Leu	Asp	Val	Ser	Asp	Gly	Lys	Ala	Leu	Leu	Leu	Ile	Met	Thr	Ala
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Thr	Arg	Ile	Gly	Glu	Leu	Tyr	Leu	Tyr	Asp	Gly	Glu	Leu	Lys	Gln	Val
				325					330					335	
Thr	Glu	Tyr	Asn	Gly	Pro	Ile	Phe	Arg	Lys	Leu	Lys	Thr	Phe	Glu	Pro
			340					345					350		
Arg	His	Phe	Arg	Phe	Lys	Ser	Lys	Asp	Leu	Glu	Ile	Asp	Gly	Trp	Tyr
		355					360					365			
Leu	Arg	Pro	Glu	Val	Lys	Glu	Glu	Lys	Ala	Pro	Val	Ile	Val	Phe	Val
	370					375					380				
His	Gly	Gly	Pro	Lys	Gly	Met	Tyr	Gly	His	Arg	Phe	Val	Tyr	Glu	Met
385					390					395					400
Gln	Leu	Met	Ala	Ser	Lys	Gly	Tyr	Tyr	Val	Val	Phe	Val	Asn	Pro	Arg
			405						410				415		
Gly	Ser	Asp	Gly	Tyr	Ser	Glu	Asp	Phe	Ala	Leu	Arg	Val	Leu	Glu	Arg
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Thr	Gly	Leu	Glu	Asp	Phe	Glu	Asp	Ile	Met	Asn	Gly	Ile	Glu	Glu	Phe

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435 440 445
 Phe Lys Leu Glu Pro Gln Ala Asp Arg Glu Arg Val Gly Ile Thr Gly
 450 455 460
 Ile Ser Tyr Gly Gly Phe Met Thr Asn Trp Ala Leu Thr Gln Ser Asp
 465 470 475 480
 Leu Phe Lys Ala Gly Ile Ser Glu Asn Gly Ile Ser Tyr Trp Leu Thr
 485 490 495
 Ser Tyr Ala Phe Ser Asp Ile Gly Leu Trp Tyr Asp Val Glu Val Ile
 500 505 510
 Gly Pro Asn Pro Leu Glu Asn Glu Asn Phe Arg Lys Leu Ser Pro Leu
 515 520 525
 Phe Tyr Ala Gln Asn Val Lys Ala Pro Ile Leu Leu Ile His Ser Leu
 530 535 540
 Glu Asp Tyr Arg Cys Pro Leu Asp Gln Ser Leu Met Phe Tyr Asn Val
 545 550 555 560
 Leu Lys Asp Met Gly Lys Glu Ala Tyr Ile Ala Ile Phe Lys Arg Gly
 565 570 575
 Ala His Gly His Ser Val Arg Gly Ser Pro Arg His Arg Pro Lys Arg
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 610 615 620

<210> 65
 <211> 1740
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

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 cagtccgcac agaccaccca gcgtttcatc gtgaagtacc gcgacggcag cgcgccgggtg 180
 gccaacacca ccgcactggc ctcttcgctg aagagcgccg ccgccggcct ggccagcagc 240
 cagggccgcg cgtgggcct gcagcaggtc cgcaagctgg ccgtcggccc caccctgggtc 300
 aagaccgatc gtccgctcga ccaggccgaa tccgagcagc tgatgcgcaa gctggccgccc 360
 gacccgaacg tgggaatacgt tgaagtgcac cagatcatgc gtgccacgct gaccccgaa 420
 gacacccgct tcagcgagca atggggcttc ggtacctcca atgccggcat caacatccgg 480
 ccggcctggg acaaggccac cggcaccggc gtggtcgtgg cggtgatcga caccggcatc 540
 accaaccacg ccgacctcaa tgccaacatc ctgcccgggt acgacttcat cagtgatgcg 600
 gcatggcgcc gcgacggcaa aggctacccg ggttccaact ccagtgaggg tgactggtac 660
 ggcgacaacg agtgccaggc aggtgaccaac aacagcaccg gcgtggcagg tactgcgttc 720
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 aacgccaagg tcgtgcccgt gtccggcgcc agcgtcagcg gcgtgccggc caatgccaat 840
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 ccggccgagg tcatcaatct ctcgctcgcc accaccgtgg tggctcgtgc cggcaacagc 1020
 aacgcgatca atggcgctgt cgggcgtggc aactgcccga acgtgatcgc agtggcggcc 1080
 aacaccaacg tgctctcgtc ggttcccggc tccaactatg gcaacggcat cgacatctcg 1140
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 1740

<210> 66
 <211> 579
 <212> PRT
 <213> Unknown

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<220>

<223> Obtained from an environmental sample.

<400> 66

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Gly Ala Ser Val Leu Ser Ser Leu Leu Ala Thr Pro Ala Leu Ala
20      25      30
Gly Asp Val Gln Leu Ser Gly Leu Gln Ser Ala Gln Thr His Gln Arg
35      40      45
Phe Ile Val Lys Tyr Arg Asp Gly Ser Ala Pro Val Ala Asn Thr Thr
50      55      60
Ala Leu Ala Ser Ser Leu Lys Ser Ala Ala Ala Gly Leu Ala Ser Ser
65      70      75      80
Gln Gly Arg Ala Leu Gly Leu Gln Gln Val Arg Lys Leu Ala Val Gly
85      90      95
Pro Thr Leu Val Lys Thr Asp Arg Pro Leu Asp Gln Ala Glu Ser Glu
100      105      110
Gln Leu Met Arg Lys Leu Ala Ala Asp Pro Asn Val Glu Tyr Val Glu
115      120      125
Val Asp Gln Ile Met Arg Ala Thr Leu Thr Pro Asn Asp Thr Arg Phe
130      135      140
Ser Glu Gln Trp Gly Phe Gly Thr Ser Asn Ala Gly Ile Asn Ile Arg
145      150      155      160
Pro Ala Trp Asp Lys Ala Thr Gly Thr Gly Val Val Val Ala Val Ile
165      170      175
Asp Thr Gly Ile Thr Asn His Ala Asp Leu Asn Ala Asn Ile Leu Pro
180      185      190
Gly Tyr Asp Phe Ile Ser Asp Ala Ala Met Ala Arg Asp Gly Asn Gly
195      200      205
Arg Asp Asn Asn Pro Asn Asp Glu Gly Asp Trp Tyr Asp Asn Glu
210      215      220
Cys Gln Ala Gly Tyr Pro Gly Ser Asn Ser Ser Trp His Gly Thr His
225      230      235      240
Val Ala Gly Thr Val Ala Val Thr Asn Asn Ser Thr Gly Val Ala
245      250      255
Gly Thr Ala Phe Asn Ala Lys Val Val Pro Val Arg Val Leu Gly Lys
260      265      270
Cys Gly Gly Tyr Thr Ser Asp Ile Ala Asp Ala Ile Val Trp Ala Ser
275      280      285
Gly Gly Ser Val Ser Gly Val Pro Ala Asn Ala Asn Pro Ala Glu Val
290      295      300
Ile Asn Leu Ser Leu Gly Gly Gly Ser Cys Ser Ser Thr Tyr Gln
305      310      315      320
Asn Ala Ile Asn Gly Ala Val Gly Arg Gly Thr Thr Val Val Ala
325      330      335
Ala Gly Asn Ser Asn Thr Asn Val Ser Ser Ser Val Pro Ala Asn Cys
340      345      350
Pro Asn Val Ile Ala Val Ala Ala Thr Thr Ser Ala Gly Ala Arg Ala
355      360      365
Ser Phe Ser Asn Tyr Gly Asn Gly Ile Asp Ile Ser Ala Pro Gly Gln
370      375      380
Gly Ile Leu Ser Thr Leu Asn Ser Gly Thr Thr Thr Pro Gly Ser Ala
385      390      395      400
Ser Tyr Ala Ser Tyr Asn Gly Thr Ser Met Ala Ala Pro His Val Ala
405      410      415
Gly Val Val Ala Leu Met Gln Ser Val Ala Pro Ser Pro Leu Ser Pro
420      425      430
Ala Gln Val Glu Ser Ile Ile Lys Ser Thr Ala Arg Pro Leu Pro Gly
435      440      445
Ala Cys Ser Gly Gly Cys Gly Ala Gly Ile Ile Asp Ala Asp Ala Ala
450      455      460
Val Ala Ala Ala Ile Asn Gly Gly Gly Pro Asn Pro Gly Gly Asn Val
465      470      475      480
Leu Gln Asn Asn Val Pro Val Thr Gly Leu Gly Ala Ala Ser Gly Ala
485      490      495
Ser Leu Ser Tyr Thr Val Asn Val Pro Ala Gly Ser Thr Gln Leu Arg
500      505      510

```


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Val Ala Ile Ser Gly Gly Ser Gly Asp Ala Asp Leu Tyr Val Arg Gln
 515 520 525
 Gly Ser Ala Pro Thr Asp Thr Ala Tyr Thr Cys Arg Pro Tyr Leu Ser
 530 535 540
 Gly Asn Ser Glu Thr Cys Thr Ile Asn Ser Pro Ala Ala Gly Thr Trp
 545 550 555 560
 Tyr Val Arg Val Lys Ala Tyr Ser Thr Phe Ser Gly Leu Thr Leu Asn
 565 570 575
 Ala Gln Tyr

<210> 67
 <211> 1854
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 67

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accgcccac	cgggcgccga	gcgcatcatc	gtcaagtacc	gggctggcgc	tgctgccgcc	180
accgaccgt	cggcgaagct	gtctaccgtg	caatcggcgc	tgacccgggc	cagcctgtcc	240
ggcgggtacct	cacgtgccag	taccctcggc	ccgcaggtgg	tacgcaagct	cgctaccggt	300
gcggacctga	tccgcgtgca	gggcccgcctg	gccccggccg	aactgcagcg	tgtgctgaag	360
gaactgcagg	ccgacccgtc	ggtgcagtac	gccgaagccg	acgtgaagct	gcgccgcacc	420
gagctgctg	ccggcgatgt	gcagccggca	ctggtgccga	acgatccctt	ctaccagcag	480
aaccagtggc	acctgcacaa	tgcggtcggc	ggcatcaacg	caccggcggc	atgggatgtc	540
tcgcaggggc	aaggcatcgt	ggtggcggtg	atcgataccg	gcacccctgc	gcagcatccg	600
gacctggttg	gcaacctgtt	ggagggttac	gatttcatca	gcgacgccga	gacctcgcg	660
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aacgagtgt	acgacggctc	gctggccgag	gacagctcct	ggcacggcac	ccatgtggcc	780
ggtaccgtcg	ccgagcagac	caacaatggc	gtcggcatgg	ccggtgtcgc	ctacaaggcc	840
aagggtgctgc	cggtgcgctg	gctggggcaag	tgcggcggtc	acctgtccga	catcgccgac	900
gcggtggtct	gggcatcggg	tggcacgggtg	accggcatcc	cggccaaacac	caaccgggcc	960
gagatcatca	acatgagcct	gggcggcagc	ggcgccctgc	gcagcaccta	ccaggacgcc	1020
atcaacggcg	ccatctcgcg	cggtaccacg	gtggtggtgg	cgcccgccaa	tgagaccgac	1080
aacgcgtcca	agtaccgtcc	ggccagctgc	gaaggcggtg	tgaccgtggg	tgcgacccgt	1140
atcaccggcg	gcacaccta	ctactccaac	tacggcaccc	gcgtggatct	gtccggcccg	1200
ggcggcggtg	gcagcgtcga	cggaatccc	ggtggctaca	tctggcagac	cggtccaat	1260
gcggcgacca	cgccggattc	gggtacgccc	ggctacatgg	gcagggcgcg	cacctcgatg	1320
gcctcgccgc	atgtggccgc	cggtgctgca	ctggtgcaga	gcgcgctgat	cgccaagggc	1380
aaggatccgc	tgaccccggc	ggccatgctg	accctgctga	aggaaaccgc	gcgtccgttc	1440
ccggtcgcca	tcccggcggc	caccccgatc	ggtaccggca	tcctcgacgc	caaggccgcg	1500
ctggccaagg	caactggaaga	gccgtgcacc	gagaactgcg	gaccggtggc	cacgccgctg	1560
accaacaagg	cgccatcggg	cggtctgtcc	ggtgcggctg	gcagcagcaa	gctttacagc	1620
ttcgaagcgg	ccgccggcaa	gcagttcagc	gtgatcacct	acggcggcac	cggcaatggt	1680
tcggtctacg	tggtgaagg	ccgtgagccc	agtgccagcg	acaacgacgc	caagtcgacc	1740
cgtccgggca	cctccgagac	agtgcgggtg	accaagccgg	tggcggccac	ctactacatc	1800
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<210> 68
 <211> 617
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(27)

<400> 68

Met	Ile	Lys	Lys	Gln	Asn	Leu	Arg	Ile	Asn	Val	Leu	Ala	Ala	Ala	Val
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Leu	Ser	Met	Thr	Ala	Val	Gly	Ala	Val	His	Ala	Ala	Gly	Leu	Pro	Thr
			20					25					30		

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Arg	Glu	Pro	Val	Arg	Gln	Ala	Ser	Thr	Ala	Gln	Pro	Gly	Ala	Glu	Arg
Ile	Ile	35	Val	Lys	Tyr	Arg	Ala	Ala	Ala	Ala	Ala	Thr	Asp	Arg	Ser
Ala	Lys	50	Leu	Ser	Thr	Val	Gln	Ser	Ala	Leu	Thr	Arg	Ala	Ser	Leu
65	Gly	Gly	Thr	Ser	Arg	Ala	Ser	Thr	Leu	Gly	Pro	Gln	Val	Val	Arg
80	Leu	Ala	Thr	Gly	Ala	Asp	Leu	Ile	Arg	Val	Gln	Gly	Arg	Leu	Ala
95	Ala	Glu	Leu	Gln	Arg	Val	Leu	Lys	Glu	Leu	Gln	Ala	Asp	Pro	Ser
110	Gln	Tyr	Ala	Glu	Ala	Asp	Val	Lys	Leu	Arg	Arg	Thr	Glu	Leu	Arg
125	Gly	Asp	Val	Gln	Pro	Ala	Leu	Val	Pro	Asn	Asp	Pro	Phe	Tyr	Gln
140	Asn	Gln	Trp	His	Leu	His	Asn	Ala	Val	Gly	Ile	Asn	Ala	Pro	Ala
155	Ala	Trp	Asp	Val	Ser	Gln	Gly	Glu	Gly	Ile	Val	Val	Ala	Val	Ile
170	Thr	Gly	Ile	Leu	Pro	Gln	His	Pro	Asp	Leu	Val	Gly	Asn	Leu	Leu
185	Gly	Tyr	Asp	Phe	Ile	Ser	Asp	Ala	Glu	Thr	Ser	Arg	Arg	Pro	Thr
200	Asp	Arg	Val	Pro	Gly	Ala	Leu	Asp	Gln	Gly	Asp	Trp	Val	Glu	Asn
215	Asn	Glu	Cys	Tyr	Asp	Gly	Ser	Leu	Ala	Glu	Asp	Ser	Ser	Trp	His
230	Thr	His	Val	Ala	Gly	Thr	Val	Ala	Glu	Gln	Thr	Asn	Asn	Gly	Val
245	Met	Ala	Gly	Val	Ala	Tyr	Lys	Ala	Lys	Val	Leu	Pro	Val	Arg	Val
260	Gly	Lys	Cys	Gly	Gly	Tyr	Leu	Ser	Asp	Ile	Ala	Asp	Ala	Val	Val
275	Ala	Ser	Gly	Gly	Thr	Val	Thr	Gly	Ile	Pro	Ala	Asn	Thr	Asn	Pro
290	Glu	Ile	Ile	Asn	Met	Ser	Leu	Gly	Gly	Ser	Gly	Ala	Cys	Gly	Ser
305	Tyr	Gln	Asp	Ala	Ile	Asn	Gly	Ala	Ile	Ser	Arg	Gly	Thr	Thr	Val
320	Val	Ala	Ala	Gly	Asn	Glu	Thr	Asp	Asn	Ala	Ser	Lys	Tyr	Arg	Pro
335	Ser	Cys	Glu	Gly	Val	Val	Thr	Val	Gly	Ala	Thr	Arg	Ile	Thr	Gly
350	Ile	Thr	Tyr	Tyr	Ser	Asn	Tyr	Gly	Thr	Arg	Val	Asp	Leu	Ser	Gly
365	Gly	Gly	Gly	Gly	Ser	Val	Asp	Gly	Asn	Pro	Gly	Gly	Tyr	Ile	Trp
380	Thr	Gly	Ser	Asn	Ala	Ala	Thr	Thr	Pro	Asp	Ser	Gly	Thr	Pro	Gly
395	Met	Gly	Met	Gly	Gly	Thr	Ser	Met	Ala	Ser	Pro	His	Val	Ala	Ala
410	Ala	Ala	Leu	Val	Gln	Ser	Ala	Leu	Ile	Ala	Lys	Gly	Lys	Asp	Pro
425	Thr	Pro	Ala	Ala	Met	Arg	Thr	Leu	Leu	Lys	Glu	Thr	Ala	Arg	Pro
440	Pro	Val	Ala	Ile	Pro	Ala	Ala	Thr	Pro	Ile	Gly	Thr	Gly	Ile	Leu
455	Ala	Lys	Ala	Ala	Leu	Ala	Lys	Ala	Leu	Glu	Glu	Pro	Cys	Thr	Glu
470	Cys	Gly	Pro	Val	Ala	Thr	Pro	Leu	Ser	Lys	Leu	Tyr	Ser	Phe	Glu
485	Leu	Ser	Gly	Ala	Ala	Gly	Ser	Ser	Lys	Leu	Tyr	Ser	Phe	Glu	Ala
500	Ala	Gly	Lys	Gln	Phe	Ser	Val	Ile	Thr	Tyr	Gly	Gly	Thr	Gly	Asn
515	Ser	Val	Tyr	Val	Ala	Glu	Gly	Arg	Glu	Pro	Ser	Ala	Ser	Asp	Asn
530	Ala	545	565												

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Ala Lys Ser Thr Arg Pro Gly Thr Ser Glu Thr Val Arg Val Thr Lys
 580 585 590
 Pro Val Ala Thr Tyr Tyr Ile Lys Val Val Gly Glu Ala Ala Tyr
 595 600 605
 Asn Gly Val Ser Ile Leu Ala Thr Gln
 610 615

<210> 69
 <211> 1740
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 69
 atgtcccagg taacgcaacc gcgtgtgcgt cgagtgtggg tggctccttgg tgcgtccggt 60
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 cagtccgcgc cgacgcatca gcgcttcctc gtgaagtacc gcgacggcag tgcgcccgtg 180
 gccagcacca ccgcactggc ttcttcgctg aagagtgcg ccgccggcct ggccagcagc 240
 cagggccgcg cgctgggcct gcaggaggtc cgcaagctgg ccgtcggccc gaccctgggtc 300
 aggaccgacc gtccgctcga ccaggccgaa tccgagctgc tgatgcgcaa gctcggcgcg 360
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 gacacccgct tcagcgaaca atggggcttc ggtacctcca acgcgtcgat caacgtgcag 480
 ccggcctggg acaaggccac cggcaccggc gtgggtgggtg ccgtgatcga taccggcatc 540
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 gtcgcccggc ccgtggcggc ggtgaccaac aacagcaccg gcgtggccgg tactgcgttc 780
 aatgccaagg tcgtcccggg gcgctgtgctc ggcaagtgcg gcggttacac ctccgacatc 840
 gccgacgcga tcgtgtgggc ttctggcggc acggtcagtg gcgtgcccgc caatgccaac 900
 ccggccgaag tcatcaacat gtcgctgggc ggcggcgga cctgctcggc cactaccag 960
 aatgcatca acggcgcggt cagccgtggt accaccgtgg tgggtgccgc cggcaacagc 1020
 aacaccaacg tgcctcgtc ggtgccggcc aactgcgcga acgtgatcgc ggtggcggcc 1080
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 agctacgcgt cctacaacgg cacctcgatg gcggcgccgc atgtggccgg cgtgggtgca 1260
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 gccaacgcgg ccgtggccgc agcgatcaat ggcggtggcc cgaacccggg cggcaatgtg 1440
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 gatgccgacc tgtacgtgcg ccagggcagt gccccgacc ataccactta cacctgccgt 1620
 ccgtacctga gcggcaacag cgagacctgc accatcaaca gccctgccgc cggcacctgg 1680
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<210> 70
 <211> 579
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(32)

<400> 70
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 Gly Ala Ser Val Leu Ser Ser Leu Leu Ala Thr Pro Ala Leu Ala
 20 25 30
 Gly Asp Val Gln Leu Ser Gly Leu Gln Ser Ala Pro Thr His Gln Arg
 35 40 45
 Phe Ile Val Lys Tyr Arg Asp Gly Ser Ala Pro Val Ala Ser Thr Thr
 50 55 60
 Ala Leu Ala Ser Ser Leu Lys Ser Ala Ala Ala Gly Leu Ala Ser Ser
 65 70 75 80

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Gln	Gly	Arg	Ala	Leu	Gly	Leu	Gln	Glu	Val	Arg	Lys	Leu	Ala	Val	Gly
Pro	Thr	Leu	Val	85	Thr	Asp	Arg	Pro	90	Leu	Asp	Gln	Ala	95	Glu
Leu	Leu	Met	Arg	100	Lys	Leu	Ala	105	Asp	Pro	Asn	Val	110	Val	Glu
Val	Asp	115	Gln	Ile	Met	Arg	Ala	120	Thr	Leu	Thr	Pro	125	Asp	Phe
Ser	130	Gln	Trp	Gly	Phe	135	Thr	Ser	Asn	Ala	140	Ile	Asn	Val	Gln
145	Glu	Gln	Trp	Asp	Lys	150	Ala	Thr	Gly	Thr	Gly	Val	Val	Val	Ile
Pro	Ala	Trp	Asp	165	Thr	Asn	His	Pro	170	Leu	Asn	Ala	Asn	175	Leu
Asp	Thr	Gly	Ile	180	Thr	Asn	His	Pro	185	Leu	Asn	Ala	Asn	190	Leu
Gly	Tyr	Asp	Phe	195	Ile	Ser	Asp	Ala	200	Met	Ala	Arg	Asp	205	Gly
Arg	Asp	210	Ser	Asn	Pro	Asn	Asp	215	Glu	Gly	Asp	Trp	Tyr	220	Gly
Cys	Gly	Ser	Gly	Ile	Pro	Ala	Ser	Asn	Ser	Ser	Trp	His	Gly	Thr	His
225	Val	Ala	Gly	Thr	Val	Ala	Ala	Val	Thr	Asn	Asn	Ser	Thr	Gly	Val
Val	Ala	Gly	Thr	245	Ala	Ala	Val	Thr	250	Asn	Asn	Ser	Thr	Gly	Val
Gly	Thr	Ala	Phe	260	Asn	Ala	Lys	Val	265	Pro	Val	Arg	Val	270	Lys
Cys	Gly	Gly	Tyr	275	Thr	Ser	Asp	Ile	280	Ala	Asp	Ala	Ile	285	Val
Gly	Gly	Thr	Val	Ser	Gly	Val	295	Pro	Ala	Asn	Ala	Asn	Pro	300	Ala
Ile	Asn	Met	Ser	Leu	Gly	Gly	Gly	Gly	Thr	Cys	Ser	Ala	Thr	Tyr	Gln
305	Asn	Ala	Ile	Asn	Gly	Ala	Val	Ser	Arg	Gly	Thr	Thr	Val	Val	Ala
Ala	Gly	Asn	Ser	325	Asn	Thr	Asn	Val	Ser	Ser	Ser	Val	Pro	Ala	Asn
Ala	Asn	Val	Ile	340	Ala	Val	Ala	Ala	Thr	Thr	Ser	Ala	Gly	Ala	Arg
Ser	Phe	Ser	Asn	Tyr	Gly	Ala	Gly	Ile	Asp	Ile	Ser	Gly	Pro	Gly	Gln
Ser	Ile	Leu	Ser	Thr	Leu	Asn	Thr	Gly	Thr	Thr	Thr	Pro	Gly	Ser	Ala
385	Ser	Tyr	Ala	Ser	Tyr	Asn	Gly	Thr	Ser	Met	Ala	Ala	Pro	His	Val
Gly	Val	Val	Ala	Leu	Met	Gln	Ser	Val	410	Ala	Pro	Ser	Ala	Leu	Ser
Ala	Gln	Val	Glu	Ser	Ile	Ile	Lys	Ser	425	Thr	Ala	Arg	Pro	430	Pro
Ala	Cys	Ser	Gly	Gly	Cys	Gly	Ala	Gly	Ile	Val	Asp	Ala	Asn	Ala	Ala
Val	Ala	Ala	Ala	Ile	Asn	Gly	Gly	Gly	Pro	Asn	Pro	Gly	Gly	Asn	Val
465	Leu	Gln	Asn	Asn	Val	Pro	Val	Thr	Gly	Leu	Gly	Ala	Ala	Thr	Gly
Glu	Leu	Asn	Tyr	Thr	Val	Ala	Val	Pro	490	Ala	Gly	Ser	Ser	Gln	Leu
Val	Ala	Ile	Ser	Gly	Gly	Ser	Gly	Asp	505	Ala	Asp	Leu	Tyr	Val	Arg
Gly	Ser	Ala	Pro	Thr	Asp	Thr	Thr	Tyr	520	Thr	Cys	Arg	Pro	Tyr	Leu
Gly	Asn	Ser	Glu	Thr	Cys	Thr	Ile	Asn	Ser	Pro	Ala	Ala	Gly	Thr	Trp
545	Tyr	Val	Arg	Val	Lys	Ala	Tyr	Ser	Thr	Phe	Ser	Gly	Leu	Thr	Leu
Ala	Gln	Tyr													Asn

<210> 71
 <211> 1620
 <212> DNA

10336256.txt

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 71

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cccgatcgga	tacccgccgc	gaccgagacg	ccggacacgc	ctctgcccgg	agccgatcgt	180
gccgctggcg	agcccccccc	cgtgctgggc	tccgaccatc	ccgaggcgat	cgagggggcg	240
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gccaccgctc	gcggcgcgac	ggtgcacgcc	acgtaccgcc	acgccctgca	cgggttcgcg	360
gccaccctcc	ccgagcaggc	gctggggggc	ctcacgcgca	acccgaacgt	cgcgttcatc	420
gacgcggacc	ttgccgtctc	gatcgagcag	gtgcagagcc	ccgcgacctg	gggcctggac	480
cgcacgcacc	agcggcgcc	gccgctggac	aaccaatacc	actacacca	caccggcgcg	540
ggcgtgcacg	cctacatcat	cgacaccggg	atccacgaca	cccacgccga	gttcggcggt	600
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cacggtaccc	acgtcgcggg	caccgtcggg	ggccagacct	acggcgtcgc	gaaggccgtg	720
cagctgtact	ccgtccgggt	gctcgactgc	ctgggcggcg	gcacgatggc	tggcgtcac	780
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ggcgccctgg	ccagctcggc	gctcgacacg	gccgtgaaca	actcgatcaa	cgccgggggtc	900
cactacgtcg	tgcccgctgc	caacagcagc	gccgacgcgt	gcggcttctc	ccccgctcgg	960
gtgagccggg	cgctgacggt	cggcgccagc	accagttcgg	acgcgcgcgc	ggcattcagc	1020
aactacggaa	cctgcgtcga	cctgttcgcc	cccggccaga	gcacacgcgc	ggcatggcac	1080
acgagcaaca	cggcgacgaa	tacgagcagc	ggcacgtcga	tggccgcgcc	gcacgtcgct	1140
gggtgctcgc	ccctgtatct	gcagcagggc	aaccagacgc	ccgcatgggt	ccacggcggt	1200
gtcacgagcc	agtcgacgca	tgggctgctg	agcgggatcg	ggccggggtc	gccgaaccgc	1260
ctgctgtact	ccctgatccc	cgcgcgcac	accaccgcgc	ccccctgcag	ctaccccgag	1320
cggttccgcg	ggttgctggc	gcggacgggt	gactggcatt	tcctgcccgt	gattccggag	1380
tacgggtaca	actcgcagge	aggggtccat	cgcgccctgc	tgaccggccc	cgccggcgcg	1440
accctaggcc	tgacactgtt	ctggtggaac	ggctcccagt	ggcaactcgt	ccgcagcgcc	1500
cagtcggtga	acggttcagt	cgccagcatc	acgcacagtg	gcgcccgcgg	gtggtacacc	1560
tggcgagtgg	attcgacgtc	cggctcgggc	acctacacct	tctcgatgca	gcgaccgtag	1620

<210> 72

<211> 539

<212> PRT

<213> Unknown

<220>

<223> obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(25)

<400> 72

Met	Gln	Arg	Ser	Arg	Arg	Leu	Val	Val	Thr	Val	Leu	Thr	Leu	Ala	Leu
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Cys	Leu	Met	Ala	Val	Pro	Ala	Gly	Ala	Ala	Ala	Pro	Asp	Gln	Pro	Ala
			20					25					30		
Ala	Pro	Glu	Gly	Val	Pro	Gly	Ala	Pro	Asp	Arg	Ile	Pro	Ala	Ala	Thr
			35				40					45			
Glu	Thr	Pro	Asp	Thr	Pro	Leu	Pro	Gly	Ala	Asp	Arg	Ala	Ala	Gly	Glu
			50			55					60				
Pro	Ala	Pro	Val	Leu	Gly	Ser	Asp	His	Pro	Glu	Ala	Ile	Glu	Gly	Arg
65					70				75						80
Tyr	Ile	Val	Val	Phe	Arg	Glu	Asp	Ala	Ala	Gln	Gly	Glu	Val	Ala	Arg
				85					90					95	
Ala	Ala	Glu	Arg	Ala	Thr	Ala	Arg	Gly	Ala	Thr	Val	His	Ala	Thr	Tyr
			100					105					110		
Arg	His	Ala	Leu	His	Gly	Phe	Ala	Ala	Thr	Leu	Pro	Glu	Gln	Ala	Leu
			115				120					125			
Gly	Ala	Leu	Thr	Arg	Asn	Pro	Asn	Val	Ala	Phe	Ile	Asp	Ala	Asp	Leu
			130			135					140				
Ala	Val	Ser	Ile	Glu	Gln	Val	Gln	Ser	Pro	Ala	Thr	Trp	Gly	Leu	Asp
145					150				155						160
Arg	Ile	Asp	Gln	Arg	Arg	Leu	Pro	Leu	Asp	Asn	Gln	Tyr	His	Tyr	Thr
				165					170					175	

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His	Thr	Gly	Ala	Gly	Val	His	Ala	Tyr	Ile	Ile	Asp	Thr	Gly	Ile	His
Asp	Thr	His	180	Glu	Phe	Gly	Gly	185	Arg	Ala	His	Leu	Ala	190	Thr
Ile	His	Asp	195	Gly	Leu	Gly	Ala	200	Arg	Asp	Cys	Ser	Gly	205	His
Val	Ala	Gly	210	Thr	Val	Gly	215	Gln	Thr	Tyr	Gly	Val	Ala	220	Lys
225	Gln	Leu	Tyr	Ser	Val	Arg	Val	Leu	Asp	Cys	235	Gly	Gly	Gly	Thr
Ala	Gly	Val	Ile	Asn	Gly	Val	Asp	Trp	Val	Thr	Ala	Asn	His	255	Val
Pro	Ala	Val	260	Ala	Asn	Met	Ser	Leu	280	Gly	Gly	Leu	Ala	Ser	Ala
Asp	Thr	Ala	275	Val	Asn	Asn	Ser	Ile	295	Asn	Ala	Gly	Val	His	Tyr
Ala	Ala	Ala	305	Asn	Ser	Ser	Ala	Asp	Ala	Cys	Gly	315	Phe	Ser	Pro
Val	Ser	Arg	Ala	Leu	Thr	Val	Gly	Ala	Ser	Thr	Ser	Ser	Asp	Ala	Arg
Ala	Ala	Phe	Ser	Asn	Tyr	Gly	Thr	Cys	345	Val	Asp	Leu	Phe	Ala	Pro
Gln	Ser	Ile	355	Thr	Ser	Ala	Trp	His	360	Thr	Ser	Asn	Thr	Ala	Thr
Ser	Ser	Gly	370	Thr	Ser	Met	Ala	Ala	375	Pro	His	Val	Ala	Gly	Val
Leu	Tyr	Leu	Gln	Gln	Gly	Asn	Gln	Thr	Pro	Ala	Trp	Val	His	Gly	Val
Val	Thr	Ser	Gln	Ser	Thr	His	Gly	Leu	Leu	Ser	Gly	Ile	Gly	Pro	Gly
Ser	Pro	Asn	Arg	Leu	Leu	Tyr	Ser	Leu	425	Ile	Pro	Ala	Arg	Ile	Thr
Ala	Ala	Pro	Cys	Ser	Tyr	Pro	Glu	Arg	Phe	Arg	Gly	Leu	Leu	Ala	Arg
Thr	Gly	Asp	Trp	His	Phe	Leu	Pro	Val	Ile	Pro	Glu	Tyr	Gly	Tyr	Asn
Ser	Gln	Ala	Gly	Val	His	Arg	Ala	Cys	Val	Thr	Gly	Pro	Ala	Gly	Ala
Thr	Leu	Gly	Leu	His	Leu	Phe	Trp	Trp	Asn	Gly	Ser	Gln	Trp	Gln	Leu
Val	Arg	Ser	Ala	Gln	Ser	Val	Asn	Gly	Ser	Val	Ala	Ser	Ile	Thr	His
Ser	Gly	Ala	Ala	Gly	Trp	Tyr	Thr	Trp	Arg	Val	Asp	Ser	Thr	Ser	Gly
Ser	Gly	Thr	Tyr	Thr	Phe	Ser	Met	Gln	Arg	Pro	525				

<210> 73

<211> 1836

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 73

atgcaacagc	acagcaagat	ggcccccg	ttgaagtttt	gcgcggcg	cctgatcgcc	60
ctggggtcga	cggcagccca	cgccggtccg	cacgacgcgg	catcaccgcc	cttcatcacc	120
cagaccgacc	gcctgatcat	ccgctacaag	gatgcggtcg	acacctcgaa	gtcccagacg	180
ccggtggccc	cgctcccat	tccccaggca	cgcaaggccc	agctcgaccg	cgccggccag	240
ggcttcggcg	cgaccctg	cgactg	gcgaccgcca	acggcgccca	cgctcctgcag	300
ctcagccgca	ccatgctgct	ggacgaagcg	aagcagctgg	cgccgac	gaaggcg	360
gacgccaacg	tcgagtacgc	cgagccggac	cgcatcatga	ccgctg	cacgcccagc	420
gacccagct	acagccagca	gtgggac	tatgaagcca	agggcg	caacgtgcag	480
gccgcctggg	acaagtgcac	cggcagcggc	atcaacgtgg	ccgtgatcga	caccggctac	540
cgctccgcatg	ccgac	cggccagatc	ctgcaaggct	acgatttc	caccaacacc	600
accatggcca	acgacggggg	cggccgcgac	agcgacgcca	gcgatccggg	cgactggacc	660
ccggccggca	gctgctcggc	aggtacgc	gcccaggacc	aggcctcgg	ctggcacggc	720

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acccacgtgg	ccggcaccat	cgccgcgcgc	gccacaacg	gcgcccggcat	cgcgggcatc	780
gcctacaacg	ccaagatcgt	cccggcgcgc	gtgctgggccc	gctgcggcgg	ctacacctcg	840
gacatcgccg	acgccatcgt	ctgggcttcg	ggcggcagcg	tgaacggcgt	gccggcgaat	900
gccaacaagg	cgcgctgct	gaacctgtcg	ctgggcggca	gcggcggtg	cgacagcacg	960
accagaacg	ccatcaacag	tgcgcgctcg	cgcggcgcgg	tggtcgtggt	cgccgccggc	1020
aattcgaacg	tcgatgccgc	gggctccagc	ccggccaact	gcgcccggcgt	gatcgcggtg	1080
gcggcggtcg	gccgcagcgg	cggcaaggcc	tcgtactcga	actacggcaa	cacggtcgac	1140
gtggcggcgc	cgggcggcga	cagcggcgcc	ggcatcctgt	cgacgctgaa	cagcggcacc	1200
accaccccg	cgggcgacag	ctacgcctac	tacatgggca	cctcgatggc	cgccccgcac	1260
gtggccggcg	tgggcgcgct	gatgctgtcg	gcgaacccga	acctgacccc	ggacgaggtc	1320
gaggccaagc	tgaagtcgac	cgcgcgcgcc	ttcccggcca	cctgcaacgg	ctgcggcagc	1380
ggcatcatcg	acgccgcagc	cgccgtcaac	gcgtcgctgc	ctgccggcag	cacgcccacg	1440
cgcccgccat	cgggctggac	cgaatgcgcg	cccgaacacg	gcacctgtc	gttcagcgcg	1500
acccgtgaag	tacgctacgg	cgccggtacc	agcttcgtct	cgaagatcgt	gaccggttcc	1560
gtcgccgtgct	cgaacgccgt	gttcggcgat	ccgctgccga	acgtgggtcaa	gtcgtgcagc	1620
tattcgaacg	ccacggtgag	cgtgccgacc	tggaaccaact	gcgcccggcga	ggcgggcacc	1680
tgctcggtta	gcggcaccgg	cgaagtgcgc	tacggcgcca	acaacaactt	cgtgtcgcgc	1740
gtcttcaccg	gcgcccgcgt	gtgctcgaat	gccaccttcg	gcgatccggg	gccgaacgtg	1800
gtcaaggcct	gcagctattc	cagcgtcacg	caataa			1836

<210> 74
 <211> 611
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(28)

<400> 74

Met	Gln	Gln	His	Ser	Lys	Met	Ala	Pro	Val	Leu	Lys	Phe	Cys	Ala	Ala
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Ala	Leu	Ile	Ala	Leu	Gly	Ser	Thr	Ala	Ala	His	Ala	Gly	Pro	His	Asp
			20					25					30		
Ala	Ala	Ser	Pro	Arg	Phe	Ile	Thr	Gln	Thr	Asp	Arg	Leu	Ile	Ile	Arg
		35					40					45			
Tyr	Lys	Asp	Ala	Val	Asp	Thr	Ser	Lys	Ser	Gln	Thr	Pro	Val	Ala	Pro
	50					55					60				
Arg	Pro	Ile	Pro	Glu	Ala	Arg	Lys	Ala	Gln	Leu	Asp	Arg	Ala	Gly	Gln
65					70					75					80
Gly	Phe	Gly	Ala	Thr	Leu	Arg	Ala	Leu	Arg	Ala	Thr	Ala	Asn	Gly	Ala
				85					90					95	
His	Val	Leu	Gln	Leu	Ser	Arg	Thr	Met	Ser	Leu	Asp	Glu	Ala	Lys	Gln
		100						105							
Leu	Ala	Ala	Asp	Leu	Lys	Ala	Arg	Asp	Ala	Asn	Val	Glu	Tyr	Ala	Glu
		115					120					125			
Pro	Asp	Arg	Ile	Met	Thr	Ala	Leu	Ala	Thr	Pro	Ser	Asp	Pro	Ser	Tyr
	130					135					140				
Ser	Gln	Gln	Trp	Asp	Leu	Tyr	Glu	Ala	Lys	Gly	Gly	Ile	Asn	Val	Gln
145					150					155					160
Ala	Ala	Trp	Asp	Lys	Ser	Thr	Gly	Ser	Gly	Ile	Asn	Val	Ala	Val	Ile
				165					170						175
Asp	Thr	Gly	Tyr	Arg	Pro	His	Ala	Asp	Leu	Ala	Gly	Gln	Ile	Leu	Gln
		180						185							
Gly	Tyr	Asp	Phe	Ile	Thr	Asn	Thr	Thr	Met	Ala	Asn	Asp	Gly	Gly	Gly
	195						200								
Arg	Asp	Ser	Asp	Ala	Ser	Asp	Pro	Gly	Asp	Trp	Thr	Pro	Ala	Gly	Ser
	210					215					220				
Cys	Ser	Ala	Gly	Thr	Pro	Ala	Gln	Asp	Gln	Ala	Ser	Gly	Trp	His	Gly
225					230					235					240
Thr	His	Val	Ala	Gly	Thr	Ile	Ala	Ala	Arg	Ala	Asn	Asn	Gly	Ala	Gly
			245						250					255	
Ile	Ala	Gly	Ile	Ala	Tyr	Asn	Ala	Lys	Ile	Val	Pro	Ala	Arg	Val	Leu
		260						265							
Gly	Arg	Cys	Gly	Gly	Tyr	Thr	Ser	Asp	Ile	Ala	Asp	Ala	Ile	Val	Trp
	275						280					285			

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Ala	Ser	Gly	Gly	Ser	Val	Asn	Gly	Val	Pro	Ala	Asn	Ala	Asn	Lys	Ala
290						295					300				
Arg	Val	Leu	Asn	Leu	Ser	Leu	Gly	Gly	Ser	Gly	Gly	Cys	Asp	Ser	Thr
305					310					315					320
Thr	Gln	Asn	Ala	Ile	Asn	Ser	Ala	Arg	Ser	Arg	Gly	Ala	Val	Val	Val
				325					330					335	
Val	Ala	Ala	Gly	Asn	Ser	Asn	Val	Asp	Ala	Ala	Gly	Ser	Ser	Pro	Ala
			340					345					350		
Asn	Cys	Ala	Gly	Val	Ile	Ala	Val	Ala	Ala	Val	Gly	Arg	Ser	Gly	Gly
		355					360					365			
Lys	Ala	Ser	Tyr	Ser	Asn	Tyr	Gly	Asn	Thr	Val	Asp	Val	Ala	Ala	Pro
	370					375					380				
Gly	Gly	Asp	Ser	Gly	Ala	Gly	Ile	Leu	Ser	Thr	Leu	Asn	Ser	Gly	Thr
385					390					395					400
Thr	Thr	Pro	Ala	Gly	Asp	Ser	Tyr	Ala	Tyr	Tyr	Met	Gly	Thr	Ser	Met
				405					410					415	
Ala	Ala	Pro	His	Val	Ala	Gly	Val	Ala	Ala	Leu	Met	Leu	Ser	Ala	Asn
			420					425						430	
Pro	Asn	Leu	Thr	Pro	Asp	Glu	Val	Glu	Ala	Lys	Leu	Lys	Ser	Thr	Ala
		435					440					445			
Arg	Ala	Phe	Pro	Ala	Thr	Cys	Asn	Gly	Cys	Gly	Ser	Gly	Ile	Ile	Asp
	450					455					460				
Ala	Ala	Ala	Ala	Val	Asn	Ala	Ser	Leu	Pro	Ala	Gly	Ser	Thr	Pro	Thr
465					470					475					480
Pro	Pro	Ala	Ser	Gly	Trp	Thr	Glu	Cys	Ala	Pro	Glu	Asn	Gly	Thr	Cys
				485					490					495	
Ser	Phe	Ser	Gly	Thr	Arg	Glu	Val	Arg	Tyr	Gly	Ala	Gly	Thr	Ser	Phe
			500					505					510		
Val	Ser	Lys	Ile	Val	Thr	Gly	Ser	Val	Ala	Cys	Ser	Asn	Ala	Val	Phe
		515					520					525			
Gly	Asp	Pro	Leu	Pro	Asn	Val	Val	Lys	Ser	Cys	Ser	Tyr	Ser	Asn	Ala
	530					535					540				
Thr	Val	Ser	Val	Pro	Thr	Trp	Thr	Asn	Cys	Ala	Gly	Glu	Gly	Gly	Thr
545					550					555					560
Cys	Ser	Phe	Ser	Gly	Thr	Arg	Glu	Val	Arg	Tyr	Gly	Ala	Asn	Asn	Asn
				565					570					575	
Phe	Val	Ser	Arg	Val	Phe	Thr	Gly	Ala	Ala	Val	Cys	Ser	Asn	Ala	Thr
			580					585					590		
Phe	Gly	Asp	Pro	Val	Pro	Asn	Val	Val	Lys	Ala	Cys	Ser	Tyr	Ser	Ser
		595					600					605			
Val	Thr	Gln													
		610													

<210> 75
 <211> 2262
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 75

atgtccagat	cacatcacac	tgtactactg	atcggcggtta	gcttactggc	aagcgcagta	60
tcaaatgcta	tggccgcatac	aacagactca	ttgcgccagg	cagcagaaca	agccagcagc	120
gacgcgtata	tcgtaaaata	taaagacaac	agtctgagta	aagatccact	tctcaaccgc	180
agtaaagctg	caaaagatag	tgcgctatca	gcattaacct	ctaacagcga	acgtttaagc	240
cggcaagggtg	cacgtgttca	ccatgtttctg	gccaaacgta	acgccatagc	agccgagcta	300
agccctgccca	cggttaaagc	gttaaaagca	gacccctaag	tggaatatgt	cgagcgcgat	360
ttaccgcggtt	ttcctatgtc	gcagcaagtg	ccttacgggtt	ataccatggt	gcaggccgat	420
ctggtcagtg	atcagtttgc	ctctaaccag	acggatatgtg	ttatcgactc	tggcctgggc	480
ttaccacatg	aagactttaa	cgatgccaat	atcaccggca	ccaatgatata	aggtaccggg	540
aactggttcg	acgccgggtg	cccacacggt	acacatgtag	ccggtaccat	tgctgcgctg	600
aataataatg	ttgggtattgt	tggcgtattg	cccaacggca	atgtgaaact	gcatatcatt	660
aaagtattta	acgccgggtg	ctgggggttac	tcttccactc	tggcacatgc	ggtagatacc	720
tgtgtgcaaa	acggctctac	cgtaattaat	atgagcttag	gcgggtgccg	ctcaaacgta	780
acagagcgta	acgccatgca	ggccgcctat	gacgccgggtg	tggtacttgt	tgcagcagcg	840
ggtaatggcg	gcaatactgc	catgtcgtat	ccggcttctt	atgattctgt	cgtatcagtt	900
gcagcgggtg	acgacaccaa	agccacagct	gacttttctgc	agcgtaatac	ccaggtagaa	960

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ctggcaggcc	cggtgttagc	ggtaatgagt	acttatccaa	ccggtacagg	cctggaaacc	1020
agcctgacgg	ttaacgggtac	aacctacagt	accaaccggt	tcgaaggctc	tgccatggcc	1080
agtttgaatg	cggaactggc	cagctgcggc	cttgcggttaa	atacctgtac	cggcgttacc	1140
gataaaatct	gtctgatcca	gcgcggcgaa	gtatctttcg	cacaaaaagt	ggaatcctgt	1200
caggctggcg	gtggtattgg	cgcggttatt	tataacaacg	aaccaggcaa	tttcagcggc	1260
accttaggtg	acgccccac	tactaatata	gtagcggttaa	gcgtatcgca	ggaagatggc	1320
cagttgttgg	ttgcagaagt	aggtaacgat	gccagcttat	ttgccggccc	gtctaactat	1380
ggcctgatgg	acggtacctc	tatggcgtcg	ccgcatgtag	ccggtgtagc	agcattggta	1440
tggagccatt	acccggtatt	tagcaatgca	caaatccgca	gtgcttttagc	agcaacagca	1500
gaagatttag	gcgcccgtgg	gcgtgataca	tcttatggct	atggcttggg	acaagccaaa	1560
gccgcggtag	attatctggc	cgagtttggc	tgtgacggcg	acggtgacga	taacgagcca	1620
ccaccaccaa	ccggcacaga	actgagtaac	ggtgtaacag	tatcaggcat	cagtgcctgt	1680
gccgggtgaag	aactgctgta	cacgctggcc	gtacctgcag	gtgccagcaa	cctgtcgttt	1740
gttatgaatg	gcggtaccgg	cgatgccgat	ctgtatgtca	agtttggcag	cgagccaacc	1800
gcatcaaaact	gggactgccg	gccttacctg	tttggttaaca	acgaaagctg	tgctatcgac	1860
ccggcacaaa	ccggtactta	ctttgttaag	ttagtagcat	acagcgcctt	taccggtgta	1920
aaccttaccg	gtagctttac	cgcaccggat	ttaccggatg	caggcggcga	aaccattacc	1980
aacatcaaca	tagcgcgccg	ggcctggcag	cactacacgc	tggacgtacc	ggaaggatg	2040
gcacagctaa	ctgttgaaat	cagtgggtggc	agcgggtgatg	ctgatctgta	cgtgaagcat	2100
ggcagccagc	ctaccagcgg	tagctatgat	tgccggccaa	ataaaaaacg	caatagcgaa	2160
acctgtgtta	ttaacaaccc	gcaagccggt	gtatggcatc	tgtcagttaa	tgccctccgg	2220
gcggtaagcg	gcttaacact	ggtaagtga	taccaaccgt	aa		2262

<210> 76

<211> 753

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(25)

<400> 76

Met	Ser	Arg	Ser	His	His	Thr	Val	Leu	Leu	Ile	Gly	Val	Ser	Leu	Leu
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Ala	Ser	Ala	Val	Ser	Asn	Ala	Met	Ala	Ala	Ser	Thr	Asp	Ser	Leu	Arg
			20					25					30		
Gln	Ala	Ala	Glu	Gln	Ala	Ser	Ser	Asp	Arg	Tyr	Ile	Val	Lys	Tyr	Lys
		35					40					45			
Asp	Asn	Ser	Leu	Ser	Lys	Asp	Pro	Leu	Leu	Asn	Arg	Ser	Lys	Ala	Ala
	50				55					60					
Lys	Asp	Ser	Ala	Leu	Ser	Ala	Leu	Thr	Ser	Asn	Ser	Glu	Arg	Leu	Ser
65				70				75						80	
Arg	Gln	Gly	Ala	Arg	Val	His	His	Val	Leu	Ala	Lys	Arg	Asn	Ala	Ile
			85					90						95	
Ala	Ala	Glu	Leu	Ser	Pro	Ala	Thr	Val	Lys	Ala	Leu	Lys	Ala	Asp	Pro
		100						105					110		
Asn	Val	Glu	Tyr	Val	Glu	Arg	Asp	Leu	Pro	Arg	Phe	Pro	Met	Ser	Gln
		115					120					125			
Gln	Val	Pro	Tyr	Gly	Tyr	Thr	Met	Val	Gln	Ala	Asp	Leu	Val	Ser	Asp
	130					135					140				
Gln	Phe	Ala	Ser	Asn	Gln	Thr	Val	Cys	Val	Ile	Asp	Ser	Gly	Leu	Gly
145				150				155						160	
Leu	Pro	His	Glu	Asp	Phe	Asn	Asp	Ala	Asn	Ile	Thr	Gly	Thr	Asn	Asp
			165					170						175	
Ile	Gly	Thr	Gly	Asn	Trp	Phe	Asp	Ala	Gly	Gly	Pro	His	Gly	Thr	His
		180					185						190		
Val	Ala	Gly	Thr	Ile	Ala	Ala	Leu	Asn	Asn	Asn	Val	Gly	Ile	Val	Gly
	195						200					205			
Val	Leu	Pro	Asn	Gly	Asn	Val	Lys	Leu	His	Ile	Ile	Lys	Val	Phe	Asn
	210				215						220				
Ala	Gly	Gly	Trp	Gly	Tyr	Ser	Ser	Thr	Leu	Ala	His	Ala	Val	Asp	Thr
225					230					235				240	
Cys	Val	Gln	Asn	Gly	Ser	Thr	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Ala
		245						250					255		
Gly	Ser	Asn	Val	Thr	Glu	Arg	Asn	Ala	Met	Gln	Ala	Ala	Tyr	Asp	Ala

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Gly Val Leu 260 Leu Val Ala Ala Ala 265 Gly Asn Gly Gly Asn 270 Thr Ala Met
 Ser Tyr 275 Pro Ala Ser Tyr Asp 280 Ser Val Val Ser Val 285 Ala Ala Val Asp
 Asp Thr 290 Lys Ala His Ala 295 Phe Ser Gln Arg Asn 300 Thr Gln Val Glu
 305 Leu Ala Gly Pro Gly 310 Val Ala Val Met Ser 315 Thr Tyr Pro Thr Gly Thr
 Gly Leu Glu Thr 325 Ser Leu Thr Val Asn 330 Gly Thr Thr Tyr Ser Thr Asn
 Pro Phe 340 Gly Ser Ala Met Ala 345 Ser Leu Asn Ala Glu 350 Leu Ala Ser
 Cys Gly 355 Leu Ala Val Asn Thr 360 Cys Thr Gly Val Thr 365 Asp Lys Ile Cys
 370 Leu Ile Gln Arg Gly Glu 375 Val Ser Phe Ala Gln Lys Val Glu Ser Cys
 385 Gln Ala Gly Gly Gly 390 Ile Gly Ala Val Ile 395 Tyr Asn Asn Glu Pro 400 Gly
 Asn Phe Ser Gly 405 Thr Leu Gly Asp Ala 410 Pro Thr Thr Asn Ile Val Ala
 Leu Ser Val 420 Ser Gln Glu Asp Gly 425 Gln Leu Leu Val Ala 430 Glu Val Gly
 Asn Asp 435 Ala Ser Leu Phe Ala 440 Gly Pro Ser Asn Tyr Gly Leu Met Asp
 450 Gly Thr Ser Met Ala Ser 455 His Val Ala Gly Val Ala Ala Leu Val
 465 Trp Ser His Tyr Pro 470 Asp Cys Ser Asn Ala Gln Ile Arg Ser Ala Leu
 Ala Ala Thr Ala 485 Glu Asp Leu Gly Ala 490 Ala Gly Arg Asp Thr Ser Tyr
 Gly Tyr Gly Leu Val Gln Ala Lys 500 Ala Ala Val Asp Tyr 510 Leu Ala Glu
 Phe Gly 515 Cys Asp Gly Asp Gly 520 Asp Asp Asn Glu Pro 525 Pro Pro Pro Thr
 530 Gly Thr Glu Leu Ser Asn 535 Gly Val Thr Val Ser 540 Gly Ile Ser Ala Ala
 545 Ala Gly Glu Glu Leu 550 Leu Tyr Thr Leu Ala Val Pro Ala Gly Ala Ser
 Asn Leu Ser Phe 560 Val Met Asn Gly Gly 570 Thr Gly Asp Ala Asp 575 Leu Tyr
 Val Lys Phe 580 Gly Ser Glu Pro Thr Ala Ser Asn Trp Asp 590 Cys Arg Pro
 Tyr Leu 595 Phe Gly Asn Asn Glu 600 Ser Cys Ala Ile Asp 605 Pro Ala Gln Thr
 610 Gly Thr Tyr Phe Val Lys 615 Leu Val Ala Tyr Ser Ala Phe Thr Gly Val
 625 Asn Leu Thr Gly Ser 630 Phe Thr Ala Pro Asp 635 Leu Pro Asp Ala Gly Gly
 Glu Thr Ile Thr 640 Asn Ile Asn Ile Ala Arg Arg Ala Trp Gln His Tyr
 Thr Leu Asp 650 Val Pro Glu Gly Met 660 Ala Gln Leu Thr Val 670 Glu Ile Ser
 Gly Gly 675 Ser Gly Asp Ala Asp 680 Leu Tyr Val Lys His 685 Gly Ser Gln Pro
 690 Thr Ser Gly Ser Tyr Asp 695 Cys Arg Pro Asn Lys 700 Asn Gly Asn Ser Glu
 705 Thr cys Val Ile Asn 710 Asn Pro Gln Ala Gly 715 Val Trp His Leu Ser Val
 Tyr Ala Phe Arg 720 Ala Val Ser Gly Leu 725 Thr Leu Val Ser Glu Tyr Gln
 730 Pro 740 745 750

<210> 77
 <211> 2136
 <212> DNA
 <213> Unknown

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<220>

<223> obtained from an environmental sample.

<400> 77

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gtcgaggtgt	accgagtgcc	cgccgctgat	cgctcactcg	accaacggaa	gctggaacta	240
cgggcgggccc	ctgacgtgca	gttcgcccgt	tcggtgctgg	tccgcccagg	ttcggacgaa	300
cctgtgctgt	atacggagaa	cctgtatatc	cgcttccggg	aggatctcga	tccggatgac	360
tgcgaagcga	tcatccgtca	ggctggcctg	acggtgaagc	aacgtctgga	tttcgccacc	420
aacgcctact	tcctggccgc	tcccaggggg	acgggacagc	gcgtcttcga	catcgcgttg	480
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tcggtggata	acgatggcta	tgcgagctac	cacaaggcca	ttgcggtggc	ggcgtgcaac	1200
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gccgcgggtgg	cctcacaagc	cgcgacagga	aaaacgaaac	gagcggctgc	gaagaaaaaca	2100
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<210> 78

<211> 711

<212> PRT

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 78

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			20					25					30		
Val	Val	Gly	Ala	Gly	Pro	Val	Met	Pro	Pro	Thr	Ala	Ala	Glu	Val	Ser
			35				40					45			
Asp	Gly	Glu	Leu	Val	Ala	Ser	Phe	Pro	Glu	Ala	Gly	Val	Glu	Val	Tyr
			50			55					60				
Arg	Val	Pro	Ala	Ala	Asp	Arg	Ser	Leu	Asp	Gln	Arg	Lys	Leu	Glu	Leu
					70					75				80	
Arg	Ala	Ala	Pro	Asp	Val	Gln	Phe	Ala	Gly	Ser	Val	Leu	Val	Arg	Pro
				85					90					95	
Gly	Ser	Asp	Glu	Pro	Val	Leu	Tyr	Thr	Glu	Asn	Leu	Tyr	Ile	Arg	Phe
			100					105					110		
Arg	Glu	Asp	Leu	Asp	Pro	Asp	Asp	Cys	Glu	Ala	Ile	Ile	Arg	Gln	Ala
			115			120						125			
Gly	Leu	Thr	Val	Lys	Gln	Arg	Leu	Asp	Phe	Ala	Thr	Asn	Ala	Tyr	Phe

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130	Leu	Ala	Ala	Pro	Glu	Gly	Thr	Gly	Gln	Arg	Val	Phe	Asp	Ile	Ala	Leu
145	Glu	Leu	Leu	Lys	Arg	Asn	Asp	Val	Ile	Tyr	Cys	His	Pro	Glu	Leu	Ile
				165	His	Lys	Gln	Arg	Ile	170	Phe	Pro	Glu	Gln	Trp	His
				180	Ile	Asn	Gly	Thr	Ala	185	Val	Asn	Ala	His	Ala	Asn
				195	Ser	Ile	Asn	Gly	Thr	200	Ala	Val	Asn	Ala	His	Ala
				210	Ala	His	Ala	Ile	Thr	215	Leu	Gly	Ala	Gly	Val	Thr
				225	Asp	Asp	Gly	Val	Asp	230	Ile	Asp	His	Pro	Glu	Phe
										235	Leu	Gln	Thr	Asn	Asp	Pro
										245	Pro	Ser	Arg	Arg	Gly	Thr
										250	Gly	Glu	Asn	His	Gly	Thr
										260	Val	Pro	Ser	Arg	Arg	Gly
										265	Gly	Thr	Asp	Gly	Ala	Gly
										270	Val	Ala	Cys	Ala	Gly	Val
										275	Leu	Ala	Arg	Leu	Met	Pro
										280	Gly	Thr	Asp	Gly	Ala	Gly
										285	Ala	Pro	Leu	Ala	Arg	Leu
										290	Val	Arg	Glu	Ala	Glu	Ala
										295	Phe	Gln	Trp	Ala	Ala	Asp
										300	Arg	Asp	Gly	Asp	Trp	Trp
										305	Ile	Ile	Ser	Cys	Ser	Trp
										310	Gly	Pro	Arg	Asp	Gly	Asp
										315	Ala	Ala	Asp	Asn	Gly	Ala
										320	Asp	Ile	Ile	Ser	Cys	Ser
										325	Leu	His	Asn	His	Val	Ser
										330	Phe	Gln	Leu	Pro	Ala	Ser
										335	Thr	Arg	Asp	Ala	Ile	Trp
										340	Pro	Asn	Asp	Pro	Gly	Ile
										345	Val	Ser	Glu	Gly	Arg	Gly
										350	Gly	Thr	Asp	Gly	Ala	Gly
										355	Val	Ile	Leu	Phe	Ala	Ala
										360	Gly	Asn	Gly	Asn	Glu	Ser
										365	Val	Ala	Ala	Cys	Asn	Thr
										370	Ile	Leu	Phe	Ala	Ala	Gly
										375	His	Lys	Val	Ile	Ala	Val
										380	Val	Ile	Ala	Ala	Cys	Asn
										385	Gly	Tyr	Ala	Ser	Tyr	Thr
										390	Thr	Arg	Ser	Val	Tyr	Ser
										395	Asp	Phe	Gly	Lys	Ala	Ile
										400	Arg	Asn	Thr	Arg	Ser	Val
										405	Ser	Ser	Asp	Phe	Gly	Thr
										410	His	Ala	Pro	Phe	Asn	His
										415	Pro	Gln	Pro	Leu	Thr	Arg
										420	Thr	Pro	Gly	Ile	Trp	Thr
										425	Thr	Thr	Asp	Arg	Met	Gly
										430	Thr	Thr	Asp	Arg	Met	Gly
										435	Thr	Thr	Asp	Arg	Met	Gly
										440	Thr	Thr	Asp	Arg	Met	Gly
										445	Thr	Thr	Asp	Arg	Met	Gly
										450	Thr	Thr	Asp	Arg	Met	Gly
										455	Thr	Thr	Asp	Arg	Met	Gly
										460	Thr	Thr	Asp	Arg	Met	Gly
										465	Thr	Thr	Asp	Arg	Met	Gly
										470	Thr	Thr	Asp	Arg	Met	Gly
										475	Thr	Thr	Asp	Arg	Met	Gly
										480	Thr	Thr	Asp	Arg	Met	Gly
										485	Thr	Thr	Asp	Arg	Met	Gly
										490	Thr	Thr	Asp	Arg	Met	Gly
										495	Thr	Thr	Asp	Arg	Met	Gly
										500	Thr	Thr	Asp	Arg	Met	Gly
										505	Thr	Thr	Asp	Arg	Met	Gly
										510	Thr	Thr	Asp	Arg	Met	Gly
										515	Thr	Thr	Asp	Arg	Met	Gly
										520	Thr	Thr	Asp	Arg	Met	Gly
										525	Thr	Thr	Asp	Arg	Met	Gly
										530	Thr	Thr	Asp	Arg	Met	Gly
										535	Thr	Thr	Asp	Arg	Met	Gly
										540	Thr	Thr	Asp	Arg	Met	Gly
										545	Thr	Thr	Asp	Arg	Met	Gly
										550	Thr	Thr	Asp	Arg	Met	Gly
										555	Thr	Thr	Asp	Arg	Met	Gly
										560	Thr	Thr	Asp	Arg	Met	Gly
										565	Thr	Thr	Asp	Arg	Met	Gly
										570	Thr	Thr	Asp	Arg	Met	Gly
										575	Thr	Thr	Asp	Arg	Met	Gly
										580	Thr	Thr	Asp	Arg	Met	Gly
										585	Thr	Thr	Asp	Arg	Met	Gly
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										650	Thr	Thr	Asp	Arg	Met	Gly
										655	Thr	Thr	Asp	Arg	Met	Gly
										660	Thr	Thr	Asp	Arg	Met	Gly
										665	Thr	Thr	Asp	Arg	Met	Gly
										670	Thr	Thr	Asp	Arg	Met	Gly

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 690 695 700
 Thr Arg Ala Lys Lys Lys Arg
 705 710

<210> 79
 <211> 1407
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 79
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 gccgcccaga tcctgcgcaa gggcatgtcc tggcaggaca agaacggcga cggcaagatc 180
 gacctcagct ataccttctt gaccgacaag cctgccaaact acaaccgaa actgggcaac 240
 ttcgggcgagt tcagcgccct gcagaaagcc caggccgtgc tcgccatgca atcctggggc 300
 gacgtggcca acgtcacctt caccgaaggc aacggcgggc acggccacat gacgttcggc 360
 aactacgacg tcagcaccgg cggcgcggcg ttgcctacc tgcccaggc cagcagctac 420
 gacggccagt cgtggtacct gatcaacgac cagtaccagg tcaacaagac tcccggcacc 480
 aacaactacg ggcgccagac cctgaccac gaaatcggcc acaccctcg cctgtcgac 540
 cccggcgccct acaacgcccg caacggcaac ccgacctac gtgacgcca gtacgcccga 600
 gacacccgcg gctacagcct catgagctac tggagcgaaa gcaacaccgc ccagaacttc 660
 agcaaggacg gcagcgggcg ctacgcgtcg gcgcggttc tggacgacat cgtggcggtg 720
 cagaaactct acggcgccaa cctgcagacc cgtgccgacg acaccgtcta cggcttcaac 780
 tccaacgccg agcgcgactt ctacagcgcc acctccaaca gctccaagg ggtgttctcg 840
 gtgtgggacg gcggcgggca cgacaccctg gacttctccg gcttcagcca caaccagaag 900
 atcaacctca atgaagggtc gttctccgac gtcggcgggc tgggtgggcaa cgtgtccatc 960
 gcctatggcg tgaccctgga gaacgccatc ggcggttcgg gcaacgacct gctgatcggc 1020
 aacgcggcgcg ccaacgaact ggtgggcgga gccggcaacg acctgatcta cggcggtggc 1080
 ggcgggcgaca cgctgtgggg cggggaaggg gccgacacct tcgtgttcgg cgcgccagc 1140
 gactcgacca tgaccgcgcc ggactggatc atggatttca ccagcggcct ggacaagatc 1200
 gacctgtcgg gcatcgccgg cttcgccagc ggcgcgcca cgtgaactt cgtcagcggc 1260
 ttaccgggcc atgcgggcga tgcgatcctc acctacttcg cgcagaccaa ccagaccagc 1320
 ctgatgatcg acctgaccgg ccaaggttcg gtggacttcg ccgtgggcgt ggtggggcag 1380
 gcgctggcaa gcgacatcgt cgcgtga 1407

<210> 80
 <211> 468
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 80
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 20 25 30
 Pro Ser Phe Thr Ala Asp Gln Ala Ala Glu Ile Leu Arg Lys Gly
 35 40 45
 Met Ser Trp Gln Asp Lys Asn Gly Asp Gly Lys Ile Asp Leu Ser Tyr
 50 55 60
 Thr Phe Leu Thr Asp Lys Pro Ala Asn Tyr Asn Pro Lys Leu Gly Asn
 65 70 75 80
 Phe Gly Glu Phe Ser Ala Leu Gln Lys Ala Gln Ala Val Leu Ala Met
 85 90 95
 Gln Ser Trp Ala Asp Val Ala Asn Val Thr Phe Thr Glu Gly Asn Gly
 100 105 110
 Gly Asp Gly His Met Thr Phe Gly Asn Tyr Asp Val Ser Thr Gly Gly
 115 120 125
 Ala Ala Phe Ala Tyr Leu Pro Gln Gly Ser Ser Tyr Asp Gly Gln Ser
 130 135 140
 Trp Tyr Leu Ile Asn Asp Gln Tyr Gln Val Asn Lys Thr Pro Gly Thr

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145 Asn Asn Tyr Gly Arg 150 Gln Thr Leu Thr His 155 Glu Ile Gly His Thr 160 Leu
 Gly Leu Ser His 165 Pro Gly Ala Tyr Asn 170 Ala Gly Asn Gly Asn 175 Pro Thr
 Tyr Gly Asp 180 Ala Lys Tyr Ala Glu 185 Asp Thr Arg Gly Tyr Ser Leu Met
 ser Tyr 195 Trp Ser Glu Ser Asn 200 Thr Ala Gln Asn Phe 205 Ser Lys Asp Gly
 ser Gly 210 Ala Tyr Ala Ser 215 Ala Pro Leu Leu Asp 220 Ile Val Ala Val
 225 Gln Lys Leu Tyr Gly 230 Ala Asn Leu Gln Thr 235 Arg Ala Asp Asp Thr Val
 Tyr Gly Phe Asn 245 Ser Asn Ala Glu Arg 250 Asp Phe Tyr Ser Ala 255 Thr Ser
 Asn Ser 260 Lys Val Val Phe 265 Ser Val Trp Asp Gly Gly 270 Gly Asn Asp
 Thr Leu 275 Asp Phe Ser Gly Phe 280 Ser His Asn Gln Lys 285 Ile Asn Leu Asn
 Glu Gly 290 Ser Phe Ser Asp 295 Val Gly Gly Leu Val Gly Asn Val Ser Ile
 305 Ala Tyr Gly Val Thr 310 Leu Glu Asn Ala Ile 315 Gly Gly Ser Gly Asn Asp
 Leu Leu Ile Gly 325 Asn Ala Ala Ala Asn 330 Glu Leu Val Gly Gly Ala Gly
 Asn Asp 340 Ile Tyr Gly Gly Gly 345 Gly Gly Asp Thr Leu Trp Gly Gly
 Glu Gly 355 Ala Asp Thr Phe Val 360 Phe Gly Ala Ala Ser 365 Asp Ser Thr Met
 Thr Ala 370 Pro Asp Trp Ile 375 Met Asp Phe Thr Ser 380 Gly Leu Asp Lys Ile
 385 Asp Leu Ser Gly Ile 390 Ala Gly Phe Ala Ser 395 Gly Ala Ala Thr Leu Asn
 Phe Val 405 Ser Gly Phe Thr Gly His 410 Ala Gly Asp Ala Ile Leu Thr Tyr
 Phe Ala 420 Gln Thr Asn Gln Thr Ser 425 Leu Met Ile Asp Leu Thr Gly Gln
 Gly Ser 435 Val Asp Phe Ala Val 440 Gly Val Val Gly Gln Ala Leu Ala Ser
 Asp Ile 450 Val Ala 455
 465

<210> 81
 <211> 1629
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 81
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 aagatgaagg ggtcttacac attaaaagg ttccatggac aagagtggag cggattgcct 180
 caagttgaag gccaaagtga ggacagccta gagcacctga acacgcttat catcgatgca 240
 aaagacgatg cagcgatctc caatctagt tcaaattccag ctgttgctta tgttgaaaga 300
 gaaatcttcc acgaaggctc tcttcaaaa acaaccttg ggcatctctg ctgtaaaagc tcctgaagca 360
 tcaaaagccg tttctcaaaa ttcacaggt tcaggggtgct cgcgttctag tacttgatac tgggatcgat 420
 tggcctctat ctaatgaagg gaaaaatttc gaagcgggca tggacttcac tggcaagtct 480
 caagctcacg ctcttttgac ctctgttagt cacggaactc acgttgctgg tactattgctg 540
 gacggttctg acttcacaga tttcacaggt ttgtctccta aagcaaaagt tttggcaggt 600
 ggtgtgaaag caagatctgg tttcacaggt atcgctatcg ctcaagggtat caactggggt 660
 cgtgtttgtt ctgaaaacgg ttgctctaac tctttgggtg gtatgtgggtc gactcctgca 720
 attactcaaa acgtagacgt tatctctatg tctttgggtg gtatgtgggtc gactcctgca 780
 gagcgtgacg ccgtttctaa agcagacgct gcgggcatca ctgttggtggc ggcttctggt 840
 aacagcggaa ctccgcgtgt ttctttccg gcggcattgc caacagttat cgcagtcggc 900
 gcgatcgaca atacattgaa aaaagctgat ttctctcaat ggggtcctga attggctgtt 960
 gttgctccgg gtgtggcggg tgtttcttct gttccaacgg gaacgggtcg tgaagcggct 1020

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aaagagatcc	tgaatgcaga	aactaatgag	ttgggttgctg	taggtcttgg	taaaactgaa	1140
gatttcgcaa	aagcaaacgt	aactggtaaa	tacgctttga	tcagccgtgg	tgagatcact	1200
ttcgggtgata	aagttaaaaa	cgcatcgcg	gcgggtgctg	cgggtgtggt	tatctacaat	1260
aacgctccag	gcttgatcca	aggttctttg	actaacgatg	gatctacatt	gtcagttcca	1320
gttttcatgg	tggaacaaac	tactggtaac	gatatcgtag	cgtctttgga	aaaaggcgaa	1380
actgtgaaag	ccactttgca	aactcttgca	actgactact	ctgctttcga	cggtacttct	1440
atggcaactc	cacacgtatc	tggtgtagtg	gctcttatga	aagcggcaaa	caaggctttg	1500
acgggcgctc	aagtaaaaga	catcttgaag	caaacagctc	aagctttggg	accaaacgat	1560
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gcaaaataa						1629

<210> 82
 <211> 542
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(20)

<400> 82

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			20					25					30		
Phe	Lys	Met	Ala	Asp	Gln	Val	Tyr	Lys	Met	Lys	Gly	Ser	Tyr	Thr	Leu
		35					40					45			
Lys	Gly	Phe	His	Gly	Gln	Glu	Trp	Ser	Gly	Leu	Pro	Gln	Val	Glu	Gly
	50					55					60				
Gln	Val	Glu	Asp	Ser	Leu	Glu	His	Leu	Asn	Thr	Leu	Ile	Ile	Asp	Ala
	65				70				75					80	
Lys	Asp	Asp	Ala	Ala	Ile	Ser	Asn	Leu	Val	Ser	Asn	Pro	Ala	Val	Ala
			85					90					95		
Tyr	Val	Glu	Arg	Glu	Ile	Phe	His	Glu	Gly	Pro	Arg	Pro	Val	Arg	Gly
			100					105					110		
Phe	Val	Ala	Ala	Pro	Leu	Ala	Lys	Ser	Lys	Ala	Val	Ser	Gln	Lys	Gln
		115					120					125			
Pro	Trp	Gly	Ile	Ser	Ala	Val	Lys	Ala	Pro	Glu	Ala	Trp	Pro	Leu	Ser
	130				135					140					
Asn	Glu	Gly	Gln	Gly	Ala	Arg	Val	Leu	Val	Leu	Asp	Thr	Gly	Ile	Asp
	145				150					155				160	
Gln	Ala	His	Ala	Ser	Leu	Thr	Lys	Asn	Phe	Glu	Ala	Gly	Met	Asp	Phe
			165					170					175		
Thr	Gly	Lys	Ser	Asp	Gly	Ser	Asp	Phe	Thr	Asp	Ser	Val	Gly	His	Gly
		180						185					190		
Thr	His	Val	Ala	Gly	Thr	Ile	Ala	Gly	Val	Lys	Ala	Arg	Ser	Gly	Phe
	195						200					205			
Thr	Gly	Val	Ala	Pro	Lys	Ala	Lys	Val	Leu	Ala	Gly	Arg	Val	Cys	Ser
	210				215						220				
Glu	Asn	Gly	Cys	Ser	Asn	Ile	Ala	Ile	Ala	Gln	Gly	Ile	Asn	Trp	Gly
	225				230				235					240	
Ile	Thr	Gln	Asn	Val	Asp	Val	Ile	Ser	Met	Ser	Leu	Gly	Gly	Met	Trp
			245					250					255		
Ser	Thr	Pro	Ala	Glu	Arg	Asp	Ala	Val	Ser	Lys	Ala	Asp	Ala	Ala	Gly
			260					265					270		
Ile	Thr	Val	Val	Ala	Ala	Ser	Gly	Asn	Ser	Gly	Thr	Pro	Arg	Val	Ser
	275						280					285			
Phe	Pro	Ala	Ala	Leu	Pro	Thr	Val	Ile	Ala	Val	Gly	Ala	Ile	Asp	Asn
	290				295						300				
Thr	Leu	Lys	Lys	Ala	Asp	Phe	Ser	Gln	Trp	Gly	Pro	Glu	Leu	Ala	Val
	305				310					315				320	
Val	Ala	Pro	Gly	Val	Ala	Val	Val	Ser	Ser	Val	Pro	Thr	Gly	Thr	Gly
			325					330					335		
Arg	Glu	Ala	Ala	Val	Glu	Ile	Ala	Phe	Ser	Ala	Lys	Ser	Gly	Lys	Val
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Asn Ala Thr Thr Phe Gln Gly Ala Lys Glu Ile Leu Asn Ala Glu Thr
      355      360      365
Asn Glu Leu Val Ala Val Gly Leu Gly Lys Thr Glu Asp Phe Ala Lys
      370      375      380
Ala Asn Val Thr Gly Lys Tyr Ala Leu Ile Ser Arg Gly Glu Ile Thr
      385      390      395
Phe Gly Asp Lys Val Lys Asn Ala Ile Ala Ala Gly Ala Ala Gly Val
      405      410      415
Val Ile Tyr Asn Asn Ala Pro Gly Leu Ile Gln Gly Ser Leu Thr Asn
      420      425      430
Asp Gly Ser Thr Leu Ser Val Pro Val Phe Met Val Glu Gln Thr Thr
      435      440      445
Gly Asn Asp Ile Val Ala Ser Leu Glu Lys Gly Glu Thr Val Lys Ala
      450      455      460
Thr Leu Gln Thr Leu Ala Thr Asp Tyr Ser Ala Phe Asp Gly Thr Ser
      465      470      475
Met Ala Thr Pro His Val Ser Gly Val Val Ala Leu Met Lys Ala Ala
      485      490      495
Asn Lys Ala Leu Thr Gly Ala Gln Val Lys Asp Ile Leu Lys Gln Thr
      500      505      510
Ala Gln Ala Leu Gly Pro Asn Asp Glu Asn Gln Tyr Gly Ala Gly Leu
      515      520      525
Val Asn Ala Glu Ala Ala Val Asn Ala Ala Ile Gln Ala Lys
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<210> 83
 <211> 3048
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 83

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gaattcaatg	ccgattgggg	gctgggagcg	gtcaacgcac	aggaggccta	cgctgccggt	180
tacaccggca	aaggcgtgaa	gctggggatc	ttcgaccaac	cggtctacgc	cgcgcatccg	240
gagttttccg	gccccaaaca	agtgatcacg	ctgggtacca	gcggcatccg	cgaatacacc	300
gatccgtaca	tcccgggtcaa	agcgggagac	gcctttcgct	acgacggttc	gccctcgata	360
ggttccgacg	gcaagctggg	ggcccacggc	acccacgttg	gcgggattgc	tgccggcagt	420
cgcgatggcg	gtccgatgca	tggtgtggcg	tttggcgcgc	agatcatcag	tgccggacaac	480
ggagatccgg	gcccgggaaga	cgcatcatt	cgcggaatg	acggtgcggt	ctacaaggcc	540
ggttgggatg	ccttgatcgc	cagcggcgcg	cggatcatca	acaacagttg	gggcatcggt	600
atcaccgatc	gcttcgacct	cggcggacgc	aatcccgcct	acccgcattt	caccgtgcag	660
gacgcgcaat	tgagttcaa	cgagatccgt	ccgttgctcg	ggaccaaacc	gggcggagcc	720
tacgacggcg	ccatcgcggc	ggcccgcagc	ggtatcgtga	cgatcttcgc	ggccggcaac	780
gactacaacc	tcaacaaccc	ggacgccatc	gccggcctgg	gctatttcgt	cccggacatc	840
gcgcccgaact	gggtcaccgt	ggcggcggtg	cagaaaaaac	cggacctcaa	cagcccggat	900
ctctacaaca	tcagcacctt	ctcatcgcg	tgccggtaca	ccgccagctt	ttgcgtgtcc	960
gcaccggggca	gcaagatcta	cagctcgatc	atcagcggtg	ccaacgccgg	cgacctgacc	1020
accgggtaca	agaattacaa	cggcacctcg	atggcgggcg	cgcatgtcgc	cggttccatg	1080
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aacctgcgca	aaggcatcga	tgcccccggc	atgtttgtca	ccgagcaaga	cattcccggag	1260
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tccatcggga	ccttgagggt	ggcgggcgac	gtcaccttcg	aacctggctc	gacctacgcc	1680
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ttcggcgcg	tgataccgga	ttacctgttc	attggaggga	cactcgggta	ctcggccaat	1920
ggcatccaac	tggcggtaga	gcgtaacgca	gcgttcctcg	ccagcgtcgg	ccaaaccccg	1980
aaccaacgcg	ctgtcgcagc	ggccgcggag	caactggcgg	ccggcaatcc	tctctatgaa	2040

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accttactgc	tttcgccgac	cgctgccgtc	gcgcaacaag	ctttccagca	actgtccggt	2100
gagattcacc	cggcgatcgg	cacgttggtg	atcaacgaca	gccgttacct	gcgcgatgcc	2160
gtcgggtgaac	gcctgcgtga	gcgtgatctg	ttcaacgctg	cggcaccgac	cgatgaccgt	2220
agcaacgcct	gggtcaaagt	cctcggcgcc	tggggcaaga	gcgatggcgg	gcatgacaac	2280
gccagttcca	acagctccat	cggcggttg	ctggccggtg	tcgacggtct	gatcactgaa	2340
aatacgcggc	tgggtttcgt	gactgggttac	agcgacagtt	cgttgagcat	gggcgatggc	2400
acgcattcct	cagcctccgt	cgatagctac	cacttgggcg	cctatctggg	ccatgaaatc	2460
gatgcgctgc	gtctgagcgt	cggcggtgca	tacagctggc	atcgcatcga	cgtgaagcgt	2520
gacctgcaat	tgggcgacgt	cagcggcaaa	cagaaatcca	aacgcgatgc	gacaaccgca	2580
caactgttta	ccgaagcggc	gtatcgctg	gacctgcagc	cgctggcgct	ggaaccgttc	2640
gccaacctgg	cttacgttca	cctcaacagc	gacagcttca	ccgagaaggg	tgatgccgca	2700
gcgctcaagg	gcggtgaaga	caaccgcgac	gccgtgctct	cgaccctcgg	cctgcggggcg	2760
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gcgttcagcg	tgcagagcgt	ttccctggac	cgtaacgctg	ccgtcatcgg	tgcgcgggcc	2940
ggtttggtcg	tggcgcagga	cgttcgttg	agcctggatt	acaacggact	gctcggctcc	3000
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<210> 84

<211> 1015

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(22)

<400> 84

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Leu	Gly	Thr	Ala	His	Ala	Ala	Pro	Tyr	Val	Glu	Asn	Gly	Arg	Ala	Gly
			20					25					30		
Asp	Pro	Asn	Ser	Trp	Arg	Ser	Thr	Glu	Phe	Asn	Ala	Asp	Trp	Gly	Leu
		35					40					45			
Gly	Ala	Val	Asn	Ala	Gln	Glu	Ala	Tyr	Ala	Ala	Gly	Tyr	Thr	Gly	Lys
	50					55					60				
Gly	Val	Lys	Leu	Gly	Ile	Phe	Asp	Gln	Pro	Val	Tyr	Ala	Ala	His	Pro
65					70				75					80	
Glu	Phe	Ser	Gly	Pro	Asn	Lys	Val	Ile	Thr	Leu	Val	Thr	Ser	Gly	Ile
			85						90					95	
Arg	Glu	Tyr	Thr	Asp	Pro	Tyr	Ile	Pro	Val	Lys	Ala	Gly	Asp	Ala	Phe
			100					105					110		
Arg	Tyr	Asp	Gly	Ser	Pro	Ser	Ile	Gly	Ser	Asp	Gly	Lys	Leu	Gly	Ala
		115					120					125			
His	Gly	Thr	His	Val	Gly	Gly	Ile	Ala	Ala	Gly	Ser	Arg	Asp	Gly	Gly
	130					135					140				
Pro	Met	His	Gly	Val	Ala	Phe	Gly	Ala	Gln	Ile	Ile	Ser	Ala	Asp	Asn
145					150					155				160	
Gly	Asp	Pro	Gly	Pro	Glu	Asp	Gly	Ile	Ile	Arg	Gly	Asn	Asp	Gly	Ala
			165						170					175	
Val	Tyr	Lys	Ala	Gly	Trp	Asp	Ala	Leu	Ile	Ala	Ser	Gly	Ala	Arg	Ile
			180					185						190	
Ile	Asn	Asn	Ser	Trp	Gly	Ile	Gly	Ile	Thr	Asp	Arg	Phe	Asp	Leu	Gly
	195						200					205			
Gly	Arg	Asn	Pro	Ala	Tyr	Pro	His	Phe	Thr	Val	Gln	Asp	Ala	Gln	Leu
	210					215					220				
Gln	Phe	Asn	Glu	Ile	Arg	Pro	Leu	Leu	Gly	Thr	Lys	Pro	Gly	Gly	Ala
225					230					235					240
Tyr	Asp	Gly	Ala	Ile	Ala	Ala	Ala	Arg	Ser	Gly	Ile	Val	Thr	Ile	Phe
			245						250					255	
Ala	Ala	Gly	Asn	Asp	Tyr	Asn	Leu	Asn	Asn	Pro	Asp	Ala	Ile	Ala	Gly
			260					265					270		
Leu	Gly	Tyr	Phe	Val	Pro	Asp	Ile	Ala	Pro	Asn	Trp	Val	Thr	Val	Ala
		275					280						285		
Ala	Leu	Gln	Lys	Asn	Pro	Asp	Leu	Asn	Ser	Pro	Asp	Leu	Tyr	Asn	Ile
	290					295					300				

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Ser Thr Phe Ser Ser Arg Cys Gly Tyr Thr Ala Ser Phe Cys Val Ser
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 Ala Pro Gly Ser Lys Ile Tyr Ser Ser Ile Ile Ser Gly Thr Asn Ala
 325 330 335
 Gly Asp Leu Thr Thr Gly Tyr Lys Asn Tyr Asn Gly Thr Ser Met Ala
 340 345 350
 Ala Pro His Val Ala Gly Ser Met Ala Val Leu Met Glu Arg Phe Pro
 355 360 365
 Tyr Met Thr Gly Ala Gln Val Ala Ser Val Leu Arg Thr Thr Ala Thr
 370 375 380
 Asp Leu Gly Ala Pro Gly Val Asp Ser Leu Tyr Gly Trp Gly Met Ile
 385 390 395 400
 Asn Leu Arg Lys Gly Ile Asp Gly Pro Ala Met Phe Val Thr Glu Gln
 405 410 415
 Asp Ile Pro Glu Gly Phe Arg Ile Gln Gly Ala Tyr Gly Ser Ser Gln
 420 425 430
 Phe Val Ala Asp Leu Pro Gly Ile Gly Ala Ile Ile Asp Ala Gly Lys
 435 440 445
 Pro Thr Glu Arg Val Cys Asn Asp Val His Cys Gly Leu Asp Thr Trp
 450 455 460
 Arg Asn Asp Ile Ser Gly His Gly Gly Leu Thr Lys Gln Gly Ile Gly
 465 470 475 480
 Thr Leu Val Leu Thr Gly Ala Asn Thr Tyr Ala Gly Pro Thr Leu Val
 485 490 495
 Asn Gln Gly Arg Leu Ala Ile Asn Gly Ser Leu Leu Ser Ala Val Thr
 500 505 510
 Val Asn Asp Ser Gly Ile Leu Gly Gly Asn Gly Arg Ile Gly Ala Leu
 515 520 525
 Thr Ala Lys Ser Gly Gly Thr Val Ala Pro Gly Asn Ser Ile Gly Thr
 530 535 540
 Leu Gln Val Ala Gly Asp Val Thr Phe Glu Pro Gly Ser Thr Tyr Ala
 545 550 555 560
 Val Glu Leu Ser Pro Thr Ser Ser Asp Arg Ile Val Ala Gly Gly Lys
 565 570 575
 Ala Val Ile Asp Gly Ala Thr Val Ser Leu Ser Leu Glu Asn Ser Pro
 580 585 590
 Thr Leu Leu Thr Thr Ser Glu Val Lys Ser Leu Leu Gly Asn Gln Tyr
 595 600 605
 Thr Ile Leu Gln Ala Ala Gly Ile Glu Gly Arg Phe Gly Ala Val
 610 615 620
 Ile Pro Asp Tyr Leu Phe Ile Gly Gly Thr Leu Gly Tyr Ser Ala Asn
 625 630 635 640
 Gly Ile Gln Leu Ala Val Glu Arg Asn Ala Ala Ser Phe Ala Ser Val
 645 650 655
 Gly Gln Thr Pro Asn Gln Arg Ala Val Ala Ala Ala Ala Glu Gln Leu
 660 665 670
 Gly Ala Gly Asn Pro Leu Tyr Glu Thr Leu Leu Leu Ser Pro Thr Ala
 675 680 685
 Ala Val Ala Gln Gln Ala Phe Gln Gln Leu Ser Gly Ile His Pro
 690 695 700
 Ala Ile Gly Thr Leu Leu Ile Asn Asp Ser Arg Tyr Leu Arg Asp Ala
 705 710 715 720
 Val Gly Glu Arg Leu Arg Glu Arg Asp Leu Phe Asn Ala Ala Ala Pro
 725 730 735
 Thr Asp Asp Arg Ser Asn Ala Trp Val Lys Val Leu Gly Ala Trp Gly
 740 745 750
 Lys Ser Asp Gly Gly His Asp Asn Ala Ser Ser Asn Ser Ile Gly
 755 760 765
 Gly Leu Leu Ala Gly Val Asp Gly Leu Ile Thr Glu Asn Thr Arg Leu
 770 775 780
 Gly Phe Val Thr Gly Tyr Ser Asp Ser Ser Leu Ser Met Gly Asp Gly
 785 790 795 800
 Thr His Ser Ser Ala Ser Val Asp Ser Tyr His Leu Gly Ala Tyr Leu
 805 810 815
 Gly His Glu Ile Asp Ala Leu Arg Leu Ser Val Gly Gly Ala Tyr Ser
 820 825 830
 Trp His Arg Ile Asp Val Lys Arg Asp Leu Gln Leu Gly Asp Val Ser
 835 840 845

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Gly	Lys	Gln	Lys	Ser	Lys	Arg	Asp	Ala	Thr	Thr	Ala	Gln	Leu	Phe	Thr
850	850					855					860				
Glu	Ala	Ala	Tyr	Arg	Leu	Asp	Leu	Gln	Pro	Leu	Ala	Leu	Glu	Pro	Phe
865					870					875					880
Ala	Asn	Leu	Ala	Tyr	Val	His	Leu	Asn	Ser	Asp	Ser	Phe	Thr	Glu	Lys
				885						890				895	
Gly	Asp	Ala	Ala	Ala	Leu	Lys	Gly	Gly	Glu	Asp	Asn	Arg	Asp	Ala	Val
			900					905					910		
Leu	Ser	Thr	Leu	Gly	Leu	Arg	Ala	Ser	Lys	Ala	Ile	Ala	Leu	Ser	Asp
		915					920					925			
Gln	Gln	Gln	Leu	Glu	Leu	Ser	Gly	Thr	Leu	Gly	Trp	Gln	His	Asn	Leu
		930				935					940				
Ser	Asn	Thr	Arg	Ser	Glu	Asp	His	Leu	Ala	Phe	Ala	Asn	Gly	Asn	Thr
945					950					955					960
Ala	Phe	Ser	Val	Gln	Ser	Val	Ser	Leu	Asp	Arg	Asn	Ala	Ala	Val	Ile
				965					970					975	
Gly	Ala	Arg	Ala	Gly	Leu	Ala	Val	Ala	Gln	Asp	Val	Arg	Leu	Ser	Leu
			980					985					990		
Asp	Tyr	Asn	Gly	Leu	Leu	Gly	Ser	Arg	Glu	Lys	Asp	His	Gly	Val	Gly
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Leu	Thr	Leu	Asp	Trp	Gln	Phe									
1010						1015									

<210> 85

<211> 2166

<212> DNA

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 85

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gatt	cc	gc	ga	tg	ga	240
ctt	gg	tg	gc	gc	gc	300
ctt	aa	gc	gc	gc	gc	360
ctt	aa	gc	gc	gc	gc	420
ctt	aa	gc	gc	gc	gc	480
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ctt	aa	gc	gc	gc	gc	660
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ctt	aa	gc	gc	gc	gc	780
ctt	aa	gc	gc	gc	gc	840
ctt	aa	gc	gc	gc	gc	900
ctt	aa	gc	gc	gc	gc	960
ctt	aa	gc	gc	gc	gc	1020
ctt	aa	gc	gc	gc	gc	1080
ctt	aa	gc	gc	gc	gc	1140
ctt	aa	gc	gc	gc	gc	1200
ctt	aa	gc	gc	gc	gc	1260
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ctt	aa	gc	gc	gc	gc	1500
ctt	aa	gc	gc	gc	gc	1560
ctt	aa	gc	gc	gc	gc	1620
ctt	aa	gc	gc	gc	gc	1680
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ctt	aa	gc	gc	gc	gc	1800
ctt	aa	gc	gc	gc	gc	1860
ctt	aa	gc	gc	gc	gc	1920
ctt	aa	gc	gc	gc	gc	1980
ctt	aa	gc	gc	gc	gc	2040
ctt	aa	gc	gc	gc	gc	2100
ctt	aa	gc	gc	gc	gc	2160

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aaataa

2166

<210> 86
 <211> 721
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(20)

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 35 40 45
 His Ala Met Asn Ile His Gly Asp Thr Arg Ile Asp Asn Tyr Tyr Trp
 50 55 60
 Met Arg Asp Asp Glu Arg Gln Asp Pro Glu Ile Leu Gln His Leu Glu
 65 70 75 80
 Gln Glu Asn Gln Tyr Ala Glu Thr Val Leu Lys His Thr Glu Ala Leu
 85 90 95
 Gln Glu Gln Leu Phe Glu Glu Ile Lys Gly Arg Ile Ala Lys Asp Asp
 100 105 110
 Asn Ser Val Pro Val Arg Lys Gly Ser Tyr Tyr Tyr Ser Asn Glu Val
 115 120 125
 Thr Gly Asp Asn Glu Tyr Glu Val His Leu Arg Ala Lys Asp Phe Ala
 130 135 140
 Gly Thr Asp Lys Gln Val Ile Leu Asp Val Asn Glu Leu Ala Lys Glu
 145 150 155 160
 His Glu Phe Phe Ser Ile Gly Gly Leu Tyr Val Ser Pro Asn Glu Asn
 165 170 175
 Met Leu Ala Tyr Gly Glu Asp Thr Leu Ser Arg Arg Ile Tyr Thr Ile
 180 185 190
 Lys Ile Lys Asp Leu Thr Thr Gly Glu Tyr Leu Lys Asp Glu Ile Glu
 195 200 205
 Gly Ala Ser Ser Ala Ile Ala Trp Gln Asn Asp Asn Gln Ala Phe Tyr
 210 215 220
 Tyr Ile Lys Lys Asp Pro Gln Thr Leu Leu Gly Tyr Gln Val Tyr Arg
 225 230 235 240
 His Val Leu Gly Thr Pro Gln Thr Ser Asp Glu Leu Ile Tyr Glu Glu
 245 250 255
 Thr Asp Ser Ala Tyr Tyr Thr Phe Leu Ser Lys Ser Lys Asp Gly Glu
 260 265 270
 Gln Val Tyr Ile Trp His Ser Ser Thr Glu Thr Ser Gly Val Ser Val
 275 280 285
 Ile Asp Ala Asn Asn Pro Asn Ala Lys Ala Glu Ala Phe Tyr Pro Arg
 290 295 300
 Glu Thr Gly Ile Glu Tyr Ser Ile Ala Lys Leu Gly Asp Trp Tyr Tyr
 305 310 315 320
 Val Tyr Thr Asn Tyr Gln Ala Val Asn Phe Arg Leu Met Lys Val Lys
 325 330 335
 Ala Glu Glu Met His Asp Arg Ser Lys Trp Val Asp Val Ile Pro Ala
 340 345 350
 Asp Asp Asn Thr Gln Leu Val Asp Phe Asp Leu Phe Asp Asp His Leu
 355 360 365
 Val Tyr Glu Gln Arg Thr Asn Gly Leu Ser Thr Val Lys Val Arg Gln
 370 375 380
 Leu Ser Thr Gly Lys Glu Phe Pro Leu Glu Phe Asn Asp Thr Ala Phe
 385 390 395 400
 Ala Ala Tyr Leu Thr Gly Asn Tyr Glu Leu Asp Asn Ser Lys Val Arg
 405 410 415
 Ile Tyr Tyr Ser Ser Leu Thr Thr Pro Gly Thr Tyr Tyr Asp Phe Asp
 420 425 430

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Leu Asn Thr Gly Glu Ser Glu Ile Met Lys Gln Thr Pro Leu Leu Gly
 435 440 445
 Asp Leu Asp Ala Asp Asn Tyr His Ser Lys Gln Ile Met Val Thr Ala
 450 455 460
 Arg Asp Gly Asn Gln Leu Pro Val Ser Leu Val Tyr Arg Lys Asp Leu
 465 470 475 480
 Phe Lys Lys Asn Gly Thr Asn Pro Ile Tyr Gln Tyr Gly Tyr Gly Ser
 485 490 495
 Tyr Gly Ser Thr Ile Glu Pro Thr Phe Arg Ser Thr Arg Leu Ser Leu
 500 505 510
 Leu Asp Arg Gly Phe Val Tyr Ala Ile Ala His Ile Arg Gly Ser Glu
 515 520 525
 Met Leu Gly Arg Pro Trp Tyr Glu Asp Gly Lys Lys Leu Thr Lys Gln
 530 535 540
 Asn Thr Phe Asn Asp Phe Ile Asp Val Thr Lys Gly Leu Val Glu Glu
 545 550 555 560
 Gly Tyr Gly Ala Lys Asp Lys Val Phe Ala Val Gly Gly Ser Ala Gly
 565 570 575
 Gly Leu Leu Met Gly Ala Ile Ile Asn Gln Ala Pro Glu Leu Tyr Arg
 580 585 590
 Gly Ile Gly Ala His Val Pro Phe Val Asp Val Val Thr Thr Met Leu
 595 600 605
 Asp Glu Ser Ile Pro Leu Thr Thr Asn Glu Tyr Asp Glu Trp Gly Asn
 610 615 620
 Pro Asn Asp Lys Thr Tyr Tyr Asp Tyr Met Val Ser Tyr Ser Pro Tyr
 625 630 635 640
 Asp Asn Val Lys Thr Gln Asn Tyr Pro Asn Met Leu Val Thr Thr Gly
 645 650 655
 Leu His Asp Ser Gln Val Gln Tyr Phe Glu Pro Met Lys Trp Val Ala
 660 665 670
 Lys Leu Arg Glu Met Lys Thr Asp Asn Val Leu Leu Phe Lys Thr
 675 680 685
 Asp Met Glu Ala Gly His Gly Gly Ala Ser Gly Arg Phe Lys Arg Leu
 690 695 700
 Lys Glu Asp Ala Leu Glu Tyr Ala Phe Phe Leu Asp Leu Leu Glu Thr
 705 710 715 720
 Lys

<210> 87
 <211> 1848
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 87

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gcgcaggggtg	ccgttggtgc	agacaagacc	gaccgcatca	tcgtcaagta	caaggacgaa	180
caggcgccgg	tggccgtgaa	gggcggttcg	atcgccgccca	tggccaagggc	cacggccgag	240
ccgatgtcga	cggcgcgcaa	ggccaagctg	gaccgcgccg	gccagcagtt	cggcttcctg	300
atgaaggaat	cgcaccgcat	cgccaccggc	gcccgcgtcg	tcaagctgga	ccgcaaggtc	360
tcgctgcagg	aagccgcgca	agtggcggcc	gacctggccg	cgcgcgaccc	ggacgtcgaa	420
tacgccgaac	cggaccgcct	gctgcatccc	ctgatgacgc	cgaacgattc	gatgtacagc	480
cagcagtggg	acttcttcga	agccaccggc	ggcatgaaca	tcccggcggc	ctgggacaag	540
tcgaccggct	ccggcatccg	cgtggccgtg	atcgataccg	gctaccgtcc	gcacgcccag	600
ctgtcggggc	agatcctggc	cggctatgac	ttcatttcgg	acgccaccat	cggcaacgac	660
ggcaacggcc	gcgacagcga	cgccagcgac	ccgggcgact	ggaccgcggc	cggcgaatgc	720
ggcgccggcg	agccggcgctc	caactcgagc	tggcacggca	cccacgtggc	cggcaccatc	780
gccgcgtcga	cgaacaacgg	cagcggcgtg	gccggcatcg	cctacggcgc	caagatcgtg	840
ccggtacgcg	tgctcggcaa	atgcggcggc	tacacctcgg	acatcgccga	cggcatcatc	900
tgggcttccg	gcggcaccgt	ctcgggcgtg	cccaacatcg	cggcgcgcg	gcaggtgatc	960
aacatgtcgc	tgggcggcgg	cggcgctcgc	ggcaccacga	cccagaacgc	gatcaacagc	1020
gcccgcctcg	cgggcaccgt	ggtcgtggtc	cgggcggcga	acgagtcgca	gaacgccagc	1080
aacagcaacc	cggccaactg	ctcgggcgtg	atcacggtgg	cggcgacgaa	ccgttcggc	1140
ggacgcgcat	cctactcgaa	ctacggcacc	gtggtcgacg	tggcgggcgc	gggcggcgac	1200

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agcggcgcg	ccatcctgtc	gacgctgaac	gccggcacca	aggcaccggg	cgccgacagc	1260
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atgctggcca	agaacgcgtc	gatgaccccg	gaccaggctcg	aagccgcgct	gaagtcgacc	1380
gcgcgcgcct	tcccggcctc	gtgcagcggc	tgcggcgccg	gcatcgtgaa	cgctcgggcc	1440
gcggctcgatg	cggccatcgg	cggcgggcggc	accacgaccg	gcccgacggg	gtcgggaaacc	1500
gagtcgaaca	acacgatcag	caccgccaac	agcgtgacga	ccacgggtac	cacgggtcaac	1560
ggcaccatgg	ccagcagcac	ggacaccgat	tacttcgtgg	tccagggtccc	ggccggcaag	1620
acgctgagcg	ccaccctgac	cccgggttcg	agcgccgact	acgacctgta	tatctacaac	1680
agcgcgggca	cccagctggc	gaccagccag	aacggcaccg	gcgcgggtcga	cagcgccagc	1740
tcggccaact	ccaccacggc	cgcttcggca	cgctacgtgc	gcgtgggtgta	ctacagcggc	1800
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<210> 88
 <211> 615
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(35)

<400> 88

Met	Lys	Ser	Lys	Gln	Ser	Met	Tyr	Pro	Ala	Val	Leu	Lys	Leu	Cys	Ala
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Ala	Ala	Val	Leu	Gly	Leu	Gly	Ala	Gly	Val	Ala	Val	Ala	Gly	Val	Ser
			20					25					30		
Ala	Thr	Ala	Gln	Gly	Thr	Pro	Val	Ala	Gln	Gly	Ala	Val	Val	Ala	Asp
			35					40					45		
Lys	Thr	Asp	Arg	Ile	Ile	Val	Lys	Tyr	Lys	Asp	Glu	Gln	Ala	Pro	Val
	50					55					60				
Ala	Val	Lys	Gly	Gly	Ser	Ile	Ala	Ala	Met	Ala	Lys	Ala	Thr	Ala	Glu
65					70				75						80
Pro	Met	Ser	Thr	Ala	Arg	Lys	Ala	Lys	Leu	Asp	Arg	Ala	Gly	Gln	Gln
				85					90					95	
Phe	Gly	Phe	Leu	Met	Lys	Glu	Ser	His	Arg	Ile	Ala	Thr	Gly	Ala	Arg
			100					105					110		
Val	Val	Lys	Leu	Asp	Arg	Lys	Val	Ser	Leu	Gln	Glu	Ala	Ala	Gln	Val
		115						120					125		
Ala	Ala	Asp	Leu	Ala	Ala	Arg	Asp	Pro	Asp	Val	Glu	Tyr	Ala	Glu	Pro
	130					135					140				
Asp	Arg	Leu	Leu	His	Pro	Leu	Met	Thr	Pro	Asn	Asp	Ser	Met	Tyr	Ser
145					150					155					160
Gln	Gln	Trp	Asp	Phe	Phe	Glu	Ala	Thr	Gly	Gly	Met	Asn	Ile	Pro	Ala
				165					170					175	
Ala	Trp	Asp	Lys	Ser	Thr	Gly	Ser	Gly	Ile	Arg	Val	Ala	Val	Ile	Asp
			180					185					190		
Thr	Gly	Tyr	Arg	Pro	His	Ala	Asp	Leu	Ser	Gly	Gln	Ile	Leu	Ala	Gly
		195					200					205			
Tyr	Asp	Phe	Ile	Ser	Asp	Ala	Thr	Ile	Gly	Asn	Asp	Gly	Asn	Gly	Arg
	210					215					220				
Asp	Ser	Asp	Ala	Ser	Asp	Pro	Gly	Asp	Trp	Thr	Ala	Ala	Gly	Glu	Cys
225					230					235					240
Gly	Ala	Gly	Glu	Pro	Ala	Ser	Asn	Ser	Ser	Trp	His	Gly	Thr	His	Val
				245					250					255	
Ala	Gly	Thr	Ile	Ala	Ala	Leu	Thr	Asn	Gly	Ser	Gly	Val	Ala	Gly	
			260					265					270		
Ile	Ala	Tyr	Gly	Ala	Lys	Ile	Val	Pro	Val	Arg	Val	Leu	Gly	Lys	Cys
		275					280					285			
Gly	Gly	Tyr	Thr	Ser	Asp	Ile	Ala	Asp	Gly	Ile	Ile	Trp	Ala	Ser	Gly
	290					295					300				
Gly	Thr	Val	Ser	Gly	Val	Pro	Asn	Ile	Ala	Ala	Arg	Ala	Gln	Val	Ile
305					310					315					320
Asn	Met	Ser	Leu	Gly	Gly	Gly	Gly	Ala	Cys	Gly	Thr	Thr	Thr	Gln	Asn
				325					330					335	
Ala	Ile	Asn	Ser	Ala	Arg	Ser	Arg	Gly	Thr	Val	Val	Val	Val	Ala	Ala
			340					345					350		

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Gly Asn Glu Ser Gln Asn Ala Ser Asn Ser Asn Pro Ala Asn Cys Ser
 355 360 365
 Gly Val Ile Thr Val Ala Ala Thr Asn Arg Ser Gly Gly Arg Ala Ser
 370 375 380
 Tyr Ser Asn Tyr Gly Thr Val Val Asp Val Ala Ala Pro Gly Gly Asp
 385 390 395 400
 Ser Gly Ala Ala Ile Leu Ser Thr Leu Asn Ala Gly Thr Lys Ala Pro
 405 410 415
 Gly Ala Asp Ser Tyr Ala Gly Tyr Met Gly Thr Ser Met Ala Thr Pro
 420 425 430
 His Val Ala Gly Val Val Ala Leu Met Leu Ala Lys Asn Ala Ser Met
 435 440 445
 Thr Pro Asp Gln Val Glu Ala Ala Leu Lys Ser Thr Ala Arg Ala Phe
 450 455 460
 Pro Ala Ser Cys Ser Gly Cys Gly Ala Gly Ile Val Asn Ala Ser Ala
 465 470 475 480
 Ala Val Asp Ala Ala Ile Gly Gly Gly Gly Thr Thr Thr Gly Pro Thr
 485 490 495
 Val Ser Glu Thr Glu Ser Asn Asn Thr Ile Ser Thr Ala Asn Ser Val
 500 505 510
 Thr Thr Thr Gly Thr Thr Val Asn Gly Thr Met Ala Ser Ser Thr Asp
 515 520 525
 Thr Asp Tyr Phe Val Val Gln Val Pro Ala Gly Lys Thr Leu Ser Ala
 530 535 540
 Thr Leu Thr Pro Gly Ser Ser Ala Asp Tyr Asp Leu Tyr Ile Tyr Asn
 545 550 555 560
 Ser Ala Gly Thr Gln Leu Ala Thr Ser Gln Asn Gly Thr Gly Ala Val
 565 570 575
 Asp Ser Ala Ser Ser Ala Asn Ser Thr Thr Ala Ala Ser Ala Arg Tyr
 580 585 590
 Val Arg Val Val Tyr Tyr Ser Gly Gly Thr Gly Ser Thr Asn Gly Lys
 595 600 605
 Tyr Thr Leu Lys Leu Ser Trp
 610 615

<210> 89
 <211> 1791
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 89
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 ccggcagcca gcggggctgc ggacgacctg ccgaccgatc agattattat tctgtacgaa 180
 gaaattgcct ccggcgcgcc ggccatgcag cagctgagct ttgccgccgg ggccgggctg 240
 acccaggtgc gcgaattgtc gggcgggtgg gcggtcatgc agctgccaga cccgctgccc 300
 gccgaagagg tcgaggttct tgcgcggcgg ctgatgaacc tgcccagagg ggcgatagcc 360
 gagcccgatc acatcaacct gccggccgtg ctgcccgaat actcgttctt ctccgcgtac 420
 caatggagcc ttaccgcgcc caagaacaat atctacggca tcgacgcccc cgccgcctgg 480
 gaaatttcga ccggctcgcc tgacatagtg gtggccgtgc tcgatacggg catcctcaac 540
 caccgccgatt tgaacgggcg aaccgtcgcc ggctatgatt tcatcacaaa tgcttgatg 600
 gccaacgacg gcgacgggcg cgaccccaac ccacggacc ccggcgactg gctgaccacc 660
 aatgacattg caaccatttg ttattatgcg ccggtgatgg acagctcgtg gcacggcacg 720
 catgtggcgg gcataatcgg cgcgccagc aataacagtc ttggcatatc cggcatcaac 780
 tggacgtcga aaatcctgcc ggtgcgctg ctgggcaagt gcggcgggta cgattcagac 840
 atcatcgacg ccatccgctg gtcggccggc ctgcccgtac ccggcgcgcc agccaacccc 900
 aacccggcca aagtaatcaa cctcagcctg ggccggccaa atacgtgcag ctcggtcatg 960
 cagtcggcca tcaatgacgc gtacgagcag ggggtcacgg ttggtggtcg cgccggcaac 1020
 agcagcatgg atcccgccgg ctttcgcgg gctcctgca gcaatgtgat ccgctggggc 1080
 gcgaccggcc cgactggctc gcgcgcgtgg tacagcaact acggcgctac cgtggccatc 1140
 tccgcgcccgg gcggcgacgg cagcagcgct atctattcgc tgcacaattc cggcaagacc 1200
 acgcccgtag ccgattccta ccagtacatg atgggcacca gccaggccgc gccgcacgtc 1260
 agcgggggtg tttcgtgctc ctattcgctc taaccccgca tgaccccgca ccaggcgcg 1320
 gccgttctga ccagcaccgc cacggccttc ccggcgggca gcagctgcgc caccgggtctg 1380
 tgcggggcgg gcatcctcaa tgccgggcag gccgtgcagg ccatgaccac cccgcccggc 1440

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accttccaga	agatcgcgcc	gctgaacaat	gccgccggcc	tgccgggtcaa	cagcgtgggtc	1500
ctggagtgga	gccccagcag	cggggcgggc	tcgtacgagt	actgctacta	cgcccccgcg	1560
cttcaggcag	cctgcgccag	ctggatcagc	gccggggcga	gcaccaaagc	cacgctcacc	1620
aatctgctcc	ccgccgtgac	ctactcctgg	cagggtgcggg	cggtaaatgc	cgcaatcacc	1680
gccaccgacg	ccgatttcgt	cgccaacagc	ggaacctggt	ggacgttctc	gaccgaggcg	1740
gtcagcttca	acgtaaccta	caacgtgttt	atgccgtcgg	tcgtgcgcta	a	1791

<210> 90
 <211> 596
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(32)

<400> 90

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Ile	Ala	Leu	Ala	Leu	Ala	Gln	Thr	Gly	Phe	Gly	Ala	Pro	Ala	Ala	Ala
			20					25					30		
Ala	Gln	Ser	Gly	Glu	Ala	Met	Pro	Pro	Ala	Ala	Ser	Gly	Ala	Ala	Asp
		35					40					45			
Asp	Leu	Pro	Thr	Asp	Gln	Ile	Ile	Ile	Leu	Tyr	Glu	Glu	Ile	Ala	Ser
	50					55					60				
Gly	Ala	Pro	Ala	Met	Gln	Gln	Leu	Ser	Phe	Ala	Ala	Gly	Ala	Gly	Leu
	65				70					75					80
Thr	Gln	Val	Arg	Glu	Leu	Ser	Gly	Gly	Gly	Ala	Val	Met	Gln	Leu	Pro
				85					90					95	
Asp	Pro	Leu	Pro	Ala	Glu	Glu	Val	Glu	Val	Leu	Ala	Arg	Arg	Leu	Met
			100					105					110		
Asn	Leu	Pro	Glu	Val	Ala	Tyr	Ala	Glu	Pro	Asp	His	Ile	Asn	Leu	Pro
		115					120					125			
Ala	Val	Leu	Pro	Asn	Asp	Ser	Phe	Phe	Ser	Ala	Tyr	Gln	Trp	Ser	Leu
	130					135					140				
Thr	Ala	Pro	Lys	Asn	Asn	Ile	Tyr	Gly	Ile	Asp	Ala	Pro	Ala	Ala	Trp
	145				150					155					160
Glu	Ile	Ser	Thr	Gly	Ser	Pro	Asp	Ile	Val	Val	Ala	Val	Leu	Asp	Thr
				165					170					175	
Gly	Ile	Leu	Asn	His	Ala	Asp	Leu	Asn	Gly	Arg	Thr	Val	Ala	Gly	Tyr
			180					185					190		
Asp	Phe	Ile	Thr	Asn	Ala	Trp	Met	Ala	Asn	Asp	Gly	Asp	Gly	Arg	Asp
	195						200					205			
Pro	Asn	Pro	Thr	Asp	Pro	Gly	Asp	Trp	Leu	Thr	Thr	Asn	Asp	Ile	Ala
	210					215					220				
Thr	His	Cys	Tyr	Tyr	Ala	Pro	Val	Met	Asp	Ser	Ser	Trp	His	Gly	Thr
	225				230					235					240
His	Val	Ala	Gly	Ile	Ile	Gly	Ala	Ala	Ser	Asn	Asn	Ser	Leu	Gly	Ile
				245					250					255	
Ser	Gly	Ile	Asn	Trp	Thr	Ser	Lys	Ile	Leu	Pro	Val	Arg	Val	Leu	Gly
			260					265					270		
Lys	Cys	Gly	Gly	Tyr	Asp	Ser	Asp	Ile	Ile	Asp	Ala	Ile	Arg	Trp	Ser
		275					280					285			
Ala	Gly	Leu	Pro	Val	Pro	Gly	Ala	Pro	Ala	Asn	Pro	Asn	Pro	Ala	Lys
	290					295					300				
Val	Ile	Asn	Leu	Ser	Leu	Gly	Gly	Pro	Asn	Thr	Cys	Ser	Ser	Val	Met
	305				310					315					320
Gln	Ser	Ala	Ile	Asn	Asp	Ala	Tyr	Glu	Gln	Gly	Val	Thr	Val	Val	Val
				325				330						335	
Ala	Ala	Gly	Asn	Ser	Ser	Met	Asp	Ala	Ala	Gly	Phe	Ser	Pro	Ala	Ser
			340					345					350		
Cys	Ser	Asn	Val	Ile	Ala	Val	Gly	Ala	Thr	Gly	Pro	Thr	Gly	Ser	Arg
		355					360					365			
Ala	Trp	Tyr	Ser	Asn	Tyr	Gly	Ala	Thr	Val	Ala	Ile	Ser	Ala	Pro	Gly
	370					375					380				
Gly	Asp	Gly	Ser	Ser	Ala	Ile	Tyr	Ser	Leu	His	Asn	Ser	Gly	Lys	Thr

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385 Thr Pro Val Ala Asp 390 Ser Tyr Gln Tyr Met Met Gly Thr Ser Gln Ala 400
 Ala Pro His Val 405 Ser Gly Val Val Ser 410 Leu Leu Tyr Ser Leu Asn Pro 415
 Ala Leu Thr 420 Pro Asp Gln Ala Arg Ala Val Leu Thr Ser Thr Ala Thr 430
 Ala Phe 435 Pro Ala Gly Ser Ser Cys Ala Thr Gly Leu Cys Gly Ala Gly 445
 Ile Leu Asn Ala Gly Gln Ala Val Gln Ala Met Thr Thr Pro Pro Gly 460
 465 Thr Phe Gln Lys Ile 470 Ala Pro Leu Asn Asn Ala Ala Gly Leu Pro Val 475
 Asn Ser Val Val Leu Glu Trp Ser Pro Ser Ser Gly Ala Ala Ser Tyr 490
 Glu Tyr Cys Tyr Tyr Ala Pro Ala Leu Gln Ala Ala Cys Ala Ser Trp 500
 Ile Ser Ala Gly Ala Ser Thr 515 Lys Ala Thr Leu Thr Asn Leu Leu Pro 525
 Ala Val Thr Tyr Ser Trp Gln Val Arg Ala Val Asn Ala Ala Ile Thr 535
 545 Ala Thr Asp Ala Asp 550 Phe Val Ala Asn Ser Gly Thr Trp Trp Thr Phe 555
 Ser Thr Glu Ala Val Ser Phe Asn Val Thr Tyr Asn Val Phe Met Pro 570
 Ser Val Val Arg 585 590

<210> 91
 <211> 1425
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 91
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 aaaagtggaa ttttttataa tttctcagct aaaactctac cttcttttga ttatgatact 120
 gcaggaaaaac atattgcacg ggaaaattcc acatggaatg ggaagtatgt tattgggcaa 180
 gcggcagaag tgacatattc attcccaact tgggctggta aaaagtttaa tgattttggt 240
 gataaaaaatc cctatggatt taattcagcg caaaaagatc atgcaagaca atctttagat 300
 gcatggtctg atattgcaaa tatcaaattt accgaagtgg caccaaattgt aaaatcagat 360
 attactttttg gtaatattac tgatccatac ggcaacttcc aagcttatgc aactttgcca 420
 aatacctata gttatggccg tgatctttca gggcaagctt ggtttagtga ttattatgat 480
 gcaaaaaata caacacctga attaggtaat tatggtcgtt taactattat ccatgaaatt 540
 ggtcatgcmc ttggtttaat gcaccctggc gattacaacg cagggcaaaa cgtacctgga 600
 tatttaaaat ctgactatgc tgaagatagt cgccaatata ctgttatgag ttattgggaa 660
 gaatatgaaa caggtgcgca cttccaaggt gcttatgcmc gcgctccitt acttcatgat 720
 atttcagcaa tgcaatatct ttatggcgca aataccacaa ccagaacagg tgatgatgtt 780
 tatgggtttta actcaaacac tgggtattaat tattacacgg caacaagtag cagtataaaa 840
 ttaatcttct cagtttgagg cagtgccggg aacgatactt ttgacttctc aggatattat 900
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 aacgtttcta ttgcacaagg cgttacaata gaaaatgcaa tcggtggctc tggtaattgat 1020
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 tatggtggcg gtggtcaaga tatattatgg ggtggtacag gtagcaatac ctttgtttat 1140
 aaaaagatca ccgactcttt aacctctgct gctgacaaga taatggactt caaatcaggt 1200
 attgataaga ttaatttatc agaattaatc gacgatacct ttggccataa attccttaac 1260
 tttgttgata attttacagg tcgctcgggt gaagcaacca ttaaataatga tcaatcaaca 1320
 aactcaagtg aacttgctat taatgcttat ggatatggat atagccctga tttcaaaatt 1380
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<210> 92
 <211> 474
 <212> PRT
 <213> Unknown

<220>

10336256.txt

<223> Obtained from an environmental sample.

<400> 92

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Leu Pro Ser Phe Asp Tyr Asp Thr Ala Gly Lys His Ile Ala Arg Glu
 40      45      50      55
Asn Ser Thr Trp Asn Gly Lys Tyr Val Ile Gly Gln Ala Ala Glu Val
 60      65      70      75
Thr Tyr Ser Phe Pro Thr Trp Ala Gly Lys Lys Phe Asn Asp Phe Gly
 80      85      90      95
Asp Lys Asn Pro Tyr Gly Phe Asn Ser Ala Gln Lys Asp His Ala Arg
100      105      110      115
Gln Ser Leu Asp Ala Trp Ser Asp Ile Ala Asn Ile Lys Phe Thr Glu
120      125      130      135
Val Ala Pro Asn Val Lys Ser Asp Ile Thr Phe Gly Asn Ile Thr Asp
140      145      150      155
Pro Tyr Gly Asn Phe Gln Ala Tyr Ala Thr Leu Pro Asn Thr Tyr Ser
160      165      170      175
Tyr Gly Arg Asp Leu Ser Gly Gln Ala Trp Phe Ser Asp Tyr Tyr Asp
180      185      190      195
Ala Lys Asn Thr Thr Pro Glu Leu Gly Asn Tyr Gly Arg Leu Thr Ile
200      205      210      215
Ile His Glu Ile Gly His Ala Leu Gly Leu Met His Pro Gly Asp Tyr
220      225      230      235
Asn Ala Gly Gln Asn Val Pro Gly Tyr Leu Lys Ser Asp Tyr Ala Glu
240      245      250      255
Asp Ser Arg Gln Tyr Thr Val Met Ser Tyr Trp Glu Glu Tyr Glu Thr
260      265      270      275
Gly Ala His Phe Gln Gly Ala Tyr Ala Gly Ala Pro Leu Leu His Asp
280      285      290      295
Ile Ser Ala Met Gln Tyr Leu Tyr Gly Ala Asn Thr Thr Thr Arg Thr
300      305      310      315
Gly Asp Asp Val Tyr Gly Phe Asn Ser Asn Thr Gly Ile Asn Tyr Tyr
320      325      330      335
Thr Ala Thr Ser Ser Ser Asp Lys Leu Ile Phe Ser Val Trp Asp Ser
340      345      350      355
Ala Gly Asn Asp Thr Phe Asp Phe Ser Gly Tyr Tyr Gln Asp Gln Val
360      365      370      375
Ile Asp Leu Arg Glu Gly His Phe Ser Asp Val Gly Gly Leu Gln Lys
380      385      390      395
Asn Val Ser Ile Ala Gln Gly Val Thr Ile Glu Asn Ala Ile Gly Gly
400      405      410      415
Ser Gly Asn Asp Thr Ile Tyr Gly Asn Asp Ala Asp Asn Ile Leu Ile
420      425      430      435
Gly Gly Gly Gly Asn Asn Ile Leu Tyr Gly Gly Gly Gly Gln Asp Ile
440      445      450      455
Leu Trp Gly Gly Thr Gly Ser Asn Thr Phe Val Tyr Lys Lys Ile Thr
460      465      470
Asp Ser Leu Thr Ser Ala Ala Asp Lys Ile Met Asp Phe Lys Ser Gly
480      485      490      495
Ile Asp Lys Ile Asn Leu Ser Glu Leu Ile Asp Asp Thr Phe Gly His
500      505      510      515
Lys Phe Leu Asn Phe Val Asp Asn Phe Thr Gly Arg Ser Gly Glu Ala
520      525      530      535
Thr Ile Lys Tyr Asp Gln Ser Thr Asn Ser Ser Glu Leu Ala Ile Asn
540      545      550      555
Ala Tyr Gly Tyr Gly Tyr Ser Pro Asp Phe Lys Ile Asp Ile Val Gly
560      565      570      575
Phe Val Asn Tyr Glu Thr Asp Ile Ile Val
580      585      590      595
465      470

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<210> 93

<211> 984

<212> DNA

<213> Unknown

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<220>

<223> Obtained from an environmental sample.

<400> 93

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cctttcaccc	ccgatcaggg	caggctcttc	ttgaacaacg	ccgccgagaa	ggcgaaggaa	180
tcgcagaaga	cgaccaccaa	gacgtttgag	gaattcaaga	aatcgggtcac	caaggagccg	240
ttccagtacg	gcaaatacat	tgtcaatggc	gacaccccca	ttgccaacga	caaggatctt	300
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atgaacaagc	tcggcatcga	catcatctgg	aaggacgccg	acaagaagaa	tctcacatac	420
tgcgtgagca	acgccccggc	ggagtccggt	ggattcggaa	atcgctacaa	caccgtcgtg	480
agcgccatgg	ccgacgcgac	caaggcatgg	gaagcagttg	ccgacatcaa	gtttattcac	540
gtgactgccg	aggattcgaa	ctgcacgccg	accaacgaga	gcgtcaaatt	cgacgtcagg	600
ccggtcaatc	tcaacgcata	tctggcgcg	gcatttttcc	ccgacgatgt	gcgcaccgcg	660
cgtaacgtcc	tcacgcgcaa	ctcgtcggtt	gagcttcccg	ccggaggaaa	gctctcgttg	720
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ttgtcgggtc	tgcactatcc	gcagtgcgac	ggaaagggcg	attggtcgtt	gaccttgacg	900
gtgcaggaca	agaacggcgt	cgcgtgcgtg	tacaaggcgg	ccccgggatt	cgtgatcgac	960
accaagatct	gcaagccgaa	gtag				984

<210> 94

<211> 327

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(36)

<400> 94

Met	Gly	Leu	Gly	Phe	Ser	Thr	Ala	Leu	Gln	Gln	Arg	Ala	His	His	Pro
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Ile	Ala	Gly	Met	Ile	Leu	Ala	Val	Ala	Val	Ser	Met	Ile	Pro	Gly	Ser
			20					25					30		
Gly	Val	Leu	Ala	Gln	Asp	Lys	Ala	Pro	Phe	Thr	Pro	Asp	Gln	Gly	Arg
		35					40					45			
Leu	Phe	Leu	Asn	Asn	Ala	Ala	Glu	Lys	Ala	Arg	Glu	Ser	Gln	Lys	Thr
	50				55					60					
Thr	Thr	Lys	Thr	Phe	Glu	Phe	Lys	Lys	Ser	Val	Thr	Lys	Glu	Pro	
65				70					75					80	
Phe	Gln	Tyr	Gly	Lys	Tyr	Ile	Val	Asn	Gly	Asp	Thr	Pro	Ile	Ala	Asn
			85					90					95		
Asp	Lys	Asp	Leu	Glu	Glu	Phe	Tyr	Lys	Gln	Asn	Val	Glu	Thr	Ala	Gly
			100					105					110		
Leu	Val	Ala	Ala	Glu	Phe	Ala	Ile	Met	Asn	Lys	Leu	Gly	Ile	Asp	Ile
		115				120						125			
Ile	Trp	Lys	Asp	Ala	Asp	Lys	Lys	Asn	Leu	Thr	Tyr	Cys	Val	Ser	Asn
	130				135						140				
Ala	Pro	Ala	Glu	Ser	Gly	Gly	Phe	Gly	Asn	Arg	Tyr	Asn	Thr	Val	Val
145					150				155						160
Ser	Ala	Met	Ala	Asp	Ala	Thr	Lys	Ala	Trp	Glu	Ala	Val	Ala	Asp	Ile
			165					170						175	
Lys	Phe	Ile	His	Val	Thr	Ala	Glu	Asp	Ser	Asn	Cys	Thr	Pro	Thr	Asn
			180					185					190		
Glu	Ser	Val	Lys	Phe	Asp	Val	Arg	Pro	Val	Asn	Leu	Asn	Ala	Tyr	Leu
		195					200					205			
Ala	Arg	Ala	Phe	Phe	Pro	Asp	Val	Arg	Thr	Ala	Arg	Asn	Val	Leu	
	210				215					220					
Ile	Asp	Asn	Ser	Ser	Phe	Glu	Leu	Pro	Ala	Gly	Gly	Lys	Leu	Ser	Leu
225					230					235					240
Ile	Gly	Ile	Leu	Arg	His	Glu	Leu	Gly	His	Thr	Ile	Gly	Ala	Arg	His
			245						250					255	
Glu	His	Thr	Arg	Pro	Gln	Ser	Gly	Thr	Cys	Phe	Glu	Asp	Lys	Asp	Trp

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260
 Arg Gly Val Thr Asp Tyr Asp Ala Leu Ser Val Met His Tyr Pro Gln
 275 280 285
 Cys Asn Gly Lys Gly Asp Trp Ser Leu Thr Leu Thr Val Gln Asp Lys
 290 295 300
 Asn Gly Val Ala Cys Val Tyr Lys Ala Ala Pro Gly Phe Val Ile Asp
 305 310 315 320
 Thr Lys Ile Cys Lys Pro Lys
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<210> 95

<211> 1806

<212> DNA

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 95

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accgcattaa	caaaacagct	gggtggcgac	gtaaaagtag	atgcagatgg	ttttatcgct	180
gctcagttca	atggtaaatc	tgttgatgaa	atcaaaggta	ttctgaaaaa	ccctcatatc	240
aaactgattg	aagaagattt	agtacgtaaa	ccaatggcgt	tatttaaatga	cgacgctggg	300
gatccaatgc	aacaacaaat	cacaccttat	gctgtgtatc	aatctcaggc	caatcagggtg	360
caatttaacc	ctggcgaggg	tatcaaagtc	tgtgtcattg	actcagggtt	agaccagtct	420
aaccctgatt	ttaactgggg	cagcatcacg	ggcgacaacg	attcaggcac	aggcaactgg	480
aatgtcaacg	gtggcccaca	cggcactcac	gtcgccggta	ccatagggtgc	ggcagacaac	540
ggttttgggtg	tgataggtat	ggcccctggc	gtagctatgc	atatcatcaa	agtatttaac	600
gctgaagggtt	ggggttattc	gtcagatctg	gcttatgccg	cacaaaaatg	taaaaacgca	660
ggctcagaca	ttatcagcat	gagcttaggc	gggtgggtgg	ccaataccac	tgaatccaac	720
gcttttataaa	cctttaccga	cgctgggtgg	ttagttatag	ccgcagcagg	taacgacggc	780
aacaatgtgc	gctcttacc	ggctgggttac	ccttctgtca	tgatgatagg	agccaacgac	840
aataacaaca	atatcgcaga	cttctcccaa	ttcccaagct	gtacagccaa	cggcaaaaaca	900
gatgagacta	tttgtgtgga	agccacagct	gggtgggtgtag	acaccttgct	cacctaccct	960
gccgatattg	caaccagcgc	caccttgagt	gccaacggta	ctccttatgc	cacctctgcg	1020
atggaaaatc	cgggttcagc	cagtgacgct	acattcttta	tgggcacagc	ggaaactgtc	1080
aactcaggcg	cagccggtaa	gatttgtatg	attgaccgtg	gtgtgatctc	tttccacgac	1140
aaagtgaata	actgccaata	ctctgggtgg	gtaggtgctg	tcattcattaa	caacacagct	1200
ggcatgttgt	acggcacttt	gggtgaagggt	tctgctaaca	ctacatcaat	ccctgcagta	1260
ggtgcggctt	ttgaagacag	gactgcgctg	ttggccgcta	ctactgcata	catcaacatc	1320
ggcaccagcg	attatgggtct	gatgagcgga	acttctatgg	caacgccggc	tgtttcagggt	1380
attgcagctc	tgggtgtgtc	aaatcacccg	ggctgtactg	gtactcaaat	ccgtaatgcg	1440
ttaaaagcga	cggcaaaaaga	cgcaggtgct	ctgggcaaa	atgtgtactt	cggttatggt	1500
attgtgcagg	ccgctgctgc	gcatacgtac	ctgacgacca	atgggtgtgg	tgggtggcact	1560
acaactccgg	gcatcagcct	gactttacag	ggcgtatcca	gcaaaggtaa	acgttatgtc	1620
gacctgacat	gggccaagtgc	gaccaccagc	tcagttgata	tttaccgcaa	caacgtcaaa	1680
gtactgacca	caaccaatga	cggcgacat	cgtgatggcc	cgttaaaccg	tggcagctat	1740
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ctgtaa						1806

<210> 96

<211> 601

<212> PRT

<213> Unknown

<220>

<223> obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(24)

<400> 96

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 Leu Gly Cys Thr Thr Val Ala Ala Ala Asp Arg Val Ile Ile Gln Val
 20 25 30
 Asp Asn Ala Asn Lys Gly Ile Val Thr Ala Leu Thr Lys Gln Leu Gly

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Gly Asp Val Lys Val Asp Ala Asp Gly Phe Ile Ala Ala Gln Phe Asn
 50 55 60
 Gly Lys Ser Val Asp Glu Ile Lys Gly Ile Leu Lys Asn Pro His Ile
 65 70 75 80
 Lys Leu Ile Glu Glu Asp Leu Val Arg Lys Pro Met Ala Leu Phe Asn
 85 90 95
 Asp Asp Ala Gly Asp Pro Met Gln Gln Ile Thr Pro Tyr Ala Val
 100 105 110
 Tyr Gln Ser Gln Ala Asn Gln Val Gln Phe Asn Pro Gly Ala Gly Ile
 115 120 125
 Lys Val Cys Val Ile Asp Ser Gly Leu Asp Gln Ser Asn Pro Asp Phe
 130 135 140
 Asn Trp Gly Ser Ile Thr Gly Asp Asn Asp Ser Gly Thr Gly Asn Trp
 145 150 155 160
 Asn Val Asn Gly Gly Pro His Gly Thr His Val Ala Gly Thr Ile Gly
 165 170 175
 Ala Ala Asp Asn Gly Phe Gly Val Ile Gly Met Ala Pro Gly Val Ala
 180 185 190
 Met His Ile Ile Lys Val Phe Asn Ala Glu Gly Trp Gly Tyr Ser Ser
 195 200 205
 Asp Leu Ala Tyr Ala Ala Gln Lys Cys Lys Asn Ala Gly Ser Asp Ile
 210 215 220
 Ile Ser Met Ser Leu Gly Gly Gly Gly Ala Asn Thr Thr Glu Ser Asn
 225 230 235 240
 Ala Phe Lys Thr Phe Thr Asp Ala Gly Gly Leu Val Ile Ala Ala Ala
 245 250 255
 Gly Asn Asp Gly Asn Asn Val Arg Ser Tyr Pro Ala Gly Tyr Pro Ser
 260 265 270
 Val Met Met Ile Gly Ala Asn Asp Asn Asn Asn Ile Ala Asp Phe
 275 280 285
 Ser Gln Phe Pro Ser Cys Thr Ala Asn Gly Lys Thr Asp Glu Thr Ile
 290 295 300
 Cys Val Glu Ala Thr Ala Gly Gly Val Asp Thr Leu Ser Thr Tyr Pro
 305 310 315 320
 Ala Asp Met Ala Thr Ser Ala Thr Leu Ser Ala Asn Gly Thr Pro Tyr
 325 330 335
 Ala Thr Ser Ala Met Glu Asn Pro Gly Ser Ala Ser Ala Ala Thr Phe
 340 345 350
 Phe Met Gly Thr Ala Glu Thr Val Asn Ser Gly Ala Ala Gly Lys Ile
 355 360 365
 Cys Met Ile Asp Arg Gly Val Ile Ser Phe His Asp Lys Val Lys Asn
 370 375 380
 Cys Gln Asn Ser Gly Gly Val Gly Ala Val Ile Ile Asn Asn Thr Ala
 385 390 395 400
 Gly Met Leu Tyr Gly Thr Leu Gly Glu Gly Ser Ala Asn Thr Thr Ser
 405 410 415
 Ile Pro Ala Val Gly Ala Ala Phe Glu Asp Arg Thr Ala Leu Leu Ala
 420 425 430
 Ala Thr Thr Ala Ser Ile Asn Ile Gly Thr Ser Asp Tyr Gly Leu Met
 435 440 445
 Ser Gly Thr Ser Met Ala Thr Pro Ala Val Ser Gly Ile Ala Ala Leu
 450 455 460
 Val Trp Ser Asn His Pro Gly Cys Thr Gly Thr Gln Ile Arg Asn Ala
 465 470 475 480
 Leu Lys Ala Thr Ala Lys Asp Ala Gly Ala Gly Lys Asp Val Tyr
 485 490 495
 Phe Gly Tyr Gly Ile Val Gln Ala Ala Ala His Gln Tyr Leu Thr
 500 505 510
 Thr Asn Gly Cys Gly Gly Gly Thr Thr Thr Pro Gly Ile Ser Leu Thr
 515 520 525
 Leu Gln Gly Val Ser Ser Lys Gly Lys Arg Tyr Val Asp Leu Thr Trp
 530 535 540
 Ala Ser Ala Thr Thr Ser Ser Val Asp Ile Tyr Arg Asn Asn Val Lys
 545 550 555 560
 Val Leu Thr Thr Thr Asn Asp Gly Ala His Arg Asp Gly Pro Leu Asn
 565 570 575
 Arg Gly Ser Tyr Ser Tyr Lys Val Cys Glu Ala Ala Ser Thr Thr Lys

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Cys Ser Ala 580 Ser Thr Ser Ile Ser 585 Leu 590
 595 600

<210> 97
 <211> 681
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 97
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 acgcccggca cgcgcacccc cagccacggc acggatatgc tcggccagcg ctacgcttat 120
 gattttatcg gcgtagcgcc aggaggcagc agcctgaagt tctaccgcat gagcccaactg 180
 cgctatttgc tgttcggcgc gcgcctggcg gactgctacg gctggggcca gccgatctac 240
 gcggcggcgg acggtacggg ggcgacggc ggcgacggc ggcccagcg caaccgggtg 300
 cacctcgccc gggatctgtt catgctcttt aagaacggcc tgtcgatccg ctcaaccgag 360
 gggctcgacc tgcgcacccct gaccggcaat tacgtcatcg tagagagcag cgcgggctat 420
 atgctctacg cccacgcgca gaacggctcg gtgcgcgtcg cgccgggcca gaagggtgacc 480
 accgggcagc acctggcgaa tgtaggccat tcgggcaatt ccaccgcgcc ccacctgcac 540
 ttccatatca tggatcagct cgacccgtgg aaagcgcagg gcatcgccctg ctgtttccgc 600
 gaatatgagg tctggcagaa cggcggctgg cagccggtgc gcaacggcat cccaccgcc 660
 gccgaacgca tccggcggtg g 681

<210> 98
 <211> 226
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 98
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 1 5 10 15
 Asn Ala Pro Asn Thr Pro Gly Thr Arg Ile Pro Ser His Gly Thr Asp
 20 25 30
 Met Leu Gly Gln Arg Tyr Ala Tyr Asp Phe Ile Gly Val Ala Pro Gly
 35 40 45
 Gly Ser Ser Leu Lys Phe Tyr Arg Met Ser Pro Leu Arg Tyr Leu Leu
 50 55 60
 Phe Gly Ala Arg Leu Ala Asp Cys Tyr Gly Trp Gly Gln Pro Ile Tyr
 65 70 75 80
 Ala Ala Ala Asp Gly Thr Val Ala Gln Ala Gly Asp Gly Trp Pro Glu
 85 90 95
 Arg Asn Pro Val His Leu Ala Arg Asp Leu Phe Met Leu Phe Lys Asn
 100 105 110
 Gly Leu Ser Ile Arg Ser Thr Glu Gly Leu Asp Leu Arg Ile Leu Thr
 115 120 125
 Gly Asn Tyr Val Ile Val Glu Ser Ser Ala Gly Tyr Met Leu Tyr Ala
 130 135 140
 His Ala Gln Asn Gly Ser Val Arg Val Ala Pro Gly Glu Lys Val Thr
 145 150 155 160
 Thr Gly Gln His Leu Ala Asn Val Gly His Ser Gly Asn Ser Thr Ala
 165 170 175
 Pro His Leu His Phe His Ile Met Asp Gln Leu Asp Pro Trp Lys Ala
 180 185 190
 Gln Gly Ile Ala Cys Cys Phe Arg Glu Tyr Glu Val Trp Gln Asn Gly
 195 200 205
 Gly Trp Gln Pro Val Arg Asn Gly Ile Pro Thr Ala Glu Arg Ile
 210 215 220
 Arg Arg
 225

<210> 99
 <211> 1944

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<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 99

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gggattaggc	tagcggtcct	tgatgacggc	ttcgaccgcc	atcatgctga	cctgcgtgca	180
aactacaacg	tcaacatcga	ccgtgatttt	gtcggccgtg	gtgactttga	cgcgattcat	240
gagcgcgga	actggcatgg	tactgctgtg	atgggcgtgg	ccggcgctga	cgacaatgga	300
gttgggggta	caggtgttgc	cacagacgtg	accctgatgg	gcctgcgtat	cggttttggc	360
tctgccggca	atccggcgca	gtacgcggcg	gctctcagcg	agagcgcaaa	agctgacgtt	420
gcaaacagtt	catggggggt	tggtggcttc	ttcattgaca	attttgatag	tcattcatttc	480
cgtgccgccc	aaagcgctct	gaagttttcg	gttgacaatg	gccgtgggtg	ccttggtact	540
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ttccagaatt	caatctatac	gatggcagtg	ggtgcgacgg	acaccgccgg	tcgggtagct	660
tcattctcga	cgccgggcgt	tgcgcttcat	gtctctgcgc	cgggtgtgtc	gattctgaca	720
actgacgtct	cgggcccgtga	cggctatagc	tctggcaatg	aggcggtggg	gcaaggcacg	780
tcctttgccc	ccccgtcggt	tgaggcatt	gtctcactca	tgctcgatgc	taatgcccgt	840
cttggatggc	gagatgttca	agagatctta	gcttattctg	cgaaggagac	gacagccggg	900
atttccgata	cattcttgat	cacgaataag	gcagacaact	ggaatgggtg	cggccttacc	960
catagcaaga	attatggcct	cggtctgggt	gatgcccatg	ctgcggtccg	ccttgccgag	1020
acttggaccg	agcagcagac	ttcgcacaa	atgatgactg	catcttttgg	agctgcgccc	1080
cgggcaacgc	tgccgggacgc	aggccgttgg	gagacgacgt	tcacgatcaa	ccgtgacatc	1140
accattgacc	gtgttgagct	tgagattgat	ctcaagcaca	actggattgg	agatctccgc	1200
ataggtcttg	tgtagccga	aggcacaacg	agttgggttg	tcgatcgtcc	gggctggcg	1260
cctggcgcg	cggggaaacg	ttcggggcta	aaaaatat	ggttcgactt	cacgaccagt	1320
cagttctggg	gcgaggaagc	gcgtggtacc	tggaagctgg	tcacgagga	cgtaagcgt	1380
ggcaatat	gtcggcttga	ctgggtccaa	gtcaacatct	ttggcgatcg	cccagacaac	1440
gatgactctt	acatctacac	caacgagttt	gcccgcctcg	gcgctcaatc	cggtcgtagc	1500
gtgatcaacg	acgcccgaag	gcgtgatgcc	atcaacgcct	cagcggtaac	cagcgatagc	1560
gttcttgatc	ttctccacgg	ctcgatcatt	gccggccggc	aggtttctta	cggggctggc	1620
accatcatcg	agcgggcttt	tgctggtgac	ggcaacgacc	aagtcctgtg	caacaccatg	1680
gataaccttc	ttcggggcgg	tcgcggaat	gatgtccttg	agggtcgagg	tggttccgat	1740
atcttcgcct	ttggcgtagc	ttcgggacgc	gatataattc	tagactttga	cgcgaaacgac	1800
cgaattctcc	taacggacgg	ggtgagtgtc	cgagctcttt	cgggcagcgt	cgccacgctc	1860
tccgacgggt	tcaccattac	tgacgctaac	ggttggcag	ggcagatgtc	caatttctac	1920
caaggcgatt	tgctctttgc	ttga				1944

<210> 100

<211> 647

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 100

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Trp	His	Leu	Ser	Leu	Arg	Ser	Asp	Val	Ser	Leu	Asn	Leu	Arg	Asp
		20					25				30			
Val	Trp	Thr	Asp	Tyr	Lys	Gly	Ala	Gly	Ile	Arg	Leu	Ala	Val	Leu
		35					40				45			
Asp	Gly	Phe	Asp	Arg	His	His	Ala	Asp	Leu	Arg	Ala	Asn	Tyr	Asn
	50					55					60			
Asn	Ile	Asp	Arg	Asp	Phe	Val	Gly	Arg	Gly	Asp	Phe	Asp	Ala	Ile
	65				70				75				80	
Glu	Arg	Gly	Asn	Trp	His	Gly	Thr	Ala	Val	Met	Gly	Val	Ala	Gly
			85						90				95	
Asp	Asp	Asn	Gly	Val	Gly	Val	Thr	Gly	Val	Ala	Thr	Asp	Val	Thr
		100						105					110	
Met	Gly	Leu	Arg	Ile	Gly	Phe	Gly	Ser	Ala	Gly	Asn	Pro	Ala	Gln
		115					120					125		
Ala	Ala	Ala	Leu	Ser	Glu	Ser	Ala	Lys	Ala	Asp	Val	Ala	Asn	Ser
	130					135						140		

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Trp	Gly	Phe	Gly	Gly	Phe	Phe	Ile	Asp	Asn	Phe	Asp	Ser	His	His	Phe
145					150					155					160
Arg	Ala	Ala	Glu	Ser	Ala	Leu	Lys	Phe	Ser	Val	Asp	Asn	Gly	Arg	Gly
				165					170					175	
Gly	Leu	Gly	Thr	Val	Gln	Val	Phe	Ala	Ala	Gly	Asn	Ser	Arg	Ala	Ser
			180					185					190		
Gly	Asp	Asp	Val	Asn	Phe	His	Asn	Phe	Gln	Asn	Ser	Ile	Tyr	Thr	Met
		195					200					205			
Ala	Val	Gly	Ala	Thr	Asp	Thr	Ala	Gly	Arg	Val	Ala	Ser	Phe	Ser	Thr
	210					215					220				
Pro	Gly	Val	Ala	Leu	His	Val	Ser	Ala	Pro	Gly	Val	Ser	Ile	Leu	Thr
225					230					235					240
Thr	Asp	Val	Ser	Gly	Arg	Asp	Gly	Tyr	Ser	Ser	Gly	Asn	Glu	Ala	Trp
				245					250					255	
Val	Gln	Gly	Thr	Ser	Phe	Ala	Ala	Pro	Ser	Val	Ala	Gly	Ile	Val	Ser
			260					265					270		
Leu	Met	Leu	Asp	Ala	Asn	Ala	Arg	Leu	Gly	Trp	Arg	Asp	Val	Gln	Glu
		275					280					285			
Ile	Leu	Ala	Tyr	Ser	Ala	Lys	Glu	Thr	Thr	Ala	Gly	Ile	Ser	Asp	Pro
	290					295					300				
Phe	Leu	Ile	Thr	Asn	Lys	Ala	Asp	Asn	Trp	Asn	Gly	Gly	Gly	Leu	Thr
305					310					315					320
His	Ser	Lys	Asn	Tyr	Gly	Phe	Gly	Leu	Val	Asp	Ala	His	Ala	Ala	Val
				325					330					335	
Arg	Leu	Ala	Glu	Thr	Trp	Thr	Glu	Gln	Gln	Thr	Ser	His	Asn	Met	Met
			340					345					350		
Thr	Ala	Ser	Phe	Gly	Ala	Ala	Pro	Arg	Ala	Thr	Leu	Arg	Asp	Ala	Gly
		355					360					365			
Arg	Trp	Glu	Thr	Thr	Phe	Thr	Ile	Asn	Arg	Asp	Ile	Thr	Ile	Asp	Arg
	370					375					380				
Val	Glu	Leu	Glu	Ile	Asp	Leu	Lys	His	Asn	Trp	Ile	Gly	Asp	Leu	Arg
385					390					395					400
Ile	Gly	Leu	Val	Ser	Ala	Glu	Gly	Thr	Thr	Ser	Trp	Leu	Val	Asp	Arg
				405						410				415	
Pro	Gly	Val	Ala	Pro	Gly	Ala	Ala	Gly	Asn	Gly	Ser	Gly	Leu	Lys	Asn
			420					425					430		
Ile	Trp	Phe	Asp	Phe	Thr	Thr	Ser	Gln	Phe	Trp	Gly	Glu	Glu	Ala	Arg
		435					440					445			
Gly	Thr	Trp	Lys	Leu	Val	Ile	Glu	Asp	Val	Lys	Arg	Gly	Asn	Ile	Gly
	450					455					460				
Arg	Leu	Asp	Trp	Phe	Gln	Val	Asn	Ile	Phe	Gly	Asp	Arg	Pro	Ser	Asn
465					470					475					480
Asp	Asp	Ser	Tyr	Ile	Tyr	Thr	Asn	Glu	Phe	Ala	Arg	Leu	Gly	Ala	Gln
				485					490					495	
Ser	Gly	Arg	Thr	Val	Ile	Asn	Asp	Ala	Gln	Gly	Arg	Asp	Ala	Ile	Asn
			500					505					510		
Ala	Ser	Ala	Val	Thr	Ser	Asp	Ser	Val	Leu	Asp	Leu	Leu	His	Gly	Ser
		515					520					525			
Ile	Ile	Ala	Gly	Arg	Gln	Val	Ser	Tyr	Gly	Ala	Gly	Thr	Ile	Ile	Glu
	530					535					540				
Arg	Ala	Phe	Ala	Gly	Asp	Gly	Asn	Asp	Gln	Val	Arg	Gly	Asn	Thr	Met
545					550					555					560
Asp	Asn	Leu	Leu	Trp	Gly	Gly	Arg	Gly	Asn	Asp	Val	Leu	Glu	Gly	Arg
				565					570					575	
Gly	Gly	Ser	Asp	Ile	Phe	Ala	Phe	Gly	Val	Arg	Ser	Gly	Arg	Asp	Ile
			580					585					590		
Ile	Leu	Asp	Phe	Asp	Ala	Asn	Asp	Arg	Ile	Leu	Leu	Thr	Asp	Gly	Val
		595					600					605			
Ser	Val	Arg	Ser	Leu	Ser	Gly	Ser	Val	Ala	Thr	Leu	Ser	Asp	Gly	Ala
	610					615					620				
Thr	Ile	Thr	Ala	Ala	Asn	Gly	Trp	Gln	Trp	Gln	Met	Ser	Asn	Phe	Tyr
625					630					635					640
Gln	Gly	Asp	Leu	Leu	Phe	Ala									
				645											

<210> 101
 <211> 1125
 <212> DNA

10336256.txt

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 101

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gtcagcaagg	tgctgcagcc	gctaagcgga	cagccgcaat	cgccaagat	gcacgtcgac	180
agcgcggggg	cgaagagcat	tcgcgtcagg	atcggcgttg	ccagcaatgc	ggcgccacgc	240
tcggattaca	ctgtcgccgt	cagggatcga	aacggcgggc	tggctggcgc	ataccgggt	300
gcggagcttc	gcgccaagcc	ggtctggagt	cctcctgtcc	cgggcgccctc	ggtcgagggtc	360
gaggtcgagg	tcgagggcgc	ggcggcggat	acggccggca	ttgcggtcgc	ggtgaccggc	420
atcatcgggc	agcgcacgcc	ggcgatccg	atgctctcgc	tgctgggcga	tacgttcgac	480
ctggaaccga	tcgagtcgtt	tcggctggaa	aagcccagaa	tattcaaggc	cgggctcgcg	540
gtagccaagc	tgatgctggt	gcgtgacggc	aagtctctgg	cgtgcacggg	cttcatgatc	600
gacgatgatc	gcatgctgac	caacgagcat	tgcatcaata	gccaggccat	ctgcgacagc	660
gcagtcgcac	tgttcggata	cgactcgaac	gcgggtatga	cgagcgacat	ggtgcgcgag	720
cagtcgcgcc	cctgtctgga	attcaagagc	atggacgaga	agctcgacgt	agcgatgatt	780
cggttgggcca	acagcccggg	caagcgggtg	ggacgactga	agctcgctgt	cgctgcgccc	840
gacgaactgt	cgatcgatgt	ccaccatccc	aatggagatc	cgaagtatgt	cacgcgagag	900
gactgcttcg	ttggcaagct	gcccgttgac	ggcgcgccca	aggacaccga	tttcagccac	960
cggtgcgaca	cgatgggagg	tagctcgggc	tcgccggtcc	tgagccgaag	gagcctggaa	1020
gtcatcggct	tgcatacctt	tgcatcgcac	ctcgtgatc	cggttggcg	ggatcaaaat	1080
cgcgcggtgc	gaatggagct	catccgcgcc	gcgctggggc	tttga		1125

<210> 102

<211> 374

<212> PRT

<213> Unknown

<220>

<223> obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(22)

<400> 102

Met	Leu	Arg	Lys	Thr	Leu	Phe	Val	Val	Val	Ala	Ala	Leu	Leu	Ala	Ser
1				5					10					15	
Ala	Gln	Pro	Val	Ala	Ala	Gln	Arg	Met	Glu	Asn	Gly	Asn	Val	Arg	Pro
		20						25					30		
Val	Asn	Asp	Gly	Ile	Val	Gln	Glu	Val	Ser	Lys	Val	Leu	Gln	Pro	Leu
		35					40					45			
Ser	Gly	Gln	Pro	Gln	Ser	Ala	Lys	Met	His	Val	Asp	Ser	Ala	Gly	Ala
	50					55				60					
Lys	Ser	Ile	Arg	Val	Arg	Ile	Gly	Val	Ala	Ser	Asn	Ala	Ala	Pro	Arg
	65				70					75				80	
Ser	Asp	Tyr	Thr	Val	Ala	Val	Arg	Asp	Arg	Asn	Gly	Gly	Leu	Val	Ala
			85						90					95	
Arg	Tyr	Pro	Ala	Ala	Glu	Leu	Arg	Ala	Lys	Pro	Val	Trp	Ser	Pro	Pro
		100						105					110		
Val	Pro	Gly	Ala	Ser	Val	Glu	Val	Glu	Val	Glu	Val	Glu	Ala	Ala	Ala
		115					120					125			
Ala	Asp	Thr	Ala	Gly	Ile	Ala	Val	Ala	Val	Thr	Gly	Ile	Ile	Gly	Gln
	130					135					140				
Arg	Thr	Pro	Gly	Asp	Pro	Met	Leu	Ser	Val	Leu	Gly	Asp	Thr	Phe	Asp
	145				150					155				160	
Leu	Glu	Pro	Ile	Glu	Ser	Phe	Arg	Leu	Glu	Lys	Pro	Glu	Ile	Phe	Lys
			165						170					175	
Ala	Gly	Leu	Ala	Val	Ala	Lys	Leu	Met	Leu	Val	Arg	Asp	Gly	Lys	Ser
		180						185					190		
Leu	Ala	Cys	Thr	Gly	Phe	Met	Ile	Asp	Asp	Asp	Arg	Met	Leu	Thr	Asn
		195					200					205			
Glu	His	Cys	Ile	Asn	Ser	Gln	Ala	Ile	Cys	Asp	Ser	Ala	Val	Ala	Leu
	210					215					220				
Phe	Gly	Tyr	Asp	Ser	Asn	Ala	Gly	Met	Thr	Ser	Asp	Met	Val	Arg	Glu
	225				230					235					240

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Gln Ser Ala Ala Cys Leu Glu Phe Lys Ser Met Asp Glu Lys Leu Asp
 Val Ala Met Ile Arg Leu Ala Asn Ser Pro Gly Lys Arg Trp Gly Arg
 Leu Lys Leu Ala Val Ala Ala Pro Asp Glu Leu Ser Ile Val Ile His
 His Pro Asn Gly Asp Pro Lys Tyr Val Thr Arg Glu Asp Cys Phe Val
 Gly Lys Leu Pro Val Asp Gly Arg Ala Lys Asp Thr Asp Phe Ser His
 Arg Cys Asp Thr Met Gly Gly Ser Ser Gly Ser Pro Val Leu Ser Arg
 Arg Ser Leu Glu Val Ile Gly Leu His His Leu Gly Ile Asp Leu Ala
 Asp Pro Ala Trp Arg Asp Gln Asn Arg Ala Val Arg Met Glu Leu Ile
 Arg Ala Ala Leu Gly Leu

<210> 103
 <211> 897
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 103
 atgaaagagt taaaggtaat gcaaaaacat caagaccaga tttttaacct gccaaatata 60
 gtcggtgtag gtatcggctg caaagtgaag gatggtatta tttctcaaga acctgccatt 120
 gtcgcttttg ttgttaagaa agtggacaaa gcttatttgc cggaagcaag catggttccg 180
 gctgaattgg atggtgtagt taccgatgtc agagaagtag gggaaattaa acttcttggg 240
 cgtaccgata aacaacggcc ggcatgtcct ggcacagca ttggtcatta taaaattacc 300
 gccggtactt tcggcgcaat gggttacgac aatcaaacag gtgatccgct tattctgtca 360
 aataatcacg ttctggccaa tgaactaat gggcgtgacg gcagaagcgc tattggtgat 420
 gcaatatatc aaccgggtag ttatgacgga ggtacgtcgg cagataccat tgcccacttg 480
 caccggtttg taccagtta ttacggttca agttcgaag cgaatctggt tgactgtgca 540
 gtagctaagc cgataagcaa tgatcttatc atcgacgaga tcatggaaat tggcaaagt 600
 gccggggtcg ctacggccga ggtaggtatg aatgtcaaga aaagcggccg gactaccgga 660
 ctaacaacag cactatcga cactgtgcat accacagtaa aggtgaacat gggcgtcgg 720
 acagctactt tcaaagatca aatcgtggcc ggtgcaatgt cccagggcgg cgacagcggg 780
 tcattggtgc ttaatgagca aaacgaagcg ataggattat tgtttgccgg ttctgattat 840
 accactatat tcaatgatat ccagaatgtt ttgaacgcac tgaaggtaag gttttag 897

<210> 104
 <211> 298
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 104
 Met Lys Glu Leu Lys Val Met Gln Lys His Gln Asp Gln Ile Phe Asn
 1 5 10 15
 Leu Pro Asn Ile Val Gly Val Gly Ile Gly Cys Lys Val Lys Asp Gly
 20 25 30
 Ile Ile Ser Gln Glu Pro Ala Ile Val Ala Leu Val Val Lys Lys Val
 35 40 45
 Asp Lys Ala Tyr Leu Pro Glu Ala Ser Met Val Pro Ala Glu Leu Asp
 50 55 60
 Gly Val Val Thr Asp Val Arg Glu Val Gly Glu Ile Lys Leu Leu Gly
 65 70 75 80
 Arg Thr Asp Lys Gln Arg Pro Ala Cys Pro Gly Ile Ser Ile Gly His
 85 90 95
 Tyr Lys Ile Thr Ala Gly Thr Phe Gly Ala Met Val Tyr Asp Asn Gln
 100 105 110
 Thr Gly Asp Pro Leu Ile Leu Ser Asn Asn His Val Leu Ala Asn Val

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115 120 125
 Thr Asn Gly Arg Asp Gly Arg Ser Ala Ile Gly Asp Ala Ile Tyr Gln
 130 135 140
 Pro Gly Ser Tyr Asp Gly Gly Thr Ser Ala Asp Thr Ile Ala His Leu
 145 150 155 160
 His Arg Phe Val Pro Val Tyr Tyr Gly Ser Ser Ser Lys Ala Asn Leu
 165 170 175
 Val Asp Cys Ala Val Ala Lys Pro Ile Ser Asn Asp Leu Ile Asp
 180 185 190
 Glu Ile Met Glu Ile Gly Lys Val Ala Gly Val Ala Gln Ala Glu Val
 195 200 205
 Gly Met Asn Val Lys Lys Ser Gly Arg Thr Thr Gly Leu Thr Thr Gly
 210 215 220
 Thr Ile Asp Thr Val His Thr Thr Val Lys Val Asn Met Gly Val Gly
 225 230 235 240
 Thr Ala Thr Phe Lys Asp Gln Ile Val Ala Gly Ala Met Ser Gln Gly
 245 250 255
 Gly Asp Ser Gly Ser Leu Val Leu Asn Glu Gln Asn Glu Ala Ile Gly
 260 265 270
 Leu Leu Phe Ala Gly Ser Asp Tyr Thr Thr Ile Phe Asn Asp Ile Gln
 275 280 285
 Asn Val Leu Asn Ala Leu Lys Val Arg Phe
 290 295

<210> 105
 <211> 2091
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 105
 gtgagcgcgc tgcacgtctg ggcgcagtac acctggttgc tggacaacgc caagaccagc 60
 caggagtgcg atgaacccca gaccgcgtcag gaaggggaca agaccatcag ctatcgggtg 120
 tgccgtcaga ccctgcccgc cgccagcgaa gtgcaggtgg tcttgaagga caccggctat 180
 caatacccg tggggggcag cgaatggcag accctgcccg aaacaaccga gtggcaggag 240
 aaccgggtgc tcaaccgccc catcgtgctg gccagcaagg aagagcagct cgactgtcgc 300
 cgtgccgacg gccgcgcctg ttccgagccg gatctgcccg gcaccgaact gctggacgcc 360
 gaagcggcca agatagtgcg ggatgccagt ggccagcccg ccccggtctg gcaggagaac 420
 tatggtcacg atgacaccaa gctgctggcc gtgtcgcgcg gcatccagag cctgctggcg 480
 gccaatcagc cgcccattcc ggccatgaag ctgctgctgg aatacgtgcg tgcccacaac 540
 taccacaact acggcaagca caaggaagac ggcccggctg ccgcccaggc gctggccgag 600
 gcattgaccg cgtggggcgc ccatccgctg ctcttcccgg agcaggccag cgacgaggta 660
 ggcgcgcgtc tgggtgcctg gagcatcgcc ctgcacggtc ctgtcgcgcg agtcaagag cccggcagt 720
 cagagccgct ttggcacctt gctcggcgag ttcaaccaga tgctggccta cagcaccgcg 780
 catgccagcg agatcaacgg tcagcacgcc tgggcgaccg gtctgttcga tctgtcaac 840
 ttcttcgact tcgccagcga ctacagcgtc cccttcgcca acgacttccg ccaacaggac 900
 ggcgagctgc gcaagcagct gcacgcctc ggcatgagcg agctcgcgtt gtggaaggga 960
 cgggatggcg ccgatctgtt cctgtcaac aacgtgctgg atgcttacac ccgctctac 1020
 cgggtcgccc gctatacccg cccggacgag ctgcacggct accgcaagct gctggatgac 1080
 tccgtcatcg cactggttcg ccaccacgac ctgatccccg gtggccagca gagccaggat 1140
 ctgctggaag acatgtcgtg gaccctctcc acctactacc tgacctacac ggaccgcacc 1200
 agcgaagcct gcatcagcgg cgactttgcc gggctctgca cccctgtccg ggtagaggac 1260
 gtgctgcccgt tcgagcacac ctgctcgccg accctgcgcc tgccgggcca ggatctcacc 1320
 atggatcagg ccgaggggat ctgccgtgaa ctgggtgccc aagagcagca gttccaccag 1380
 cagatggaga ccggctggca gccggtggcg gacgatcaca acgaggcgtt ggaactggtg 1440
 gtcttcaact cctccgcccga ctggaaaacg tacggcagtg ccctgttcgg cggcgtctcc 1500
 accgacaacg gcggcatcta cctcgaaggg gatccggctc gcccgggcaa ccaggcccgc 1560
 ttctttgcct acgaggcgga gtggaagcgc ccagcgttcc aggtgtggaa cctgcgccac 1620
 gagtacgtgc actacctgga cggccgcttc aaccagtacg gcagcttcgg ccactaccgc 1680
 ctcaaccgta ccacctggtg gtcggaaagg gtcgggagtg tcgtcgccca cggtcagtgc 1740
 ttgcgccgcg gtctggacaa cgtcgccggc cgtccggcca gtgagcgtcc ggccctggcc 1800
 gacatcctgc acctggatta cgacaagggc ggcgagatgg tctactcctg gtcctacacg 1860
 gtgcaccgct tccctgaacga gaccggtcgc ggcgaccagc ggctggccat ggcccaggcc 1920
 ctgcgcaacc cggatcagca gcaggccatg agcgcttctg aagccgagct ggaccagctg 1980
 attgccaatg acagcgaggc ctaccagcag tggctcgccc gcgagctgct gccctggtgg 2040
 gaagccaaca aggactccga cgagtgaag gccaacgact cctcccactg a 2091

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<210> 106
 <211> 696
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 106
 Met Ser Glu Leu His Val Trp Arg Gln Tyr Thr Trp Leu Leu Glu Gln
 1 5 10 15
 Ala Lys Thr Gln Gln Glu Cys Asp Glu Pro Gln Thr Arg Gln Glu Gly
 20 25 30
 Asp Lys Thr Ile Ser Tyr Arg Val Cys Arg Gln Thr Leu Pro Ala Gly
 35 40 45
 Ser Glu Val Gln Val Val Leu Lys Asp Thr Gly Tyr Gln Tyr Pro Val
 50 55 60
 Gly Gly Ser Glu Trp Gln Thr Leu Pro Glu Thr Thr Glu Trp Gln Glu
 65 70 75 80
 Asn Arg Val Leu Asn Arg Pro Ile Val Leu Ala Ser Lys Glu Glu Gln
 85 90 95
 Leu Asp Cys Arg Arg Ala Asp Gly Arg Ala Cys Ser Glu Pro Asp Leu
 100 105 110
 Pro Gly Thr Glu Leu Leu Asp Ala Glu Ala Ala Lys Ile Val Gln Asp
 115 120 125
 Ala Ser Gly Gln Pro Ala Pro Val Trp Gln Glu Asn Tyr Gly His Asp
 130 135 140
 Asp Thr Lys Leu Leu Ala Val Ser Arg Gly Ile Gln Ser Leu Leu Ala
 145 150 155 160
 Ala Asn Gln Pro Ala His Pro Ala Met Lys Leu Leu Leu Glu Tyr Val
 165 170 175
 Arg Ala His Asn Tyr His Asn Tyr Gly Lys His Lys Glu Asp Gly Pro
 180 185 190
 Ala Ala Ala Glu Ala Leu Ala Glu Ala Leu Thr Ala Leu Gly Ala His
 195 200 205
 Pro Leu Leu Phe Pro Glu Gln Ala Ser Asp Glu Val Gly Ala Val Met
 210 215 220
 Gly Ala Trp Ser Ile Ala Leu His Gly Gln Phe Lys Ser Pro Ala Val
 225 230 235 240
 Gln Ser Arg Phe Gly Thr Leu Leu Gly Glu Phe Asn Gln Met Leu Ala
 245 250 255
 Tyr Ser Thr Arg His Ala Ser Glu Ile Asn Gly Gln His Ala Trp Ala
 260 265 270
 Thr Gly Leu Phe Asp Leu Leu Asn Phe Leu Asp Phe Ala Ser Asp Tyr
 275 280 285
 Ser Asp Pro Phe Ala Asn Asp Phe Arg Gln Gln Asp Gly Glu Leu Arg
 290 295 300
 Lys Gln Leu His Ala Leu Gly Met Ser Glu Leu Ala Leu Trp Lys Gly
 305 310 315 320
 Arg Asp Gly Ala Asp Leu Phe Leu Leu Asn Asn Val Leu Asp Ala Tyr
 325 330 335
 Thr Arg Leu Tyr Arg Val Ala Arg Tyr Thr Arg Pro Asp Glu Leu Asp
 340 345 350
 Gly Tyr Arg Lys Leu Leu Asp Asp Ser Val Ile Ala Leu Val Arg His
 355 360 365
 His Asp Leu Ile Pro Gly Gly Gln Gln Ser Gln Asp Leu Leu Glu Asp
 370 375 380
 Met Ser Leu Thr Leu Ser Thr Tyr Tyr Leu Thr Tyr Thr Asp Arg Thr
 385 390 395 400
 Ser Glu Ala Cys Ile Ser Gly Asp Phe Ala Gly Leu Cys Thr Pro Val
 405 410 415
 Arg Val Glu Asp Val Leu Pro Phe Glu His Thr Cys Ser Pro Thr Leu
 420 425 430
 Arg Leu Arg Ala Gln Asp Leu Thr Met Asp Gln Ala Glu Gly Ile Cys
 435 440 445
 Arg Glu Leu Gly Ala Glu Glu Gln Gln Phe His Gln Gln Met Glu Thr
 450 455 460

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Gly 465	Trp	Gln	Pro	Val	Ala 470	Asp	Asp	His	Asn	Glu 475	Ala	Leu	Glu	Leu	Val 480
Val	Phe	Asn	Ser	Ser 485	Ala	Asp	Trp	Lys	Arg	Tyr	Gly	Ser	Ala	Leu	Phe 495
Gly	Gly	Val	Ser 500	Thr	Asp	Asn	Gly	Gly 505	Ile	Tyr	Leu	Glu	Gly 510	Asp	Pro
Ala	Arg	Pro 515	Gly	Asn	Gln	Ala	Arg 520	Phe	Phe	Ala	Tyr	Glu 525	Ala	Glu	Trp
Lys	Arg	Pro 530	Ala	Phe	Gln	Val 535	Trp	Asn	Leu	Arg	His 540	Glu	Tyr	Val	His
Tyr 545	Leu	Asp	Gly	Arg	Phe 550	Asn	Gln	Tyr	Gly	Ser 555	Phe	Gly	His	Tyr	Pro 560
Leu	Asn	Arg	Thr	Thr 565	Trp	Trp	Ser	Glu	Gly 570	Leu	Ala	Glu	Phe	Val 575	Ala
His	Gly	Gln	Cys 580	Phe	Ala	Arg	Gly	Leu 585	Asp	Asn	Val	Ala	Gly 590	Arg	Pro
Ala	Ser	Glu 595	Arg	Pro	Ala	Leu	Ala 600	Asp	Ile	Leu	His	Leu 605	Asp	Tyr	Asp
Lys	Gly 610	Gly	Glu	Met	Val	Tyr 615	Ser	Trp	Ser	Tyr	Thr 620	Val	His	Arg	Phe
Leu 625	Asn	Glu	Thr	Gly	Arg 630	Gly	Ala	Ser	Trp	Leu 635	Ala	Met	Ala	Gln	Ala 640
Leu	Arg	Asn	Pro	Asp 645	Gln	Gln	Gln	Ala	Met	Ser 650	Ala	Phe	Glu	Ala 655	Glu
Leu	Asp	Gln	Leu 660	Ile	Ala	Asn	Asp	Ser 665	Glu	Ala	Tyr	Gln	Gln 670	Trp	Leu
Gly	Arg	Glu 675	Leu	Leu	Pro	Trp	Trp 680	Glu	Ala	Asn	Lys	Asp 685	Ser	Asp	Glu
Cys	Lys	Ala	Asn	Asp	Ser	Ser 695	His								

<210> 107
 <211> 1116
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 107	
atggctacat	atatacgttac
ggcaaagtag	gtaagccgca
aagcaaacac	tagagggtat
cctgaagaag	cacgtcctac
tcacgcagca	acacaacata
gtagatgatg	gtatgagaga
agaaatgttg	acgggtgtgc
tctttatttg	gggcagcctt
gcagatacaa	ttaaagctat
ccttccgtgt	tgaatttatc
gacagagctt	ttagttaggg
tccctaaaaa	gattccctgc
gatatggtaa	gagcttctta
cacgatggaa	gagcggcgtc
tcacccgctg	cacctgttat
ctgacgaacg	tagaggttcg
ggtcgagttg	gatacgctca
cctgaaccag	agcctattga
gcaatgcaaa	ccttcacctc
attagaagag	ggtcaaacaa
atctgtacct	gaatgcgtta
agatggcggt	gtcagtgtaa
taataataaac	tggttcctag
cataccaacc	cgttcgggca
atcacacaga	gatttctcag
aagggcacat	ggtacttttg
tgaagcagaa	atctatatgg
ggatgcttgt	attgaccact
attcacatca	atgtcctccg
tatgactgtt	gtagcagcag
aaatccttgc	aacgtaatat
cagtaactac	ggagaactgg
agccgtagat	aacaactcag
agctgggtgc	tgtgcaatga
taaagaactt	atgacaaatg
agttacaaat	acagcacctc
tacgtcagca	atagaacaag
tagtttgaat	aagtga
gagattgcct	actaggttgt
ttgttgacac	cctgcttact
tagaggatca	tcctgtgcag
accgtatcca	caaccaacag
aggggggtatg	tatctatatc
gacgtgtagc	acaaacgatt
ttgcaagttg	tgcagcaggg
ctgaaacatt	gtggacgtat
atatccaaaa	tggacgtaaa
caggatatag	agtagttata
caggcaacca	taacgacgat
cagtaggatg	cttgactaaa
tgatatatg	ggcacctgga
cgagaatggc	cacaggcact
ttcttgaagg	gaaccctaac
gttcattacc	ctttgcacta
ttcccgaacc	agaaccttgc
cattagcaga	ttttaatgct

60
120
180
240
300
360
420
480
540
600
660
720
780
840
900
960
1020
1080
1116

<210> 108
 <211> 371
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

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<400> 108
 Met Ala Thr Tyr Ile Val Thr Leu Glu Glu Gly Gln Thr Arg Asp Cys
 1 5 10 15
 Leu Leu Gly Cys Gly Lys Val Gly Lys Pro Gln Ser Val Pro Glu Cys
 20 25 30
 Val Ile Val Asp Thr Leu Leu Thr Lys Gln Thr Leu Glu Gly Ile Asp
 35 40 45
 Gly Val Val Ser Val Ile Glu Asp His Pro Val Gln Pro Glu Glu Ala
 50 55 60
 Arg Pro Thr Asn Asn Asn Trp Phe Leu Asp Arg Ile His Asn Gln Gln
 65 70 75 80
 Ser Arg Ser Asn Thr Thr Tyr Ile Pro Thr Arg Ser Gly Lys Gly Val
 85 90 95
 Cys Ile Tyr Ile Val Asp Asp Gly Met Arg Glu Ser His Arg Asp Phe
 100 105 110
 Ser Gly Arg Val Ala Gln Thr Ile Arg Asn Val Asp Gly Val Ser Arg
 115 120 125
 Ala His Gly Thr Leu Val Ala Ser Cys Ala Ala Gly Ser Leu Phe Gly
 130 135 140
 Ala Ala Phe Glu Ala Glu Ile Tyr Met Ala Glu Thr Leu Trp Thr Tyr
 145 150 155 160
 Ala Asp Thr Ile Lys Ala Met Asp Ala Cys Ile Asp His Tyr Ile Gln
 165 170 175
 Asn Gly Arg Lys Pro Ser Val Leu Asn Leu Ser Phe Thr Ser Met Ser
 180 185 190
 Ser Ala Gly Tyr Arg Val Val Ile Asp Arg Ala Phe Ser Glu Gly Met
 195 200 205
 Thr Val Val Ala Ala Ala Gly Asn His Asn Asp Asp Ser Leu Lys Arg
 210 215 220
 Phe Pro Ala Asn Leu Asp Asn Val Ile Ser Val Gly Cys Leu Thr Lys
 225 230 235 240
 Asp Met Val Arg Ala Ser Tyr Ser Asn Tyr Gly Glu Leu Val Asp Ile
 245 250 255
 Trp Ala Pro Gly His Asp Gly Arg Ala Ala Ser Ala Val Asp Asn Asn
 260 265 270
 Ser Ala Arg Met Ala Thr Gly Thr Ser Ser Ala Ala Pro Val Ile Ala
 275 280 285
 Gly Val Cys Ala Met Ile Leu Glu Gly Asn Pro Asn Leu Thr Asn Val
 290 295 300
 Glu Val Arg Lys Glu Leu Met Thr Asn Gly Ser Leu Pro Phe Ala Leu
 305 310 315 320
 Gly Arg Val Gly Tyr Ala Gln Val Thr Asn Thr Ala Pro Leu Pro Glu
 325 330 335
 Pro Glu Pro Cys Pro Glu Pro Glu Pro Ile Asp Thr Ser Ala Ile Glu
 340 345 350
 Gln Ala Leu Ala Asp Phe Asn Ala Ala Met Gln Thr Phe Ile Ser Ser
 355 360 365
 Leu Asn Lys
 370

<210> 109
 <211> 1215
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 109
 atgaagtaca ttgtcattct aaagaaagggt tacaatagag attcacttac agactattgc 60
 acaaaagtag gcaagccgtg tgagctacac aatctcgtaa tcattaacac tgacgagtgt 120
 acggcaaaaga ttattgctga cttagattgt gtggaatcta ttgagaaaga ttctgtatgt 180
 acatctgatg aggaatttta caagtcattct cgtactactg ataattgggc attgacacga 240
 ttcaatttta cagaacctca acgagagtat cctgagagtt accgttacaa tcgcacaggc 300
 aaagggtgtg gcatctacgt tattgacagt ggtgtacgta ctactcatca agagttagta 360
 ggacgtgtag aaactatcta cagtaccctt gaaggtaagc attttgacag tgataatgag 420
 ctaaaccatta accgtagtca tggtagagcc gtagcgtag cagcagcagg gaagaagcta 480
 ggtattgcaa gtgaagctac tgtctacaac ttattcgtag atttttctat gtcagacatt 540

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atcaaagcgt	ttgatactgt	attgcacccat	tacaaaaagt	ctaagagtgc	tgctgtactt	600
gtgacatcat	tctcaacttt	gtcactagca	atgaaaccta	tctcagacgc	actctaccaa	660
gcagggtctcg	ttcatgtatc	tagtgcaggt	aatcagtcta	cagatactcc	aagataccct	720
gctgcattcc	ctcagactat	ctctgtaggt	gctactgaca	agcaggacaa	taaagcatca	780
ttcagtaact	ttggcaatac	cgtagacgta	tatgcacccg	gagtgaatgt	gaaggtagcg	840
gatcatgcaa	gagatgttcg	tactcgtatt	gcaagaggaa	cctcattctc	tgcaccttat	900
gttgctggta	tcattgcact	catgctagaa	ggctcagaca	agcctcgtaa	gagtgagcat	960
gtcgatacca	tacgacaatc	cttcctagac	aatgctgcaa	gtgcctctaa	ggcagataag	1020
cgtgtgccac	atacacgttt	tgacattgaa	ccattcaagt	ttcctaaacc	ttctcctgta	1080
gaaaaaattg	tacaaaaggt	gtctgacaat	aaggaatcgt	caactatttc	agacaaaggt	1140
tctaagaaga	attacgtcaa	agaaattgta	gcagggtgta	tcctagtagc	tactatagct	1200
gcaattcttc	tgtaa					1215

<210> 110

<211> 404

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 110

Met	Lys	Tyr	Ile	Val	Ile	Leu	Lys	Lys	Gly	Tyr	Asn	Arg	Asp	Ser	Leu
1				5					10					15	
Thr	Asp	Tyr	Cys	Thr	Lys	Val	Gly	Lys	Pro	Cys	Glu	Leu	His	Asn	Leu
			20					25					30		
Val	Ile	Ile	Asn	Thr	Asp	Glu	Cys	Thr	Ala	Lys	Ile	Ile	Ala	Asp	Leu
			35				40					45			
Asp	Cys	Val	Glu	Ser	Ile	Glu	Lys	Asp	Ser	Val	Cys	Thr	Ser	Asp	Glu
			50			55					60				
Glu	Phe	Tyr	Lys	Ser	Ser	Arg	Thr	Thr	Asp	Asn	Trp	Ala	Leu	Thr	Arg
					70					75					80
Phe	Asn	Phe	Thr	Glu	Pro	Gln	Arg	Glu	Tyr	Pro	Glu	Ser	Tyr	Arg	Tyr
				85					90					95	
Asn	Arg	Thr	Gly	Lys	Gly	Val	Gly	Ile	Tyr	Val	Ile	Asp	Ser	Gly	Val
			100					105					110		
Arg	Thr	Thr	His	Gln	Glu	Leu	Val	Gly	Arg	Val	Glu	Thr	Ile	Tyr	Ser
			115				120					125			
Thr	Leu	Glu	Gly	Lys	His	Phe	Asp	Ser	Asp	Asn	Glu	Leu	Asn	Ile	Asn
			130			135					140				
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Gly	Ile	Ala	Ser	Glu	Ala	Thr	Val	Tyr	Asn	Leu	Phe	Val	Asp	Phe	Ser
				165					170					175	
Met	Ser	Asp	Ile	Ile	Lys	Ala	Phe	Asp	Thr	Val	Leu	His	His	Tyr	Lys
			180					185					190		
Lys	Ser	Lys	Ser	Ala	Ala	Val	Leu	Val	Thr	Ser	Phe	Ser	Thr	Leu	Ser
			195				200					205			
Leu	Ala	Met	Lys	Pro	Ile	Ser	Asp	Ala	Leu	Tyr	Gln	Ala	Gly	Leu	Val
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					230					235					240
Ala	Ala	Phe	Pro	Gln	Thr	Ile	Ser	Val	Gly	Ala	Thr	Asp	Lys	Gln	Asp
				245					250					255	
Asn	Lys	Ala	Ser	Phe	Ser	Asn	Phe	Gly	Asn	Thr	Val	Asp	Val	Tyr	Ala
				260				265					270		
Pro	Gly	Val	Asn	Val	Lys	Val	Ala	Asp	His	Ala	Arg	Asp	Val	Arg	Thr
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Arg	Ile	Ala	Arg	Gly	Thr	Ser	Phe	Ser	Ala	Pro	Tyr	Val	Ala	Gly	Ile
					295					300					
Ile	Ala	Leu	Met	Leu	Glu	Gly	Ser	Asp	Lys	Pro	Arg	Lys	Ser	Glu	His
					310					315					320
Val	Asp	Thr	Ile	Arg	Gln	Ser	Phe	Leu	Asp	Asn	Ala	Ala	Ser	Ala	Ser
				325					330					335	
Lys	Ala	Asp	Lys	Arg	Val	Pro	His	Thr	Arg	Phe	Asp	Ile	Glu	Pro	Phe
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Lys	Phe	Pro	Lys	Pro	Ser	Pro	Val	Glu	Lys	Ile	Val	Gln	Lys	Val	Ser
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Asp Asn Lys Glu Ser Ser Thr Ile Ser Asp Lys Gly Ser Lys Lys Asn
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 Tyr Val Lys Glu Ile Val Ala Gly Val Ile Leu Val Ala Thr Ile Ala
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 Ala Ile Leu Leu

<210> 111
 <211> 1596
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 111
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 acctccgaag accccatcga aggacgctac atcgtcgtgc tcagggagca ggctgcacgt 180
 ctgtcatccc aattcaccgg ccgcgccgac gtgcccgcga ttgccgatgt ggcgcgacag 240
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 gtggctcgatg ccgacgacag gacgctggcg caactgctgg ccgatccacg cgtggagtac 360
 gtcgaggagg acggccatgt gctgctgaac tcgacgacgc agccgaacgc gacctggggg 420
 ctggatcgag tcgaccagcg ctttcttcca ctcaacagca cctacgtcta cgacaccacg 480
 gccgccaacg tgcgcgccta catcatcgat tcgggctgctg tgaccgcgca cagccagttc 540
 ggccggacgca tcggcaacgg gttcagcgcg atcaacgacg gtcgtggcgt acaggactgc 600
 aatggccacg gcacacatgt ggccgggacg gtcgcccgca gtacatgggg cgtggccaag 660
 ggctgtgatcg tgcattccagt gcgcgtgttc ggctgtctcg gcggctcggc ctggctcgacg 720
 atcatcgccg gcatcgactg ggtacgcggc aaccacgtca agccggcggg ggcaaacatg 780
 agcctgggtg tcggcgggcaa ttcttcggcg gatacggcga ccaacaacct catcaacgcc 840
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<210> 112
 <211> 531
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(36)

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 Thr Ala Val Ala Ser Glu Leu Arg Thr Ser Glu Asp Pro Ile Glu Gly
 35 40 45
 Arg Tyr Ile Val Val Leu Arg Glu Gln Ala Ala Arg Leu Ser Ser Glu
 50 55 60
 Phe Thr Gly Arg Ala Asp Val Pro Ala Ile Ala Asp Val Ala Arg Thr
 65 70 75 80
 Leu Ala Ser Arg His Gly Ala Thr Leu Leu Phe Ser Tyr Glu His Ala
 85 90 95

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Leu Arg Gly Phe Val Val Asp Ala Asp Asp Arg Thr Leu Ala Gln Leu
 100 105 110
 Leu Ala Asp Pro Arg Val Glu Tyr Val Glu Glu Asp Gly His Val Leu
 115 120 125
 Leu Asn Ser Thr Thr Gln Pro Asn Ala Thr Trp Gly Leu Asp Arg Val
 130 135 140
 Asp Gln Arg Phe Leu Pro Leu Asn Ser Thr Tyr Val Tyr Asp Thr Thr
 145 150 155 160
 Ala Ala Asn Val Arg Ala Tyr Ile Ile Asp Ser Gly Val Leu Thr Ala
 165 170 175
 His Ser Gln Phe Gly Gly Arg Ile Gly Asn Gly Phe Ser Ala Ile Asn
 180 185 190
 Asp Gly Arg Gly Val Gln Asp Cys Asn Gly His Gly Thr His Val Ala
 195 200 205
 Gly Thr Val Ala Gly Ser Thr Trp Gly Val Ala Lys Gly Val Ile Val
 210 215 220
 His Pro Val Arg Val Phe Gly Cys Ser Gly Gly Ser Ala Trp Ser Thr
 225 230 235 240
 Ile Ile Ala Gly Ile Asp Trp Val Arg Gly Asn His Val Lys Pro Ala
 245 250 255
 Val Ala Asn Met Ser Leu Gly Gly Gly Asn Ser Ser Ala Asp Thr
 260 265 270
 Ala Thr Asn Asn Leu Ile Asn Ala Gly Val Thr Val Val Ala Ala
 275 280 285
 Gly Asn Ser Asn Asp Asn Ala Cys Leu Tyr Ser Pro Ala Arg Val Ala
 290 295 300
 Asn Ala Ile Thr Val Gly Ser Thr Gln Ser Asn Asp Ala Arg Ser Trp
 305 310 315 320
 Phe Ser Asn Trp Gly Asn Cys Leu Asp Leu Phe Ala Pro Gly Ser Ala
 325 330 335
 Ile Thr Ser Ala Trp Trp Thr Ser Thr Ala Ser His Thr Ile Asp
 340 345 350
 Gly Thr Ser Met Ala Ala Pro His Val Ala Gly Ala Ala Leu Tyr
 355 360 365
 Leu Ala Asn Asn Pro Gly Ala Ser Pro Ala Thr Val Arg Asn Ala Ile
 370 375 380
 Ile Thr Asn Ala Thr Thr Asn Val Val Ser Asn Pro Gly Ala Gly Ser
 385 390 395 400
 Pro Asn Arg Leu Leu Tyr Thr Arg Phe Ala Ala Pro Pro Pro Pro
 405 410 415
 Pro Pro Gly Cys Gly Arg Leu Asn Gly Gly Gln Thr Leu Gln Thr Gly
 420 425 430
 Gln Ser Ala Val Ser Cys Asp Gly Arg Phe Thr Phe Val Ile Gln Gly
 435 440 445
 Asp Gly Asn Leu Val Leu Tyr Gln Ala Gly Val Gly Ala Ile Trp Ala
 450 455 460
 Asn His Val Tyr Gly Ser Gly His Arg Leu Ser Met Gln Gly Asp Gly
 465 470 475 480
 Asn Leu Val Val Tyr Asn Ser Val Asn Gln Ala Arg Trp His Thr Gly
 485 490 495
 Thr His Gly His Pro Gly Ala Trp Leu Ala Val Gln Asn Asp Gly Asn
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 Cys Cys Arg
 530

<210> 113
 <211> 4818
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

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<210> 114
 <211> 1606
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(32)

<400> 114

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			20					25					30		
Ala	Leu	Leu	Lys	Gln	Pro	Phe	Lys	Thr	Asn	Pro	Gln	Asp	Ala	Ser	Ala
		35					40					45			
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	50					55					60				
Asp	Ala	Arg	Leu	His	Lys	Asp	Leu	Gln	Gly	Leu	Ser	Gly	Ser	Gln	Glu
65					70					75				80	
Val	Pro	Val	Ile	Ile	His	Leu	Ser	Glu	Lys	Ala	Val	Gly	Leu	Glu	Gln
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Gly	Ile	His	Lys	Leu	Asn	Gly	Lys	Lys	Met	Ser	Gln	Ser	Glu	Ile	Thr
			100					105					110		
Leu	Lys	Lys	Gly	Lys	Ile	Gln	Ala	Gln	Gln	Asn	Thr	Ala	Arg	Lys	Glu
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145					150					155				160	
Leu	Leu	Thr	Ile	Ser	Gly	Val	Lys	Tyr	Val	Glu	Pro	Asp	Thr	Thr	Val
			165						170					175	
Tyr	Ala	Gln	Glu	Gly	Leu	Gln	Lys	Val	Asp	Pro	Lys	Val	Asp	Ala	Lys
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Asp	Gly	Ser	Glu	Thr	Ser	Pro	Leu	Asp	Arg	Pro	Ala	Asn	Lys	Pro	Glu
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Val	Asn	Glu	Arg	Gly	Ser	Ser	Phe	Tyr	Thr	Thr	His	Gly	Thr	His	Val
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Glu	Ala	530	Leu	Arg	Ala	Ala	Leu	Ala	Ala	Pro	Ser	Thr	Ile	Ser	Phe
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Ser	Ala	580	Pro	Gly	Thr	Asn	Ile	Met	Ser	Thr	Ile	Pro	Met	Tyr	Gly
Asp	Phe	595	Pro	Asp	Ala	Asp	Tyr	Ser	Glu	Ala	Tyr	Ser	Arg	Lys	Thr
Thr	Ser	610	Met	Ala	Thr	Pro	His	Ile	Ala	Gly	Ile	Ala	Ala	Leu	Val
Gln	Ala	625	Asn	Pro	Thr	Trp	Asn	Ala	Phe	Asp	Val	Lys	Val	Ala	Leu
Asn	Thr	645	Ala	Thr	Val	Leu	Asp	Thr	Lys	Lys	Tyr	Asp	Val	Phe	Ala
Gly	Ala	660	Gly	Arg	Val	Asp	Ala	Tyr	Lys	Ala	Ala	Arg	Ala	Asp	Val
Ala	Tyr	675	Ala	Ile	Asp	Thr	Ala	Ser	Asn	Asp	Gly	Thr	Glu	Val	Glu
Leu	Lys	690	Gly	Thr	Val	Thr	Phe	Gly	Pro	Gln	Lys	Leu	Asp	Lys	Asn
Ser	Val	705	Thr	Lys	Lys	Ile	Asn	Val	Lys	Asp	Leu	Lys	Ser	Ala	Gly
Asp	Tyr	725	Thr	Val	Ser	Val	Asp	Val	Thr	Lys	Gly	Phe	Gly	Asp	Ala
Val	Thr	740	Val	Asp	Gln	Ser	Glu	Phe	Thr	Leu	Asn	Gly	Glu	Gln	Leu
Asn	Val	755	Thr	Leu	Thr	Ala	Ser	Lys	Ala	Glu	Thr	Lys	Ala	Gly	Asp
Ile	Leu	770	Gly	Tyr	Ile	His	Ile	Lys	Gly	Asn	Gly	Lys	Asp	Leu	Ser
Pro	Phe	785	Ala	Ala	Asp	Phe	Gly	Gly	Ala	Ala	Ala	Val	Ala	Val	Lys
Met	Glu	805	Ile	Thr	Lys	Thr	Asp	Leu	Ser	Phe	Asn	Gly	Asp	Gly	Val
Asp	Asp	820	Ala	Met	Leu	Tyr	Phe	Thr	Ile	Thr	Gly	Asp	Val	Gly	Phe
Thr	Ile	835	Glu	Leu	Trp	Asp	Ile	Met	Asn	Pro	Thr	Gly	Gly	Lys	Tyr
Asp	Gly	850	Tyr	Ile	Gly	Tyr	Leu	His	Ala	Ser	Asp	Thr	Leu	Thr	Ala
Ser	Tyr	865	Gln	Leu	Pro	Ile	Leu	Gly	Lys	Tyr	Thr	Gln	Trp	Gly	Gly
Ala	Ser	885	Glu	Val	Ile	Pro	Asp	Gly	Leu	Tyr	Ile	Asp	Phe	Ser	Ala

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Glu Thr Lys Ser Gly Asn Pro Lys Thr Ile Ala Asp Tyr Val Gly Pro
 Val Val Val⁹⁰⁰ Lys Ser Thr Ala Gly⁹⁰⁵ Thr Ile Glu Gly Ala Val Ala Asp
 Gly Lys Val⁹¹⁵ Thr Gly Lys Ile Thr Asp Lys Tyr Val⁹²⁵ Asp Tyr Gln Lys
 Glu⁹³⁰ Leu Val Lys Tyr Gly⁹³⁵ Met Gly Tyr Asp Leu⁹⁴⁰ Asn Thr Lys Leu Ser
 Ala⁹⁴⁵ Thr Tyr Glu Val⁹⁵⁰ Thr Ala Asn Asp Ala⁹⁵⁵ Val Val Asp Ser Gly⁹⁶⁰ Ala
 Val Lys Leu Ala⁹⁶⁵ Gln Asp Gly Thr Phe Ala⁹⁷⁰ Phe Asp Leu Pro Thr Phe
 Asp Lys Thr⁹⁸⁰ Lys Asn Asn Val Thr⁹⁸⁵ Val Lys Tyr Ala Asp Ala Ala Gly
 Asn Lys Ala⁹⁹⁵ Glu Glu Val Ile¹⁰⁰⁰ Tyr Thr Ala Ile Asp Glu Pro Val Asp
 Thr¹⁰¹⁰ Val Ser Val Ala Val¹⁰¹⁵ Asp Gln Thr Ala Leu Asp Leu Lys Val Gly
 Asp¹⁰²⁵ Thr Ala Gln Leu¹⁰³⁰ Leu Val Thr Glu Thr¹⁰³⁵ Thr Thr Lys Pro Asp Gly
 Thr Ser Thr Asp¹⁰⁴⁵ Arg Asp Val Thr Ala¹⁰⁵⁰ Glu Ala Thr Phe Ala Ser Ser
 Asp Ala Ala Val¹⁰⁶⁰ Ala Thr Val Val¹⁰⁶⁵ Asn Gly Lys Val Thr Ala Val Ala
 Ala Gly Lys Ala Glu Ile Thr¹⁰⁸⁰ Val Thr Tyr Asn Asp Phe Thr Gln Thr
 Val¹⁰⁹⁰ Pro Val Thr Val Thr¹⁰⁹⁵ Ala Glu Pro Val Lys¹¹⁰⁰ Glu Glu Ile Ser Tyr
 Ala¹¹⁰⁵ Leu Asn Lys Lys¹¹¹⁰ Ser Leu Ser Leu Gly Val Gly Gln Gln Glu Gln
 Leu Thr Ile Thr¹¹²⁵ Glu Thr Lys Val Lys¹¹³⁰ Ala Asp Gly Thr Val Val Lys
 Thr Asp Val Thr¹¹⁴⁰ Pro Thr Val Ser Phe Asn Val Val Asp Asn Ser Ile
 Ala Thr Val His Lys Gly¹¹⁵⁵ Leu Val Thr Ala His Lys¹¹⁶⁰ Ala Gly Lys Thr
 Gln Val Arg Val Met Ile¹¹⁷⁵ Pro Gly Gln Asp Thr Arg Phe Val Tyr Leu
 Glu¹¹⁸⁵ Val Lys Asp Leu¹¹⁹⁰ Pro Gln Asp Val Val¹¹⁹⁵ Thr Tyr Ser Val Asp Lys
 Thr Ala Leu Lys¹²⁰⁵ Leu Gly Val Gly¹²¹⁰ Gln Gln Glu Gln Leu Thr Val Lys
 Gln Thr Thr Val¹²²⁰ Lys Pro Asp Gly¹²²⁵ Thr Val Val Glu Lys Asp Phe Thr
 Pro Ser Thr Ser Phe Asn Val¹²⁴⁰ Val Asp Lys Lys Ile Ala Thr Val Ser
 Lys¹²⁵⁰ Gly Leu Val Thr Ala¹²⁵⁵ His Lys Ala Gly Lys Thr Gln Val Arg Val
 Met¹²⁶⁵ Ile Pro Gly Glu¹²⁷⁰ Asp Thr Ile Phe Val Tyr Leu Glu Val Val Thr
 Pro Pro Gln Asn Ile Val Thr Tyr Ser Val Asp Lys Thr Asp Val Lys
 Met Gln Val Asn Gln Gln Thr Gln Ile Lys Ile Thr Glu Lys Thr Val
 Thr¹³¹⁵ Pro Asp Gly Lys Ile Thr¹³²⁰ Glu Lys Asp Val Thr Gly Ala Ser Lys
 Phe Ser Val Val Asn Asn Lys Ile Ala Thr Val Asn Lys Gly Leu Ile
 Ser Ala Leu Thr Pro Gly Lys Thr Gln Val Lys Val Val Leu Pro Asn
 Gly Glu Ser Leu¹³⁶⁵ Val Tyr Leu Ala Val Lys Gly Glu Pro Ala Pro
 Ile Ile Thr Tyr Ser Leu Asp Lys¹³⁸⁰ Asp Ser Val Ser Leu Lys Ala Gly
 Asp Ser Ala Asn Val Gln Leu Val Glu Thr Thr Thr Lys Ala Asp Gly
 Thr Ser Thr Thr Lys Asp Val¹⁴¹⁰ Thr Thr Glu Ala Thr Tyr Gln Thr Asn
 Thr¹⁴²⁵ Ser Thr Thr Lys Asp¹⁴³⁰ Val Thr Thr Glu Ala Thr Tyr Gln Thr Asn
 Thr¹⁴³⁵ Ser Thr Thr Lys Asp¹⁴⁴⁰ Val Thr Thr Glu Ala Thr Tyr Gln Thr Asn

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Asn Ala Asp Val Ala Thr Val Thr Gln Gly Lys Ile Ser Ala Ile Ala
1445 1450 1455
Ala Gly Asp Thr Glu Ile Ser Val Thr Leu Gly Ala Phe Glu Thr Thr
1460 1465 1470
Val Lys Val His Val Glu Ala Val Ala Pro Lys Ala Ile Val Val Thr
1475 1480 1485
Asp Glu Met Ile Asn Ala Phe Ile Ala Asp Lys Lys Ala Lys Gln Ile
1490 1495 1500
Ile Ile Glu Val Pro Ala Ala Val Gly Leu Met Asp Val Glu Phe Ser
1505 1510 1515 1520
Lys Ala Ile Leu Lys Lys Ile Glu Lys Ser Glu Lys Asp Leu Val Leu
1525 1530 1535
Lys Ala Gly Asn Ala Val Tyr Thr Leu Glu Asp Asp Ala Val Glu Glu
1540 1545 1550
Leu Met Asn Arg Ser Gly Gly Asp Ala Val Ile Thr Leu Gly Thr Ser
1555 1560 1565
Ser Ser Ala Asn Val Lys Asp Ala Val Ser Glu Val Tyr Thr Ile Glu
1570 1575 1580
Phe Ser Thr Gly Thr Ala Ala Asn Lys Ser Ala Leu Lys Lys Phe Asp
1585 1590 1595 1600
Glu Glu Ile Leu Val Ala
1605

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<210> 115
 <211> 2487
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 115

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gcgcacgtcg	cggcggagca	cccggaggac	gcaggacccc	caccgcgtagc	gcagtccccc	180
acagccgaga	cggagcacgt	cgcgacgga	cgcacgaagg	tgtccgagct	tccgccactg	240
gccgcgagca	aggaccgct	caaggaggtg	tacggcaaga	ccgcgaaggc	gccggctccgt	300
ccctcgaagt	cgatggagaa	ggcggttgcc	ggcaagaccg	gcaagtcccg	tgcgcttgcc	360
gccgcgtgca	acgtctccga	cttcaccagc	cgaagcggcg	gcgcgctggg	ccagcagatc	420
aaggcgtcta	caaccgactg	cgtcaacacc	ctgttcaacc	tgaccgggtc	ggacgcctac	480
tacgccttcc	gcgagtcgca	gatggcctcg	gtcgcctacg	ccctgcgcga	cggtctcgacg	540
tcctacccgg	gtaacgcctc	caccggtatg	ccgcagctcg	tgctctacct	gcgcgccggc	600
tactacgtcc	actactacaa	cgcaagcacg	gtgggctcct	acggcagcag	cctgcagacc	660
gcgatacgcg	ccgggctcga	cgcttcttc	gccagcccgc	gctcacgcga	cgtaacgcac	720
gccaacggcg	agacgctcgc	cgaggcggtc	acgctcatcg	acagtgcga	ggagaacgcc	780
cgctacatcc	acgtcgtcaa	gcgcctgctg	gcggattacg	actccacctg	gaactcctcc	840
tggtggatgc	tcaacgcggt	caacaacgtg	tacaccgtga	ccttcgcggg	ccatcaggtg	900
cccgcgttcg	tgagtgcggt	gcagtcggag	cccggctctga	tcgacgcgct	ctacaacttc	960
gcgagcgggc	acctcgcgct	gctgggaacg	gctggtcctt	acctcacgtc	gaacgcggga	1020
cgcgaaactcg	gcaggttcct	gcagcactcc	ccactgcgct	ccaagggtccg	ccccctggcc	1080
gcgggcctgc	tcaactccag	ctccatcaag	ggccgaacgg	ccccgctgtg	ggtcggtgtg	1140
gccgagatga	ccgactacta	cgacaaggcc	aactgctcct	actacggcac	ctgcgacctc	1200
caggcccaac	tggcccgtc	cgtcctgacg	gtgacctacc	cctgcagctc	cagcatcacc	1260
atcaaggcgc	agcagatgac	ctcgggagag	ctgtcctcca	gctgcagcag	cctgcgcaac	1320
caggacgcct	acttccacaa	cgtggcccgt	gacaacggcc	ccgtcgcgaa	cgacaacaac	1380
agcaccatcg	aggtcgtggt	cttcgactcc	agcaccgact	accagacctc	cgccggcgcc	1440
atgtacggga	tcgacaccaa	caacggcgcg	atgtacctgg	aagggaaccc	gtcggcgggc	1500
ggcaaccagc	gcagattcat	cgcctacgag	gccgattggc	tgccggcccga	cttcagatc	1560
tggaacctca	accacgagta	cacgcactac	ctcgacggtc	gcttcaacat	gtacggcgac	1620
ttcaacgcc	acatcaccac	cccgaacctc	tggtggatcg	aaggcttcgc	cgagtacgtc	1680
tcctactcct	accgcggtct	cccctatacg	gaggcgacga	ccgaagcagg	ccgtcgcacg	1740
tacgcgtgga	gcaccttggt	cgacaccacg	tacagccacg	acaccacgcg	catctaccgc	1800
tggggctacc	tcgccgtgcg	gtacatgctc	gagaaccacc	gcgccgacat	ggacaccgtc	1860
ctcggctact	accgcgcggg	aaactggaac	gccgcacgtt	cctacctgac	cggcaccatc	1920
ggcaccgcgt	acgacaacga	ctggtacacc	tggtggcgcg	cctgcgcggc	cggaactgac	1980
ggaggcgggg	gcaccaaccc	gcccggcaac	caggcgccca	ccgccgcgtt	caccaccgcc	2040
gtccagggcc	tggacgtcac	cttcaccgac	cagtcacagg	acgccgacgg	caccatcgcc	2100
tcccggctct	ggagcttcgg	tgacggcacc	acctccacgg	ccaccaacc	cgtcaagagg	2160

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tacgggtcgg	ccgggtccta	cacgggtgaag	ctgaccgtca	ccgacgacaa	gggagccacc	2220
gccaccgcaa	cgaggacggt	caccgtagcc	agcggcggag	gcggcggcac	cgagtgcacc	2280
ggaaccgaca	cccgggaact	gggccagaac	tgccaacgcg	gcaaccagtc	cgccaccgcc	2340
ggcaactacg	cctacctgta	cctctacgtc	ccggccggca	ccacccagct	gaagatcacc	2400
acctccggcg	ggacgggcca	cgcggacctc	tactacagca	ccagcggctg	gcccggcacc	2460
acgagctaca	cgcagcgtgc	gacggga				2487

<210> 116
 <211> 829
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(33)

<400> 116

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Ala	Leu	Thr	Val	Ala	Met	Ser	Met	Gly	Leu	Leu	Ser	Gln	Pro	Ala	Gly
			20					25					30		
Ala	Ala	Gly	Asn	Thr	Gly	Ser	Val	Ala	His	Val	Ala	Ala	Asp	Asp	Pro
		35					40				45				
Glu	Asp	Ala	Gly	Pro	Pro	Pro	Val	Ala	Gln	Ser	Pro	Thr	Ala	Glu	Thr
	50					55					60				
Glu	His	Val	Ala	His	Gly	Arg	Thr	Lys	Val	Ser	Glu	Leu	Pro	Pro	Leu
	65				70					75					80
Ala	Ala	Ser	Lys	Asp	Pro	Leu	Lys	Glu	Val	Tyr	Gly	Lys	Thr	Ala	Lys
			85						90					95	
Ala	Pro	Val	Arg	Pro	Ser	Lys	Ser	Met	Glu	Lys	Ala	Val	Ala	Gly	Lys
			100					105					110		
Thr	Gly	Lys	Ser	Arg	Ala	Leu	Ala	Ala	Cys	Asn	Val	Ser	Asp	Phe	
		115				120					125				
Thr	Ser	Arg	Ser	Gly	Gly	Ala	Leu	Val	Gln	Gln	Ile	Lys	Ala	Ser	Thr
	130					135					140				
Thr	Asp	Cys	Val	Asn	Thr	Leu	Phe	Asn	Leu	Thr	Gly	Ser	Asp	Ala	Tyr
	145				150					155					160
Tyr	Ala	Phe	Arg	Glu	Ser	Gln	Met	Ala	Ser	Val	Ala	Tyr	Ala	Leu	Arg
				165					170					175	
Asp	Gly	Ser	Thr	Ser	Tyr	Pro	Gly	Asn	Ala	Ser	Thr	Gly	Met	Pro	Gln
			180					185					190		
Leu	Val	Leu	Tyr	Leu	Arg	Ala	Gly	Tyr	Tyr	Val	His	Tyr	Tyr	Asn	Ala
		195					200					205			
Ser	Thr	Val	Gly	Ser	Tyr	Gly	Ser	Ser	Leu	Gln	Thr	Ala	Ile	Arg	Ala
	210					215					220				
Gly	Leu	Asp	Ala	Phe	Phe	Ala	Ser	Pro	Arg	Ser	Arg	Asp	Val	Asn	Asp
	225				230					235					240
Ala	Asn	Gly	Glu	Thr	Leu	Ala	Glu	Ala	Val	Thr	Leu	Ile	Asp	Ser	Ala
			245						250					255	
Glu	Glu	Asn	Ala	Arg	Tyr	Ile	His	Val	Val	Lys	Arg	Leu	Leu	Ala	Asp
		260						265					270		
Tyr	Asp	Ser	Thr	Trp	Asn	Ser	Ser	Trp	Trp	Met	Leu	Asn	Ala	Val	Asn
		275					280					285			
Asn	Val	Tyr	Thr	Val	Thr	Phe	Arg	Gly	His	Gln	Val	Pro	Ala	Phe	Val
	290					295					300				
Ser	Ala	Val	Gln	Ser	Asp	Pro	Gly	Leu	Ile	Asp	Ala	Leu	Tyr	Asn	Phe
	305				310					315					320
Ala	Ser	Gly	His	Leu	Ala	Leu	Leu	Gly	Thr	Asp	Gln	Ser	Tyr	Leu	Thr
			325						330					335	
Ser	Asn	Ala	Gly	Arg	Glu	Leu	Gly	Arg	Phe	Leu	Gln	His	Ser	Pro	Leu
		340						345					350		
Arg	Ser	Lys	Val	Arg	Pro	Leu	Ala	Ala	Gly	Leu	Leu	Asn	Ser	Ser	Ser
		355					360					365			
Ile	Lys	Gly	Arg	Thr	Ala	Pro	Leu	Trp	Val	Gly	Val	Ala	Glu	Met	Thr
	370					375					380				
Asp	Tyr	Tyr	Asp	Lys	Ala	Asn	Cys	Ser	Tyr	Tyr	Gly	Thr	Cys	Asp	Leu

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385      390      395      400
Gln Ala Gln Leu Ala Arg Ser Val Leu Thr Val Thr Tyr Pro Cys Ser
      405
Ser Ser Ile Thr Ile Lys Ala Gln Gln Met Thr Ser Gly Glu Leu Ser
      420
Ser Ser Cys Ser Ser Leu Arg Asn Gln Asp Ala Tyr Phe His Asn Val
      435
Ala Arg Asp Asn Gly Pro Val Ala Asn Asp Asn Asn Ser Thr Ile Glu
      450
Val Val Val Phe Asp Ser Ser Thr Asp Tyr Gln Thr Tyr Ala Gly Ala
      465
Met Tyr Gly Ile Asp Thr Asn Asn Gly Gly Met Tyr Leu Glu Gly Asn
      485
Pro Ser Ala Ala Gly Asn Gln Pro Arg Phe Ile Ala Tyr Glu Ala Glu
      500
Trp Leu Arg Pro Asp Phe Gln Ile Trp Asn Leu Asn His Glu Tyr Thr
      515
His Tyr Leu Asp Gly Arg Phe Asn Met Tyr Gly Asp Phe Asn Ala Asn
      530
Ile Thr Thr Pro Thr Ile Trp Trp Ile Glu Gly Phe Ala Glu Tyr Val
      545
Ser Tyr Ser Tyr Arg Gly Leu Pro Tyr Thr Glu Ala Thr Thr Glu Ala
      565
Gly Arg Arg Thr Tyr Ala Leu Ser Thr Leu Phe Asp Thr Thr Tyr Ser
      580
His Asp Thr Arg Ile Tyr Arg Trp Gly Tyr Leu Ala Val Arg Tyr
      595
Met Leu Glu Asn His Arg Ala Asp Met Asp Thr Val Leu Gly Tyr Tyr
      610
Arg Ala Gly Asn Trp Asn Ala Ala Arg Ser Tyr Leu Thr Gly Thr Ile
      625
Gly Thr Arg Tyr Asp Asn Asp Trp Tyr Thr Trp Leu Ala Ala Cys Ala
      645
Ala Gly Asn Cys Gly Gly Gly Gly Thr Asn Pro Pro Gly Asn Gln Ala
      660
Pro Thr Ala Phe Thr Thr Ala Val Gln Gly Leu Asp Val Thr Phe
      675
Thr Asp Gln Ser Thr Asp Ala Asp Gly Thr Ile Ala Ser Arg Ser Trp
      690
Ser Phe Gly Asp Gly Thr Thr Ser Thr Ala Thr Asn Pro Val Lys Arg
      705
Tyr Gly Ser Ala Gly Ser Tyr Thr Val Lys Leu Thr Val Thr Asp Asp
      725
Lys Gly Ala Thr Ala Thr Ala Thr Arg Thr Val Thr Val Ala Ser Gly
      740
Gly Gly Gly Gly Thr Glu Cys Thr Gly Thr Asp Thr Arg Glu Leu Gly
      755
Gln Asn Cys Gln Arg Gly Asn Gln Ser Ala Thr Ala Gly Asn Tyr Ala
      770
Tyr Leu Tyr Leu Tyr Val Pro Ala Gly Thr Thr Gln Leu Lys Ile Thr
      785
Thr Ser Gly Gly Thr Gly Asp Ala Asp Leu Tyr Tyr Ser Thr Ser Gly
      805
Trp Pro Gly Thr Thr Ser Tyr Thr Gln Arg Ala Thr Gly
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      825

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<210> 117
 <211> 1356
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 117
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 gaacatccgc agggccatac cggccgctac atcgcgatca tgcgtgagga tgccgaaggc 180

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gatactgaag	cggtgatgtc	gaattccttt	gccgccacct	cggtcaaacag	ccgtgacttc	240
ggcaccgcgc	gtttcgcgat	ggatgagatt	tcgggggcgc	actcgtggt	gctgaacacg	300
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tctggcgaca	gtttcgggac	tgctgccgag	ttgccctatg	tgctcgaacc	cgaaaccatc	420
gaatgggtgc	tgatcgacct	ggccagctat	ctcatgggct	ttcgtgctgc	ctcggaccgg	480
atcgcgaccg	atcttctggg	gcaacctgtg	ccgtcgcagt	tcgaaccggc	ccccgccgac	540
gtcactgctg	ctgccggcgc	gatgacctgg	ggcctttcgc	cgaccgcgct	cggtgccagc	600
acggcgaccg	ggcgcgccat	ccgcgtggcg	atccttgata	ccgggcttga	tctcggccac	660
ccggatttcg	cgggcccgcg	gatcctggcg	cagtcgttca	tcgcgggcga	gacaccgcag	720
gatgtcaacg	gccacggcac	tcacgtgacc	ggcaccgctt	gcggcccgcg	ggtgcccgcg	780
accggcgcca	accgctatgg	catcgcccac	gagtgcgaaa	tcctggtcgc	caagggtgctg	840
agcaacgccg	gtgccggacc	gggccttggc	atcgtgatgg	gcatcgactg	ggcgctggcg	900
aacggcgcg	atatcatcaa	catgtctctt	ggcagcccgc	cagcggcggc	caatctcaag	960
tacacccagg	cgggtaagcg	ggccttgacc	cgcggcgctt	tgattgtcgc	ggcgccgggc	1020
aacgacaacg	cgccgaccgg	ccagcccgc	aattcgccga	cgatcctgtc	ggtggccctcg	1080
gtgaactcgt	tcctgcagaa	gtcgggcttt	tcaaacttcg	gcaaggtcga	acttgccgca	1140
ccggggctct	ccatcgattc	gtccctgccc	cgtccgcgca	ggcgcggtt	cctcagcggt	1200
accagctagg	cgcggccgca	gttcacggcg	attgctgccc	ttcatgcca	ggccactggc	1260
ctgcgcggca	aggcgctgtg	ggcccatctc	gagtcctcgc	ccaaggcgct	gtcgtgccc	1320
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<210> 118

<211> 451

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 118

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Gly	Thr	Asp	Asp	Thr	Gly	Thr	Gly	Ala	Pro	Gly	Leu	Asp	Cys	Pro	Val
			20					25					30		
Gln	Arg	Leu	Ile	Asp	Ala	Ala	Leu	Glu	His	Pro	Gln	Gly	His	Thr	Gly
		35					40					45			
Arg	Tyr	Ile	Ala	Ile	Met	Arg	Glu	Asp	Ala	Glu	Gly	Asp	Thr	Glu	Ala
	50				55						60				
Val	Met	Ser	Asn	Ser	Phe	Ala	Ala	Thr	Ser	Ala	Asn	Ser	Arg	Asp	Phe
65					70				75					80	
Gly	Thr	Arg	Gly	Phe	Ala	Met	Asp	Glu	Ile	Ser	Gly	Ala	Asp	Ser	Leu
			85						90					95	
Val	Leu	Asn	Thr	Leu	Gly	Met	Ala	Val	Leu	Gly	Gly	Ser	Ala	Ala	Asp
			100					105					110		
Ala	Ala	Arg	Glu	Ser	Met	Thr	Arg	Ser	Gly	Asp	Ser	Phe	Gly	Thr	Ala
		115					120					125			
Ala	Glu	Leu	Pro	Tyr	Val	Leu	Glu	Pro	Glu	Thr	Ile	Glu	Trp	Val	Leu
	130					135					140				
Ile	Asp	Pro	Ala	Ser	Tyr	Leu	Met	Gly	Phe	Arg	Ala	Ala	Ser	Asp	Arg
145					150					155				160	
Ile	Ala	Thr	Asp	Leu	Leu	Gly	Gln	Pro	Val	Pro	Ser	Gln	Phe	Glu	Pro
			165						170					175	
Ala	Pro	Ala	Asp	Val	Thr	Ala	Ala	Ala	Gly	Gly	Met	Thr	Trp	Gly	Leu
			180					185					190		
Ser	Ala	Thr	Arg	Val	Gly	Ala	Ser	Thr	Ala	Thr	Gly	Arg	Gly	Ile	Arg
		195					200					205			
Val	Ala	Ile	Leu	Asp	Thr	Gly	Leu	Asp	Leu	Gly	His	Pro	Asp	Phe	Ala
	210					215					220				
Gly	Arg	Arg	Ile	Leu	Ala	Gln	Ser	Phe	Ile	Ala	Gly	Glu	Thr	Pro	Gln
225					230					235				240	
Asp	Val	Asn	Gly	His	Gly	Thr	His	Val	Thr	Gly	Thr	Ala	Cys	Gly	Pro
			245						250					255	
Arg	Val	Pro	Ala	Thr	Gly	Gly	Asn	Arg	Tyr	Gly	Ile	Ala	His	Glu	Cys
			260					265					270		
Glu	Ile	Leu	Val	Gly	Lys	Val	Leu	Ser	Asn	Ala	Gly	Ala	Gly	Pro	Gly
	275						280					285			
Leu	Gly	Ile	Val	Met	Gly	Ile	Asp	Trp	Ala	Leu	Ala	Asn	Gly	Ala	His
	290					295					300				

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Ile	Ile	Asn	Met	Ser	Leu	Gly	Ser	Pro	Ala	Ala	Ala	Ala	Asn	Leu	Lys
305					310				315						320
Tyr	Thr	Gln	Ala	Gly	Lys	Arg	Ala	Leu	Thr	Arg	Gly	Ala	Leu	Ile	Val
				325					330					335	
Ala	Ala	Ala	Gly	Asn	Asp	Asn	Ala	Pro	Thr	Gly	Gln	Pro	Ala	Asn	Ser
			340					345					350		
Pro	Thr	Ile	Leu	Ser	Val	Ala	Ser	Val	Asn	Ser	Phe	Leu	Gln	Lys	Ser
		355					360					365			
Gly	Phe	Ser	Asn	Phe	Gly	Lys	Val	Glu	Leu	Ala	Ala	Pro	Gly	Ser	Ser
	370					375					380				
Ile	Asp	Ser	Ser	Leu	Pro	Arg	Pro	Arg	Arg	Arg	Gly	Phe	Leu	Ser	Gly
385					390					395					400
Thr	Ser	Met	Ala	Ala	Pro	His	Val	Thr	Gly	Ile	Ala	Ala	Leu	His	Ala
			405						410					415	
Gln	Ala	Thr	Gly	Leu	Arg	Gly	Lys	Ala	Leu	Trp	Ala	His	Leu	Glu	Ser
			420					425					430		
Arg	Ala	Lys	Ala	Leu	Ser	Leu	Pro	Pro	Gln	Asn	Arg	Gly	Ala	Gly	Leu
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Val	Gln	Ala													
	450														

<210> 119
 <211> 1590
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 119

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gcgacacttc	gcactcgtct	gcagaaaacg	atttctgcag	gagccagtgc	ggtgcggggg	180
gccggaaaca	aattgaaact	gaaagctgaa	aaggcgcaga	aatcagcctt	tgaaatcgct	240
tcctcactca	acgaagacgg	ggtcaagctg	gtgagtgtca	cgcccgaat	gatagccgct	300
atgcgatttg	atcagccggg	cttgcgagtg	gtgcctgaag	cattttgttc	tccggcgaga	360
gcagttgtgc	gccttctcag	gacggtcacg	aaaacggccg	ctgcagcgac	cgccgtccag	420
cgcaaattga	aaattaccgt	gctccggagc	gatacgcagc	agccggtgtc	aggtgttgac	480
atcattgggt	ttacgaattt	cgaacaacga	gagggagtac	aggggggtcac	gtcggcgagc	540
ggcaagggtga	cgctgacagt	ttccgggagt	ctgaaattcc	agcggctcta	tgtacaacat	600
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aatcatcctg	atcttcgggt	gagtggcgga	ttgggctgcg	ttcctggcga	accagaaagt	840
gattttggtc	cccgcggcgg	aattcacggc	tcacacgttg	cgggaataat	tgcgggacgt	900
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gtttttggaa	acacctcttc	gtcgggggtca	aattttgccc	tcgtgaaagc	gattcagcga	1020
ggagtgcgcg	atggctgtga	cttacttaat	atgagcctga	gttttgatcc	cgatgtgaac	1080
ggcgttcctc	aagtcgatgc	cgcggtgcag	gaggcaatcc	gcgaggcaca	tcagaagggc	1140
gtgctgggtga	tcgcggcggc	aggggaatgat	ggacgtcgct	cggtaagtta	tccagccatg	1200
gatgacatgg	ttgttgcggt	ttccgcagtg	gggcgaaaag	ggacgtttcc	ggcgaaatcc	1260
ggcgagtacg	gtgatgttct	cgcaccattt	ggagccgccc	ctaaagattt	cctcgcggca	1320
ttttcaaacg	tcggaaccga	actcgatgta	accggtgctg	gcgtcggagt	tgtttcgaca	1380
gcaccgggcg	gctacatccc	gatgagtggt	acgtcgatgg	cttgtcctgc	tgtgacgggt	1440
gtcctggcgc	gcctgctggc	aaatactccc	gccgtactca	atatgcaacg	agactcgaat	1500
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<210> 120
 <211> 529
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 120
 Met Thr Met Ala Asp Pro Lys Arg Tyr Leu Ile Leu Pro Ala Arg Gly

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			20								25					30			
Met	Ser	Leu	Asn	Ala	Gly	Ser	Ala	Ala	Thr	Leu	Arg	Thr	Arg	Leu	Gln				
		35					40												
Lys	Thr	Ile	Ser	Ala	Gly	Ala	Ser	Ala	Val	Arg	Gly	Ala	Gly	Asn	Lys				
		50				55													
Leu	Lys	Leu	Lys	Ala	Glu	Lys	Ala	Gln	Lys	Ser	Ala	Phe	Glu	Ile	Val				
		65			70														
Ser	Ser	Leu	Asn	Glu	Asp	Gly	Val	Lys	Leu	Val	Ser	Ala	Thr	Pro	80				
			85																
Met	Ile	Ala	Ala	Met	Arg	Phe	Asp	Gln	Pro	Gly	Leu	Arg	Val	Val	Pro				
			100																
Glu	Ala	Phe	Cys	Ser	Pro	Ala	Arg	Ala	Val	Val	Arg	Leu	110	Arg	Thr				
		115																	
Val	Thr	Lys	Thr	Ala	Ala	Ala	Ala	Thr	Ala	Val	Gln	Arg	Lys	Leu	Lys				
		130																	
Ile	Thr	Val	Leu	Arg	Ser	Asp	Thr	Gln	Gln	Pro	Val	Ser	Gly	Val	Asp				
		145			150														
Ile	Ile	Gly	Phe	Thr	Asn	Phe	Glu	Gln	Arg	Glu	Gly	Val	Gln	Gly	Val				
			165																
Thr	Ser	Ala	Ser	Gly	Lys	Val	Thr	Leu	Thr	Val	Ser	Gly	Ser	Leu	Lys				
			180																
Phe	Gln	Arg	Leu	Tyr	Val	Gln	His	Glu	Gln	Val	Gly	Leu	Trp	Ser	Phe				
		195																	
Leu	Gly	Lys	Asn	Val	Ser	Thr	Asp	Gly	Thr	Leu	Thr	Ile	Thr	Leu	Gln				
		210																	
Ala	Leu	Ser	Leu	Ala	Thr	Val	Asp	Ser	Leu	Arg	His	Phe	His	Gly	Leu				
		225			230														
Gly	Gly	Asn	Ala	Asp	Gly	Thr	Gly	Val	Lys	Val	Gly	Val	Ile	Asp	Ser				
			245																
Gly	Ile	Ala	Leu	Asn	His	Pro	Asp	Leu	Arg	Val	Ser	Gly	Gly	Leu	Gly				
		260																	
Cys	Val	Pro	Gly	Glu	Pro	Glu	Ser	Asp	Phe	Gly	Pro	Arg	Gly	Gly	Ile				
		275																	
His	Gly	Ser	His	Val	Ala	Gly	Ile	Ile	Ala	Gly	Arg	Gly	Asn	Ala	Pro				
		290																	
Thr	Gly	Met	Arg	Gly	Gln	Ala	Pro	Asn	Ala	Glu	Ile	Phe	Ser	Tyr	Arg				
		305			310														
Val	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Gly	Ser	Asn	Phe	Ala	Leu	Val	Lys				
			325																
Ala	Ile	Gln	Arg	Gly	Val	Ala	Asp	Gly	Cys	Asp	Leu	Leu	Asn	Met	Ser				
			340																
Leu	Ser	Phe	Asp	Pro	Asp	Val	Asn	Gly	Val	Pro	Gln	Val	Asp	Ala	Ala				
		355																	
Val	Gln	Glu	Ala	Ile	Arg	Glu	Ala	His	Gln	Lys	Gly	Val	Leu	Val	Ile				
		370																	
Ala	Ala	Ala	Gly	Asn	Asp	Gly	Arg	Arg	Ser	Val	Ser	Tyr	Pro	Ala	Met				
		385			390														
Asp	Asp	Met	Val	Val	Ala	Val	Ser	Ala	Val	Gly	Arg	Lys	Gly	Thr	Phe				
			405																
Pro	Ala	Lys	Ser	Gly	Glu	Ser	Gly	Asp	Val	Leu	Ala	Pro	Phe	Gly	Ala				
			420																
Ala	Pro	Lys	Asp	Phe	Leu	Ala	Ala	Phe	Ser	Asn	Val	Gly	Thr	Glu	Leu				
		435																	
Asp	Val	Thr	Gly	Ala	Gly	Val	Gly	Val	Val	Ser	Thr	Ala	Pro	Gly	Gly				
		450																	
Tyr	Ile	Pro	Met	Ser	Gly	Thr	Ser	Met	Ala	Cys	Pro	Ala	Val	Thr	Gly				
		465			470														
Val	Leu	Ala	Arg	Leu	Leu	Ala	Asn	Thr	Pro	Ala	Val	Leu	Asn	Met	Gln				
			485																
Arg	Asp	Ser	Asn	Arg	Thr	Asp	Ala	Ile	Lys	Ala	Leu	Leu	Phe	Ser	Asn				
			500																
Ala	Gln	Thr	Leu	Gly	Phe	Asp	Leu	Arg	Phe	Glu	Gly	Lys	Gly	Leu	Pro				
		515																	
Lys																			

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<210> 121
 <211> 1557
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 121
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 gtagtgctga aggaatcggc agcccgttc agcagcgaag cgtcgatcgc ccaccggcgc 180
 aatgtgccgg aggtggcgca ggtggccagc caattggccg ctggcgggcg gggcatgcgg 240
 gtatcgcgca gcttcaacaa tgcgtgcgc gggtttgcg ctgataacac cagtgacgcc 300
 gatctggcgc gcctgctgca ggacccgcgg gtcgactacg tcgaagaaga cggcgtgggtg 360
 catgcctttg ccaccagag cggggcgacc tggggcctgg accggatcga tcagacggcg 420
 ctgccgtga atggtcaata tgtctatgac agcaccgcca gcaatgtgaa tgcctacatc 480
 atcgataccg gcatccgcgc cagtcacagc gatttcggcg gccgggtcag cggcggttat 540
 gacgcggtca acgacggcaa cggcaccaat gactgccagg gccatggcac ccattgctgcc 600
 ggcacggctc gcagcgccac ctatggcgtc gccaaaggcg tgcacctggg tccggtagcg 660
 gtgctgggct gtgatggttc cggcaccaac tcgggcgtca tctccggcat cgactgggtt 720
 cggagcaacc acagccgcc ggcggtggcc aatatgagcc tgggcggcgg cgctcaacg 780
 gcggttgaca gcgcggtggc caatctcagc gccgcccggc tcgtgggtgg ggtcgccgcc 840
 ggcaacgaca ataccagcgc ctgcgactat tcaccggcgc gggcgccaag cgcgatcacg 900
 gtcggctcca ccaccaatac cgatgcgcgc tcgtcgttct ccaactacgg ccagtgtctg 960
 gatatcttcg cgcccggctc caacatcctg tcgactgcca acagcagcaa cagcgccacc 1020
 accacgatga gtggcacgtc gatggcctcg ccgcatgttg ctggcgccgc cgcgctctac 1080
 ctggccagta accccagcgc atcgccggcc gcggtggcga cggcgttggg caaccaggcg 1140
 gtcgccaatg cggtgagcaa tccgggctcc ggctcaccga accgactact gcaaagtcgc 1200
 gccggcgga gcaaccggcc accgccacc ccgcccggcg gcggtgacct ctgcacggcc 1260
 tgcgccaagt acagtggcag cttgtattac agcggcgact acggctacca acctgacggg 1320
 aacttctact atgcctccag cggccaacaa cagggctggc tgcgcggccc cgccagcacc 1380
 gacttcgacc tcgaactgct gcgctggagt ggctatgggt ggaccaaggt ggcgcagagc 1440
 gtgggctcga ccagcagcga acaggtcagc tactacggca gcgctggcta ctacatgtgg 1500
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<210> 122
 <211> 518
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(25)

<400> 122
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 20 25 30
 Thr Pro Val Ser Gly Arg Tyr Ile Val Val Leu Lys Glu Ser Ala Ala
 35 40 45
 Arg Phe Ser Ser Glu Ala Ser Ile Ala His Arg Arg Asn Val Pro Glu
 50 55 60
 Val Ala Gln Val Ala Ser Gln Leu Ala Ala Gly Arg Gly Met Arg
 65 70 75 80
 Val Ser Arg Ser Phe Asn Asn Ala Leu Arg Gly Phe Val Ala Asp Asn
 85 90 95
 Thr Ser Asp Ala Asp Leu Ala Arg Leu Leu Gln Asp Pro Arg Val Asp
 100 105 110
 Tyr Val Glu Glu Asp Gly Val Val His Ala Phe Ala Thr Gln Ser Gly
 115 120 125
 Ala Thr Trp Gly Leu Asp Arg Ile Asp Gln Thr Ala Leu Pro Leu Asn
 130 135 140
 Gly Gln Tyr Val Tyr Asp Ser Thr Ala Ser Asn Val Asn Ala Tyr Ile
 145 150 155 160

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Ile Asp Thr Gly Ile Arg Ala Ser His Ser Asp Phe Gly Gly Arg Val
 165 170 175
 Ser Gly Gly Tyr Asp Ala Val Asn Asp Gly Asn Gly Thr Asn Asp Cys
 180 185 190
 Gln Gly His Gly Thr His Val Ala Gly Thr Val Gly Ser Ala Thr Tyr
 195 200 205
 Gly Val Ala Lys Gly Val His Leu Val Pro Val Arg Val Leu Gly Cys
 210 215 220
 Asp Gly Ser Gly Thr Asn Ser Gly Val Ile Ser Gly Ile Asp Trp Val
 225 230 235 240
 Arg Ser Asn His Ser Arg Pro Ala Val Ala Asn Met Ser Leu Gly Gly
 245 250 255
 Gly Ala Ser Thr Ala Val Asp Ser Ala Val Ala Asn Leu Ser Ala Ala
 260 265 270
 Gly Val Val Val Val Val Ala Ala Gly Asn Asp Asn Thr Ser Ala Cys
 275 280 285
 Asp Tyr Ser Pro Ala Arg Ala Pro Ser Ala Ile Thr Val Gly Ser Thr
 290 295 300
 Thr Asn Thr Asp Ala Arg Ser Ser Phe Ser Asn Tyr Gly Gln Cys Leu
 305 310 315 320
 Asp Ile Phe Ala Pro Gly Ser Asn Ile Leu Ser Thr Ala Asn Ser Ser
 325 330 335
 Asn Ser Ala Thr Thr Thr Met Ser Gly Thr Ser Met Ala Ser Pro His
 340 345 350
 Val Ala Gly Ala Ala Ala Leu Tyr Leu Ala Ser Asn Pro Ser Ala Ser
 355 360 365
 Pro Ala Ala Val Ala Thr Ala Leu Gly Asn Gln Ala Val Ala Asn Ala
 370 375 380
 Val Ser Asn Pro Gly Ser Gly Ser Pro Asn Arg Leu Leu Gln Ser Arg
 385 390 395 400
 Ala Gly Gly Ser Asn Pro Pro Pro Pro Gly Gly Gly Asp
 405 410 415
 Pro Cys Thr Ala Cys Ala Lys Tyr Ser Gly Ser Leu Tyr Tyr Ser Gly
 420 425 430
 Asp Tyr Gly Tyr Gln Pro Asp Gly Asn Phe Tyr Tyr Ala Ser Ser Gly
 435 440 445
 Gln Gln Gln Gly Trp Leu Arg Gly Pro Ala Ser Thr Asp Phe Asp Leu
 450 455 460
 Glu Leu Leu Arg Trp Ser Gly Tyr Gly Trp Thr Lys Val Ala Gln Ser
 465 470 475 480
 Val Gly Ser Thr Ser Ser Glu Gln Val Ser Tyr Tyr Gly Ser Ala Gly
 485 490 495
 Tyr Tyr Met Trp Arg Val Val Ser Tyr Ser Gly Ser Gly Asn Phe Asp
 500 505 510
 Phe Tyr Leu Ser Ile Pro
 515

<210> 123
 <211> 1656
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 123

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gttttcttat	tcctaattgat	tataccgacg	gatagaaccg	tagggcaagc	aatcagtttt	180
ggagcgcagt	aggagtttagc	gagtggttaac	ggagatgaaa	ttccttactt	attttttggc	240
gatgtcgcagg	acacccctct	tgagtatgat	ggttacatca	ttgagttaca	cgaaaaaccc	300
ctcgcgcgaag	taatagctat	gcaagagaat	attccttcag	gtgatttttg	agctatgagc	360
acttcatcaa	gcgcagtgat	taatcacgaa	gcaattattg	tatcagaaca	acaaaacgcg	420
ctagcggaca	taactatgcg	acttagtcaa	gcacagtcct	catcgggaatt	cggagcgcaa	480
gcaaccacat	catcccagga	attaattggt	cgagagtcct	acagcgttgt	tttcaacgga	540
ttctctctcg	acattacaga	tgaacaagca	ctagcaataa	atcaatcacc	ctacgtgaaa	600
aacgtacatc	ctaaccgtcg	cgtgagcatt	gcgcttcaag	atgccgtacc	cctcatccaa	660
gacggaattc	tcgcaggcag	agtggatgaa	gacgggaatg	attgtgaact	aacacaaaaa	720

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ccctgtttaa	caggtgaagg	cgttaccatc	gctattatag	atacaggcgt	tgattacacg	780
cacccagatt	tgggggggtg	cacaacacaa	gagtttttag	gtggagcgtg	cgaaaaagta	840
attggagggt	atgatttcac	taataatgat	gatgatgcc	tggtatgataa	tggtcatgga	900
acacacgtcg	cagggattgc	tgaggaaat	ggcttactaa	aaggcgttgc	gcccgcgcg	960
aaaatactag	cgtataaagt	tttaggtgct	gggtggttatg	gaacctggga	aggaataatt	1020
gctggaatag	aacaagcagt	tattgatggc	gcggatattt	taagtttaag	tcttggttgt	1080
gttcactctt	cctgtaatcc	tgatgatatc	gcttctcaag	cagttgataa	cgcagtactt	1140
gctggaaaag	tagtgggtgt	tgctgcagga	aattcaggac	cttcttctcg	aacgatcgga	1200
agtcctggga	ctgcacgaaa	agcaataact	gttgggttcta	caactaaatc	agataattatt	1260
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cctgaaatcg	tgtttgataa	tagaatttgt	gctgcttggc	ttaataaaga	atatcttgcc	1440
atttcaggta	ctcaatggc	aacaccttta	gtttccggag	caatagcatt	acttaaaca	1500
aaacatcccc	attggacacc	tgaagaaatt	aaaggagcag	taaaagggaac	cgcgattaat	1560
ttaggttatg	acccaacga	gcaaggcgt	ggaagaatta	atgtgagaga	aatgattggt	1620
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<210> 124

<211> 552

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(56)

<400> 124

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Ser	Phe	Lys	Gln	Phe	Leu	Leu	Asn	Lys	Asn	Asp	Ile	Phe	Ile	Leu	Gly
			20					25					30		
Ile	Ser	Phe	Leu	Leu	Ile	Val	Gly	Val	Phe	Leu	Phe	Leu	Met	Ile	Ile
			35				40					45			
Pro	Thr	Asp	Arg	Thr	Val	Gly	Gln	Ala	Ile	Ser	Phe	Gly	Ala	Ser	Glu
						55					60				
Glu	Leu	Ala	Ser	Val	Asn	Gly	Asp	Glu	Ile	Pro	Tyr	Leu	Phe	Phe	Gly
65					70					75					80
Asp	Val	Glu	Asp	Thr	Pro	Leu	Glu	Tyr	Asp	Gly	Tyr	Ile	Ile	Glu	Leu
				85					90					95	
His	Glu	Lys	Pro	Leu	Ala	Gln	Val	Ile	Ala	Met	Gln	Glu	Asn	Ile	Pro
			100					105					110		
Ser	Gly	Asp	Phe	Gly	Ala	Met	Ser	Thr	Ser	Ser	Ser	Ala	Val	Ile	Asn
		115					120					125			
His	Glu	Ala	Ile	Ile	Val	Ser	Glu	Gln	Gln	Asn	Ala	Leu	Ala	Asp	Ile
		130				135					140				
Thr	Met	Arg	Leu	Ser	Gln	Ala	Gln	Ser	Ser	Ser	Glu	Phe	Gly	Ala	Gln
145					150					155					160
Ala	Thr	Thr	Ser	Ser	Gln	Glu	Leu	Ile	Val	Arg	Glu	Ser	Tyr	Ser	Val
				165					170					175	
Val	Phe	Asn	Gly	Phe	Ser	Leu	Asp	Ile	Thr	Asp	Glu	Gln	Ala	Leu	Ala
			180					185					190		
Ile	Asn	Gln	Ser	Pro	Tyr	Val	Lys	Asn	Val	His	Pro	Asn	Arg	Arg	Val
		195					200					205			
Ser	Ile	Ala	Leu	Gln	Asp	Ala	Val	Pro	Leu	Ile	Gln	Asp	Gly	Ile	Leu
		210				215					220				
Ala	Gly	Arg	Val	Asp	Glu	Asp	Gly	Asn	Asp	Cys	Glu	Leu	Thr	Gln	Lys
225					230					235					240
Pro	Cys	Leu	Thr	Gly	Glu	Gly	Val	Thr	Ile	Ala	Ile	Ile	Asp	Thr	Gly
				245					250					255	
Val	Asp	Tyr	Thr	His	Pro	Asp	Leu	Gly	Gly	Cys	Thr	Thr	Gln	Glu	Phe
			260					265					270		
Leu	Gly	Gly	Ala	Cys	Glu	Lys	Val	Ile	Gly	Gly	Tyr	Asp	Phe	Ile	Asn
		275					280					285			
Asn	Asp	Asp	Asp	Ala	Met	Asp	Asp	Asn	Gly	His	Gly	Thr	His	Val	Ala
		290				295					300				
Gly	Ile	Ala	Ala	Gly	Asn	Gly	Leu	Leu	Lys	Gly	Val	Ala	Pro	Asp	Ala

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305      310      315      320
Lys Ile Leu Ala Tyr Lys Val Leu Gly Ala Gly Gly Tyr Gly Thr Trp
      325      330      335
Glu Gly Ile Ile Ala Gly Ile Glu Gln Ala Val Ile Asp Gly Ala Asp
      340      345      350
Ile Leu Ser Leu Ser Leu Gly Cys Val His Ser Ser Cys Asn Pro Asp
      355      360      365
Asp Ile Ala Ser Gln Ala Val Asp Asn Ala Val Leu Ala Gly Lys Val
      370      375      380
Val Val Val Ala Ala Gly Asn Ser Gly Pro Ser Ser Arg Thr Ile Gly
385      390      395      400
Ser Pro Gly Thr Ala Arg Lys Ala Ile Thr Val Gly Ser Thr Thr Lys
      405      410      415
Ser Asp Ile Ile Ser Trp Phe Ser Ser Arg Gly Pro Val Val Trp Met
      420      425      430
Asp Glu Ala Gly Ile Glu Gln Ala Ile Met Lys Pro Asp Val Leu Ala
      435      440      445
Pro Gly Gly Thr Asp Ser Gly Ser Glu Phe Cys Asn Pro Glu Met Met
      450      455      460
Phe Asp Asn Arg Ile Cys Ala Ala Trp Leu Asn Lys Glu Tyr Leu Ala
465      470      475      480
Ile Ser Gly Thr Ser Met Ala Thr Pro Leu Val Ser Gly Ala Ile Ala
      485      490      495
Leu Leu Lys Gln Lys His Pro Asp Trp Thr Pro Glu Glu Ile Lys Gly
      500      505      510
Ala Val Lys Gly Thr Ala Ile Asn Leu Gly Tyr Asp Pro Asn Glu Gln
      515      520      525
Gly Ala Gly Arg Ile Asn Val Arg Glu Met Ile Gly Leu Glu Glu Arg
      530      535      540
Ala Leu Ile Ala Ser Ile Leu Trp
545      550

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<210> 125

<211> 1215

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 125

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acagcaaaaa ttgttgctga tttagattgt gtagaatcta ttgagaaaga ttctgtatgt      180
acatctgatg aggaatttta caagtcattc cgtactactg ataattgggc attgacacga      240
ttcaatttta cagaacctca acgagagtat cctgagaggt accgttacaa tcgcacagga      300
aaaggtgtgg gcatctacgt tattgacagt ggtgtccgta ctactcatca agagtttagta      360
ggacgtgtag agactgtcta cagtgttctc gaaggtaagc aatttgacag tgataatgag      420
ctaaacatta accgtagcca tggcacagca gtggcgtcag cagcagcagg gaagaagcta      480
ggtattgcaa gtgaagctac tgtctacaac ttattcgtag atttttctat gtcagacatt      540
atcaaagcgt ttgatactgt attgcaccat taaaaaagt ctaagagtgc tgctgtactt      600
gtgacatcat tctcaacttt gtcactagca atgaaaccta tctcagacgc actctaccaa      660
gcaggtctcg ttcattgtatc tagtgcaggc aatcagtcta cagatactcc aagataccct      720
gctgcattcc ctcagactat ctctgtaggt gctactgaca agcaggacaa taaagcatca      780
ttcagtaact ttggcaatac cgtagacgta tatgcacccg gagtgaatgt gaaggtagcg      840
gatcatgcaa gagatgttcg tactcgtatt gcaagaggga cttctttctc tgcaccttat      900
gttgctggta tcattgcact catgctagaa gattcagaca agcctcgtaa gcgcgagcat      960
gtcgatacca taccgacaatc cttcctagac aatgctacaa gtatttccaa ggcagataag      1020
cgtgtgccac atacacgttt tgacattgaa ccgttcaagt ttctctgta      1080
gaaaaaattg taaaaaagggt gtctgacaat aaggatacgt caagtatttc agacaaaaaa      1140
cgtaaaaaga gttacacgaa acagattgta gcaggcgtta tcctagcagc tactatagtt      1200
gcaattcttg tgtaa

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<210> 126

<211> 404

<212> PRT

<213> Unknown

10336256.txt

<220>

<223> obtained from an environmental sample.

<400> 126

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Met Lys Tyr Ile Val Ile Leu Lys Lys Gly Tyr Asn Arg Asp Ser Leu
 1      5      10      15
Thr Asp Tyr Cys Thr Lys Val Gly Lys Pro Cys Glu Leu His Asn Leu
      20      25      30
Val Ile Ile Asn Thr Asp Glu Ala Thr Ala Lys Ile Val Ala Asp Leu
      35      40      45
Asp Cys Val Glu Ser Ile Glu Lys Asp Ser Val Cys Thr Ser Asp Glu
      50      55      60
Glu Phe Tyr Lys Ser Ser Arg Thr Thr Asp Asn Trp Ala Leu Thr Arg
65      70      75      80
Phe Asn Phe Thr Glu Pro Gln Arg Glu Tyr Pro Glu Ser Tyr Arg Tyr
      85      90      95
Asn Arg Thr Gly Lys Gly Val Gly Ile Tyr Val Ile Asp Ser Gly Val
      100      105      110
Arg Thr Thr His Gln Glu Leu Val Gly Arg Val Glu Thr Val Tyr Ser
      115      120      125
Val Leu Glu Gly Lys Gln Phe Asp Ser Asp Asn Glu Leu Asn Ile Asn
      130      135      140
Arg Ser His Gly Thr Ala Val Ala Ser Ala Ala Ala Gly Lys Lys Leu
145      150      155      160
Gly Ile Ala Ser Glu Ala Thr Val Tyr Asn Leu Phe Val Asp Phe Ser
      165      170      175
Met Ser Asp Ile Ile Lys Ala Phe Asp Thr Val Leu His His Tyr Lys
      180      185      190
Lys Ser Lys Ser Ala Ala Val Leu Val Thr Ser Phe Ser Thr Leu Ser
      195      200      205
Leu Ala Met Lys Pro Ile Ser Asp Ala Leu Tyr Gln Ala Gly Leu Val
210      215      220
His Val Ser Ser Ala Gly Asn Gln Ser Thr Asp Thr Pro Arg Tyr Pro
225      230      235      240
Ala Ala Phe Pro Gln Thr Ile Ser Val Gly Ala Thr Asp Lys Gln Asp
      245      250      255
Asn Lys Ala Ser Phe Ser Asn Phe Gly Asn Thr Val Asp Val Tyr Ala
      260      265      270
Pro Gly Val Asn Val Lys Val Ala Asp His Ala Arg Asp Val Arg Thr
      275      280      285
Arg Ile Ala Arg Gly Thr Ser Phe Ser Ala Pro Tyr Val Ala Gly Ile
290      295      300
Ile Ala Leu Met Leu Glu Asp Ser Asp Lys Pro Arg Lys Arg Glu His
305      310      315      320
Val Asp Thr Ile Arg Gln Ser Phe Leu Asp Asn Ala Thr Ser Ile Ser
      325      330      335
Lys Ala Asp Lys Arg Val Pro His Thr Arg Phe Asp Ile Glu Pro Phe
      340      345      350
Lys Phe Pro Lys Pro Ser Pro Val Glu Lys Ile Val Gln Lys Val Ser
      355      360      365
Asp Asn Lys Asp Thr Ser Ser Ile Ser Asp Lys Lys Arg Lys Lys Ser
370      375      380
Tyr Thr Lys Gln Ile Val Ala Gly Val Ile Leu Ala Ala Thr Ile Val
385      390      395      400
Ala Ile Leu Val

```

<210> 127

<211> 1236

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 127

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atgttcaacc gtcgttccat gcttgccgtc gccattggcg ccggcgtcct gagcaccttc
ggcgcgggg ccctgcaggc ctccgagctc cgcttcgcgg agaaccgat cgaaggccag

```

60
120

10336256.txt

tacatcgctcg	tcctgaagga	tgacgccgcc	acgctcgagg	gcgagacctc	gatcgcgtcc	180
aaccgtccca	acgtggccac	ggccgcacgc	aacctcgccc	gcgcgcaccg	cgccgaggtt	240
cgccacacct	acaaccgcgc	cctgcgcgga	ttcgtggccc	gtgccgacga	gcgtgcccctg	300
gcccgcctgc	tgaggaccc	cagcgtcgcc	tatgtcgaag	aggacggcat	cgtcaccacc	360
caggccacgc	agaccggcgc	gacctggggc	atcgaccgca	tcgaccagcg	caccctgccg	420
ctgaaccaga	cctacgtcta	cgacaccacc	gcgtcgaacg	tgaacgtcta	catcgtcgac	480
accggcatcc	gctcggcgca	caacgacttc	ggtggccgcg	tcgctcggg	ctacaccgcc	540
atcaacgacg	gccagggcac	caacgactgc	aacggccacg	gcacccacgt	cgctccacc	600
gccgcccgcg	ccacctatgg	cgtggccaag	gccgcccgcg	tgtatccggt	gcgcgtgctc	660
ggctgcaacg	gctcgggcac	caactccggc	gtgatcgccg	gcatggactg	ggtcgccagc	720
aaccacgtca	agccggccgt	ggccaacatg	agcctgggcg	gcggcgctc	gtccgccacc	780
gactcggccg	tcacccgcat	gcgcaatgcc	ggcgtgaccg	tggctcgtggc	cgcgggcaac	840
gacagcggca	ccacgtgcaa	ctactcgccg	gcgcgctcga	cctcggcgat	caccgtgggt	900
tccaccacca	gcaccgacgc	gcgctcgaac	ttctccaact	tcggcacctg	cgtgaacatc	960
ttcgcgccgg	gttcctcgat	caactgccgcg	tggcacacca	gcaacaccgc	gaccaacacc	1020
atcagcggca	cctcgatggc	ggcgccgcac	gtggccggcg	tggccgcgct	gttcctggcc	1080
accaacccca	acgccacccc	ggcccaggtc	gagcaggcga	tctacagcaa	ctccacgccc	1140
aaccgcgtca	ccaatccggg	cagcggctcg	cccaatcgcc	tgctgtactc	ccgattcggc	1200
ggcggcaccg	acccgggtcc	cgatccggat	ccaaag			1236

<210> 128
 <211> 412
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(27)

<400> 128

Met	Phe	Asn	Arg	Arg	Ser	Met	Leu	Ala	Val	Ala	Ile	Gly	Ala	Gly	Val
1				5					10					15	
Leu	Ser	Thr	Phe	Gly	Ala	Gly	Ala	Leu	Gln	Ala	Ser	Glu	Leu	Arg	Phe
			20					25					30		
Ala	Glu	Asn	Pro	Ile	Glu	Gly	Gln	Tyr	Ile	Val	Val	Leu	Lys	Asp	Asp
		35					40					45			
Ala	Ala	Thr	Leu	Glu	Gly	Glu	Thr	Ser	Ile	Ala	Ser	Asn	Arg	Pro	Asn
	50					55					60				
Val	Ala	Thr	Ala	Ala	Arg	Asn	Leu	Ala	Arg	Ala	His	Arg	Ala	Glu	Val
65					70				75					80	
Arg	His	Thr	Tyr	Asn	Arg	Ala	Leu	Arg	Gly	Phe	Val	Ala	Arg	Ala	Asp
			85						90					95	
Glu	Arg	Ala	Leu	Ala	Arg	Leu	Leu	Gln	Asp	Pro	Ser	Val	Ala	Tyr	Val
			100					105					110		
Glu	Glu	Asp	Gly	Ile	Val	Thr	Thr	Gln	Ala	Thr	Gln	Thr	Gly	Ala	Thr
		115					120					125			
Trp	Gly	Ile	Asp	Arg	Ile	Asp	Gln	Arg	Thr	Leu	Pro	Leu	Asn	Gln	Thr
130						135					140				
Tyr	Val	Tyr	Asp	Thr	Thr	Ala	Ser	Asn	Val	Asn	Val	Tyr	Ile	Val	Asp
145					150				155					160	
Thr	Gly	Ile	Arg	Ser	Ala	His	Asn	Asp	Phe	Gly	Gly	Arg	Val	Arg	Ser
			165						170					175	
Gly	Tyr	Thr	Ala	Ile	Asn	Asp	Gly	Gln	Gly	Thr	Asn	Asp	Cys	Asn	Gly
			180					185					190		
His	Gly	Thr	His	Val	Ala	Ser	Thr	Ala	Ala	Gly	Ala	Thr	Tyr	Gly	Val
		195					200					205			
Ala	Lys	Ala	Ala	Arg	Leu	Tyr	Pro	Val	Arg	Val	Leu	Gly	Cys	Asn	Gly
	210					215					220				
Ser	Gly	Thr	Asn	Ser	Gly	Val	Ile	Ala	Gly	Met	Asp	Trp	Val	Ala	Ser
225					230					235				240	
Asn	His	Val	Lys	Pro	Ala	Val	Ala	Asn	Met	Ser	Leu	Gly	Gly	Gly	Ala
			245						250					255	
Ser	Ser	Ala	Thr	Asp	Ser	Ala	Val	Thr	Arg	Met	Arg	Asn	Ala	Gly	Val
			260					265					270		
Thr	Val	Val	Val	Ala	Ala	Gly	Asn	Asp	Ser	Gly	Asn	Ala	Cys	Asn	Tyr
		275					280						285		

10336256.txt

```

Ser Pro Ala Arg Ser Thr Ser Ala Ile Thr Val Gly Ser Thr Thr Ser
290 295 300
Thr Asp Ala Arg Ser Asn Phe Ser Asn Phe Gly Thr Cys Val Asn Ile
305 310 315
Phe Ala Pro Gly Ser Ile Thr Ala Ala Trp His Thr Ser Asn Thr
325 330 335
Ala Thr Asn Thr Ile Ser Gly Thr Ser Met Ala Ala Pro His Val Ala
340 345 350
Gly Val Ala Ala Leu Phe Leu Ala Thr Asn Pro Asn Ala Thr Pro Ala
355 360 365
Gln Val Glu Gln Ala Ile Tyr Ser Asn Ser Thr Pro Asn Arg Val Thr
370 375 380
Asn Pro Gly Ser Gly Ser Pro Asn Arg Leu Leu Tyr Ser Arg Phe Gly
385 390 395 400
Gly Gly Thr Asp Pro Gly Pro Asp Pro Asp Pro Lys
405 410

```

<210> 129
 <211> 1248
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 129

atggatctgg	ccgcgcctgc	gacgcccgcg	gtgacggtgt	gggaatactc	gatggacgag	60
cgctaccgca	atccccgctc	gccgctgttc	aaggtgctgc	ccaacggcgg	cagggctctg	120
cgccgcgacg	gcgatgcggt	gttcctgctc	ggcagcggcg	cgaccgcgca	gggcgaccgc	180
cccttcctcg	atcgccacga	cctgaagacc	ggccagacca	ggcgccctgt	ccgcagcgcg	240
ccggaatgcct	tcgagcgcgt	cgccagcgct	tccgacgacg	gccagcgcct	gtacacgctg	300
cgcgaaaccc	cgaaggaccc	gccgaacctg	ttcgtgcgca	cgctgggcgc	gccggctcgcc	360
gatgccgccc	aaggcgaagc	cgtcgtcgct	tcctcgccgc	ggcaggctcac	gagctacgtc	420
gacccgaccc	cggaagtgcg	cggcattccag	cgccggctgg	tgacctacaa	gcgcaaggac	480
ggcgtggacc	tgctcgttcac	gctctacctg	ccgctgggct	accaggccgg	gacgcgcgtg	540
cccgcctgct	tctacgccta	tcccgcgcag	tatgccgatc	cgggcaaggc	cgggcaggtc	600
accgggtcgc	agcagagctt	cacccgcttc	ccggagtacc	gcctgtgctg	gctcgccggc	660
tacgcgatca	tcgacaacac	ctcgttcccc	atcgtcggcg	acccgcgcac	cgccctacgac	720
acctacctgc	agcagctcgt	cgacaacgcg	caggcgggcg	tcgacaaggc	cgctcgagctg	780
ggcgtggtcg	atcgcgaccg	catcggcgtg	accgggcaca	gccatggcgc	gctgatgacc	840
gccaacctgc	tcgcgcactc	ggacctgttc	cgccgcgggt	tcgccagcag	cggcggctac	900
aacaagacgc	tcacgccctt	cggtttccag	aacgagcgcc	gctcgctgtg	gaacgccaag	960
cgcgtgtacg	aagaggcgct	gacctactac	tacgccgaca	aggtggacga	gccgctgctg	1020
atcgtgcacg	gcgaggacga	tgccaacccc	ggcaccgaac	cggtgcagtc	gccgaagctc	1080
ttccaggcca	tccgcggcaa	cggcggcacc	gcgcgcctgg	tgatgctgcc	cttcgagccg	1140
cactggtaca	ccgcgaagga	aaccaatgag	cacttcgccg	cggaatgctg	gatgtgggtc	1200
gaccgctggg	tgaagaacgc	cggcccgcgc	gaggcgaaga	aggagtga		1248

<210> 130
 <211> 415
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 130

Met Asp Leu Ala Ala Pro Ala Thr Pro Pro Val Thr Val Trp Glu Tyr	1	5	10	15
Ser Met Asp Glu Arg Tyr Arg Asn Pro Gly Ser Pro Leu Phe Lys Val	20	25	30	
Leu Pro Asn Gly Gly Arg Val Val Arg Arg Asp Gly Asp Ala Val Phe	35	40	45	
Leu Arg Gly Ser Gly Ala Thr Ala Gln Gly Asp Arg Pro Phe Leu Asp	50	55	60	
Arg His Asp Leu Lys Thr Gly Gln Thr Arg Arg Leu Phe Arg Ser Ala	65	70	75	80
Pro Asp Ala Phe Glu Arg Val Ala Ser Val Ser Asp Asp Gly Gln Arg				

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Leu	Tyr	Thr	Leu	85	Arg	Glu	Thr	Pro	Lys	90	Asp	Pro	Pro	Asn	Leu	95	Phe	Val
Arg	Thr	Leu	100	Gly	Ala	Pro	Val	Ala	105	Asp	Ala	Ala	Glu	Gly	110	Glu	Ala	Val
Val	Ala	Ser	115	Ser	Pro	Arg	Gln	Val	120	Thr	Ser	Tyr	Val	125	Asp	Pro	Thr	Pro
Glu	Val	Arg	130	Gly	Ile	Gln	Arg	Arg	135	Leu	Val	Thr	Tyr	140	Lys	Arg	Lys	Asp
Gly	Val	Asp	145	Leu	Ser	Phe	Thr	Leu	150	Tyr	Leu	Pro	Leu	155	Gly	Tyr	Gln	Ala
Gly	Thr	Arg	160	Val	Pro	Ala	Val	Leu	165	Tyr	Ala	Tyr	Pro	170	Ala	Asp	Tyr	Ala
Asp	Pro	Gly	175	Lys	Ala	Gly	Gln	Val	180	Thr	Gly	Ser	Gln	185	Gln	Ser	Phe	Thr
Arg	Phe	Pro	190	Glu	Tyr	Arg	Leu	Leu	195	Leu	Leu	Ala	Gly	200	Tyr	Ala	Ile	Ile
Asp	Asn	Thr	205	Ser	Phe	Pro	Ile	Val	210	Gly	Asp	Pro	Arg	215	Thr	Ala	Tyr	Asp
Thr	Tyr	Leu	220	Gln	Gln	Leu	Val	Asp	225	Asn	Ala	Gln	Ala	230	Ala	Val	Asp	Lys
Ala	Val	Glu	235	Leu	Gly	Val	Val	Asp	240	Arg	Asp	Arg	Ile	245	Gly	Val	Thr	Gly
His	Ser	His	250	Gly	Ala	Leu	Met	Thr	255	Ala	Asn	Leu	Leu	260	Ala	His	Ser	Asp
Leu	Phe	Arg	265	Ala	Gly	Val	Ala	Ser	270	Ser	Gly	Gly	Tyr	275	Asn	Lys	Thr	Leu
Thr	Pro	Phe	280	Gly	Phe	Gln	Asn	Glu	285	Arg	Arg	Ser	Leu	290	Trp	Asn	Ala	Lys
Arg	Val	Tyr	295	Glu	Ala	Ser	Thr	Tyr	300	Tyr	Tyr	Ala	Asp	305	Lys	Val	Asp	310
Glu	Pro	Leu	315	Leu	Ile	Val	His	Gly	320	Glu	Asp	Asp	Ala	325	Asn	Pro	Gly	330
Glu	Pro	Val	335	Gln	Ser	Pro	Lys	Leu	340	Phe	Gln	Ala	Ile	345	Arg	Gly	Asn	Gly
Gly	Thr	Ala	350	Arg	Leu	Val	Met	Leu	355	Pro	Phe	Glu	Pro	360	His	Trp	Tyr	Thr
Ala	Lys	Glu	365	Thr	Asn	Glu	His	Phe	370	Ala	Ala	Glu	Met	375	Leu	Met	Trp	Phe
Asp	Arg	Trp	380	Val	Lys	Asn	Ala	Gly	385	Pro	Arg	Glu	Ala	390	Lys	Lys	Glu	400
			405						410									415

<210> 131
 <211> 903
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 131																		
atgattatga	ataagtggcc	ccttctgcta	ttgcttagtt	ttctctcttc	tttgcaaac													60
gcacaggaaa	aagagagaca	atcttacatt	ataccatattg	ttggttggaa	tcaggaaaaa													120
ctcaactgga	atattgctgg	taatgaaaat	ggacaataacc	ccaatgtatt	atctgaatta													180
aaatggcagc	agttgctgg	cccggaaatg	ggaattatct	ccgctgtatc	aatttcacatca													240
aggtttcagg	tgaggtggaa	tttcagctac	caggcaatta	cctccggaac	agtaaattgat													300
acagattacg	caggcgataa	cagagcgctt	aaaactgctg	aattcaattt	acaagcagat													360
aaaggctata	caattaaaac	ccgtctggaa	ttatcttattc	ttctctggac	taaccaaaaca													420
ttctctttta	gaccacatgc	aggatatttc	ggaagttacc	agaagcttta	tatgctggat													480
ggtgatactc	cgcttatttc	cggaaaagaa	ttaaaaagca	cctataaacc	cgaatggcac													540
ggtgcagttc	ttggcttaga	aacaaacttc	aaaaaggaaa	actggaatgt	taatctcgac													600
atcagcggca	tgattttccc	ccaatattct	gccactgcaa	actggaatct	tcgggaagaa													660
ctcagaaggc	ctgtcagctt	cgaacacaga	tccaaaggaa	aaggcttcga	tactggactt													720
cgtattgggt	accagctcgg	tcaacgcatt	cagcctttta	tatctgcaag	atatacacag													780
atagaagcag	gaaaaggaac	ggataaatta	tatatggcaa	acggagatat	ttacaaaagc													840
aggctgaacg	aagttaattc	tacaagcatt	agttttggca	tcggtgttaa	agtactattc													900
tag																		903

10336256.txt

<210> 132
 <211> 300
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(21)

<400> 132
 Met Ile Met Asn Lys Trp Pro Leu Leu Leu Leu Ser Phe Leu Ser
 1 5 10 15
 Ser Leu Ala Asn Ala Gln Glu Lys Glu Arg Gln Ser Tyr Ile Ile Pro
 20 25 30
 Tyr Val Gly Trp Asn Gln Glu Lys Leu Asn Trp Asn Ile Ala Gly Asn
 35 40 45
 Glu Asn Gly Gln Tyr Pro Asn Val Leu Ser Glu Leu Lys Trp Gln Gln
 50 55 60
 Leu Arg Gly Pro Glu Met Gly Ile Ile Ser Ala Val Ser Ile Ser Ser
 65 70 75 80
 Arg Phe Gln Val Arg Trp Asn Phe Ser Tyr Gln Ala Ile Thr Ser Gly
 85 90 95
 Thr Val Asn Asp Thr Asp Tyr Ala Gly Asp Asn Arg Ala Leu Lys Thr
 100 105 110
 Ala Glu Phe Asn Leu Gln Ala Asp Lys Gly Tyr Thr Ile Lys Thr Arg
 115 120 125
 Leu Glu Leu Ser Tyr Leu Leu Trp Thr Asn Gln Thr Phe Ser Phe Arg
 130 135 140
 Pro His Ala Gly Tyr Phe Gly Ser Tyr Gln Lys Leu Tyr Met Leu Asp
 145 150 155 160
 Gly Asp Thr Pro Leu Ile Pro Gly Lys Glu Leu Lys Ser Thr Tyr Lys
 165 170 175
 Pro Glu Trp His Gly Ala Val Leu Gly Leu Glu Thr Asn Phe Lys Lys
 180 185 190
 Glu Asn Trp Asn Val Asn Leu Asp Ile Ser Gly Met Tyr Phe Pro Gln
 195 200 205
 Tyr Ser Ala Thr Ala Asn Trp Asn Leu Arg Glu Glu Leu Arg Arg Pro
 210 215 220
 Val Ser Phe Glu His Arg Ser Lys Gly Lys Gly Phe Asp Thr Gly Leu
 225 230 235 240
 Arg Ile Gly Tyr Gln Leu Gly Gln Arg Ile Gln Pro Phe Ile Ser Ala
 245 250 255
 Arg Tyr Thr Gln Ile Glu Ala Gly Lys Gly Thr Asp Lys Leu Tyr Met
 260 265 270
 Ala Asn Gly Asp Ile Tyr Lys Ser Arg Leu Asn Glu Val Asn Ser Thr
 275 280 285
 Ser Ile Ser Phe Gly Ile Gly Val Lys Val Leu Phe
 290 295 300

<210> 133
 <211> 939
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 133
 atgaaccccg tgtatcgcag cctcttcgcc ccggccctgc tggccggcgt gatgctggcc 60
 catgtgcctg cagccctggc acagacggca ggccccgcc cgctccgcat cgccgacctg 120
 cgcccgccca gcctgcagat cgaaggacgc gacccgcca gtctgatcgc gtcgcacgtg 180
 ccgctgctgg agatcagcac cgaggacgcc tccttcatca aggtgcattt cgaccacttc 240
 tccctgcccc ccggcctggc cctgggtggc gagaaccccc acggcagcga ggcctaccgc 300
 tacagcagcc accagcgcga cgccacacc ttcgaccgca gcctcggcca caacggccgg 360
 accagtttct cggccatgtc gatcagcggc ccgctgctgc tgctgcgcct ggagggcacg 420
 gccaccgagc gctggcggcc ccaccacggc atccgcgtga gcggatacca cgagggctac 480

10336256.txt

ccggacgaga	tgatcgagac	cctgcagtcg	gagggcctgc	tcgacgaggt	cggcaccag	540
gccatctgcg	gcagcaacga	caagcgcggc	gtggcctgct	acgccagctc	cgagcctgcc	600
gcggtcgacc	gctcgcgcc	ggtggccgcg	ctgggtgatga	gcggctcgct	ctgcaccgcg	660
tggcgctgg	gcccgaacaa	ccgcatgttc	accaacaacc	actgcatgtc	cacggcggcg	720
cgctggccg	cctcggaagt	gtggttcaac	caccaggcgc	cctcctgcgg	tggcaccagc	780
gcaggcaccg	tgggtcaaggt	ggccgggtgac	cagatgctgg	ccaccaacag	ctcgtctggac	840
tacaccctgt	tcacgggtgcg	cgacttcgcc	tcgatcgcca	gcttcggcta	cctgggcctg	900
gacatcgcca	gcactggcgt	gggcgaccag	atccaaaga			939

<210> 134

<211> 313

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(27)

<400> 134

Met	Asn	Pro	Val	Tyr	Arg	Ser	Leu	Phe	Ala	Pro	Ala	Leu	Leu	Ala	Gly
1				5					10					15	
Val	Met	Leu	Ala	His	Val	Pro	Ala	Ala	Leu	Ala	Gln	Thr	Ala	Gly	Pro
			20					25					30		
Ala	Pro	Leu	Arg	Ile	Ala	Asp	Leu	Arg	Pro	Ala	Ser	Leu	Gln	Ile	Glu
		35					40					45			
Gly	Arg	Asp	Pro	Pro	Met	Ser	Ile	Ala	Ser	His	Val	Pro	Leu	Leu	Glu
	50					55					60				
Ile	Ser	Thr	Glu	Asp	Ala	Ser	Phe	Ile	Lys	Val	His	Phe	Asp	His	Phe
65					70				75						80
Ser	Leu	Pro	Ala	Gly	Leu	Ala	Leu	Val	Val	Glu	Asn	Pro	Asp	Gly	Ser
			85						90					95	
Glu	Ala	Tyr	Arg	Tyr	Ser	Ser	His	Gln	Arg	Asp	Gly	His	Thr	Phe	Asp
			100					105					110		
Arg	Ser	Leu	Gly	His	Asn	Gly	Arg	Thr	Ser	Phe	Ser	Ala	Met	Ser	Ile
		115					120					125			
Ser	Gly	Pro	Arg	Ala	Val	Leu	Arg	Leu	Glu	Gly	Thr	Ala	Thr	Glu	Arg
	130					135					140				
Trp	Arg	Pro	His	His	Gly	Ile	Arg	Val	Ser	Gly	Tyr	His	Glu	Gly	Tyr
145					150					155					160
Pro	Asp	Glu	Met	Ile	Glu	Thr	Leu	Gln	Ser	Glu	Gly	Leu	Leu	Asp	Glu
			165						170					175	
Val	Gly	Thr	Gln	Ala	Ile	Cys	Gly	Ser	Asn	Asp	Lys	Arg	Gly	Val	Ala
		180						185					190		
Cys	Tyr	Ala	Ser	Ser	Glu	Pro	Ala	Ala	Val	Asp	Arg	Ser	Arg	Pro	Val
		195					200					205			
Ala	Arg	Leu	Val	Met	Ser	Gly	Ser	Leu	Cys	Thr	Ala	Trp	Arg	Val	Gly
	210					215					220				
Pro	Thr	Asn	Arg	Met	Phe	Thr	Asn	Asn	His	Cys	Met	Ser	Thr	Ala	Ala
225					230					235					240
Arg	Val	Ala	Ala	Ser	Glu	Val	Trp	Phe	Asn	His	Gln	Ala	Pro	Ser	Cys
			245						250					255	
Gly	Gly	Thr	Ser	Ala	Gly	Thr	Val	Val	Lys	Val	Ala	Gly	Asp	Gln	Met
		260						265					270		
Leu	Ala	Thr	Asn	Ser	Ser	Leu	Asp	Tyr	Thr	Leu	Phe	Thr	Val	Arg	Asp
		275					280					285			
Phe	Ala	Ser	Ile	Ala	Ser	Phe	Gly	Tyr	Leu	Gly	Leu	Asp	Ile	Ala	Ser
	290					295					300				
Thr	Gly	Val	Gly	Asp	Gln	Ile	Gln	Arg							
305					310										

<210> 135

<211> 3105

<212> DNA

<213> Unknown

<220>

10336256.txt

<223> Obtained from an environmental sample.

<400> 135

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acagttccta	tattagaaca	atattataga	gaaatgaaca	aatatccaaa	ggataaatta	180
aaagcggatg	ctgtatataa	tcttatgaaa	gagataaatt	atgatata	acaatatata	240
tatgatcata	atattagaga	tggtaaaaat	acaccttggt	ccagcaaaat	agatcctttc	300
ataaatacaa	tttcaaaatt	tgcagggtata	tctaaagtta	cagaagataa	tggtctggatt	360
ataaataatg	gtattttatta	tactagttaa	ttcgctatat	atcatagcag	tccatctatt	420
cctcattcag	taatagacaa	atgtcttgaa	atccttcctg	cttatagtga	gcaatattat	480
attgcagtag	aaagaataaa	ggaagatttt	aattgtaaag	attcaaagg	aaatgttata	540
gacattgata	aattacttga	agatggttaa	aaacattatt	tacctaanaac	ttatactttt	600
gataacggaa	aaatgattat	aaaagctgga	gataaagtag	aagaatcaaa	aattcaaagg	660
ctttattggg	catctaaaga	agtaaaatcc	caatttcata	ggataatagg	taatgataaa	720
cctttagaag	caggtaatgc	tgatgatgtc	ctaactatgg	taatatataa	tagtccagaa	780
gaatataaac	taaatagaac	tttatatgga	tatagtgtag	acaatgggtg	aatatatatt	840
gaaggaattg	gtacttttct	tacttatgaa	agaactccag	aggaaagcat	atatagtcta	900
gaagaacttt	tccgtcatga	gtttactcat	tacttaacag	gacgttattt	agtaccagga	960
ttattttaatg	aagggtgattt	ttataaagga	aatagcggaa	gaatcacatg	gtttgaagaa	1020
ggttctgccc	aatttttttgc	aggctcaact	agaacttctg	tattaccaag	aaaatcaatg	1080
gttgggtggac	tttctgaaac	ccctaagaaa	agattttagt	cagataagat	attacattca	1140
aaatatgatg	atggatggga	attctacaaa	tatggatatg	ctttctcaga	ttatatgtat	1200
aataacaaca	aaaaactatt	tagcgattta	gtatctacta	tgaaaaataa	tgatgttaaa	1260
ggttatgaaa	acctaataga	aaatgcaagt	aaggatccta	atgttaacaa	aagctatcaa	1320
gatcacatgc	aaaaattagt	ggataattac	aataattaca	caataccact	agtatctgac	1380
gattacatga	aaaaatatag	taacaaaagc	ttaaatgaaa	taaaatcaga	tattgaaagt	1440
actatgaatt	taacaaattc	gcaaataact	aaagaaagt	ctcaatactt	tgatacttat	1500
actctaaaag	caaattacac	attagattcc	aacaaagggtg	aaattgataa	ttggaattgt	1560
atgaataata	aagttaatga	atctctagag	aaactaaaca	aattaggatg	gggcggatat	1620
aaaacagtta	ctgcttattt	ctcaaatcct	aaagtaaact	cacacaatca	ggtagaatat	1680
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aaattagatt	ttcctaagga	ggcaaataca	aacgaaaaaa	ttaaattttc	tagcgaaggc	1800
tcaactgatg	atggaaaaat	agtttcctat	gcttgggatc	ttggagatgg	tgaaactagc	1860
tcagaaaaaa	atcctactca	tgtttataaa	gctcctggta	cttacacagt	gaaacttaca	1920
gtaacagacg	acaaaggcat	taaatcagaa	aaaagtgc	ctataaacat	aaagaaagta	1980
cttacaggaa	atgcagtatc	agaaaaagaa	aataacaatg	attacgtaaa	tgctaaccga	2040
gtttattcta	aagatttagt	aagtggatct	gttagttcat	ccgacgatag	agatattttt	2100
tatttcaatg	ttactaagcc	ttcagatata	actataaatg	cggaaaaaat	taataaagat	2160
aaaagtgaat	ttacttggct	tttattttagc	gaagaagata	aatcaaaacta	tatagcctat	2220
ccaaataaaa	aactagaaaa	cttatttttat	agcactgtaa	aaatagataa	acctggtaaa	2280
tactatttag	taattttataa	agttagtggg	gaaaaatcag	attatagatt	taatatagaa	2340
ggagatatat	cagcatctcc	aaaagatgat	actgataaag	atgaattagt	tatatctgaa	2400
aaggaagata	ataattcttt	tgacaaagct	aatagagttt	gtaaaaatca	atcagtaata	2460
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gatataaaaa	aagctaaaga	tttagacata	aaactaaata	attttaaata	tttaggatta	2940
gcttggaaatc	tttataaaga	atcagatttg	aataattata	ttgcttatgg	atcagtttca	3000
ggcaataacta	taaaagggaa	atgcaatgta	actcctggta	aatattactt	gtatgtatat	3060
aaatactctg	gtgacaatgg	caattattca	ttaacaataa	aataa		3105

<210> 136

<211> 1034

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 136

Met	Leu	Ala	Ile	Glu	Asn	Asn	Lys	Asn	Phe	Lys	Leu	Gly	Glu	Lys	Gly
1				5				10						15	
Gln	Asp	Thr	Val	Ile	Ser	Ala	Leu	Gly	Lys	Leu	Ile	Gly	Asn	Ala	Ser

10336256.txt

Cys Asn Ala Glu Val Val Asn Lys Thr Val Pro Ile Leu Glu Gln Tyr
 Tyr Arg 35 Glu Met Asn Lys Tyr 40 Pro Lys Asp Lys Leu 45 Lys Ala Asp Ala
 Val Tyr Asn Leu Met Lys 55 Glu Ile Asn Tyr Asp Ile Leu Gln Tyr Thr
 65 Tyr Asp His Asn Ile Arg Asp Gly Lys Asn Thr Pro Trp Ser Ser Lys
 Ile Asp Pro Phe 85 Ile Asn Thr Ile Ser Lys Phe Ala Gly Ile Ser Lys
 Val Thr Glu Asp Asn Gly Trp Ile 105 Ile Asn Asn Gly Ile Tyr Tyr Thr
 Ser Lys 115 Phe Ala Ile Tyr His 120 Ser Ser Pro Ser Ile 125 Pro His Ser Val
 Ile 130 Asp Lys Cys Leu Glu 135 Ile Leu Pro Ala Tyr Ser Glu Gln Tyr Tyr
 145 Ile Ala Val Glu Arg 150 Ile Lys Glu Asp Phe 155 Asn Cys Lys Asp Ser Lys
 Gly Asn Val Ile Asp Ile Asp Lys Leu 170 Leu Glu Asp Gly Lys Lys His
 Tyr Leu Pro 180 Lys Thr Tyr Thr Phe 185 Asp Asn Gly Lys Met Ile Ile Lys
 Ala Gly Asp Lys Val Glu Glu Ser Lys Ile Gln Arg Leu Tyr Trp Ala
 Ser 210 Lys Glu Val Lys Ser 215 Gln Phe His Arg Ile Ile Gly Asn Asp Lys
 225 Pro Leu Glu Ala Gly Asn Ala Asp Asp Val Leu Thr Met Val Ile Tyr
 Asn Ser Pro Glu Tyr Lys Leu Asn Arg Thr Leu Tyr Gly Tyr Ser
 Val Asp Asn 260 Gly Gly Ile Tyr Ile Glu Gly Ile Gly Thr Phe Phe Thr
 Tyr Glu Arg Thr Pro Glu Glu Ser Ile Tyr Ser Leu Glu Glu Leu Phe
 Arg 290 His Glu Phe Thr His 310 Tyr Leu Gln Gly Arg Tyr Leu Val Pro Gly
 305 Leu Phe Asn Glu Gly Asp Phe Tyr Lys Gly Asn Ser Gly Arg Ile Thr
 Trp Phe Glu Glu Gly Ser Ala Glu Phe 345 Phe Ala Gly Ser Thr Arg Thr
 Ser Val Leu Pro Arg Lys Ser Met Val Gly Gly Leu Ser Glu Asn Pro
 Lys Glu Arg Phe Ser Ala Asp 375 Lys Ile Leu His Ser Lys Tyr Asp Asp
 Gly Trp Glu Phe Tyr Lys Tyr Gly Tyr Ala Phe Ser Asp Tyr Met Tyr
 385 Asn Asn Asn Lys Lys 390 Leu Phe Ser Asp Leu Val Ser Thr Met Lys Asn
 Asn Asp Val Lys Gly Tyr Glu Asn Leu Ile Glu Asn Ala Ser Lys Asp
 Pro Asn Val 420 Asn Lys Ser Tyr Gln Asp His Met Gln Lys Leu Val Asp
 Asn Tyr Asn Asn Tyr Thr Ile 455 Pro Leu Val Ser Asp Asp Tyr Met Lys
 Lys Tyr Ser Asn Lys Ser Leu Asn Glu Ile Lys Ser Asp Ile Glu Ser
 465 Thr Met Asn Leu Thr 485 Asn Ser Gln Ile Thr Lys Glu Ser Ser Gln Tyr
 Phe Asp Thr Tyr Thr Leu Lys Ala Asn Tyr Thr Leu Asp Ser Asn Lys
 Gly Glu Ile Asp Asn Trp Asn Cys 520 Met Asn Asn Lys Val Asn Glu Ser
 Leu Glu Lys Leu Asn Lys Leu Gly Trp Gly Gly Tyr Lys Thr Val Thr
 530 Ala Tyr Phe Ser Asn Pro Lys Val Asn Ser His Asn Gln Val Glu Tyr
 545 Asn Ile Val Phe His Gly Leu Leu Thr His Asn Lys Asn Phe Asn Glu

10336256.txt

565
 Ala Pro Thr Ile Lys Leu Asp Phe Pro Lys Glu Ala Asn Thr Asn Glu
 570
 Lys Ile Lys Phe Ser Ser Glu Gly Ser Thr Asp Asp Gly Lys Ile Val
 585
 Ser Tyr Ala Trp Asp Leu Gly Asp Gly Glu Thr Ser Ser Glu Lys Asn
 595
 Pro Thr His Val Tyr Lys Ala Pro Gly Thr Tyr Thr Val Lys Leu Thr
 600
 610
 615
 620
 625
 Val Thr Asp Asp Lys Gly Ile Lys Ser Glu Lys Ser Ala Ser Ile Asn
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 1030

<210> 137
 <211> 705
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

10336256.txt

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<400> 137
ttgaaagctg taccacaggc agatatccct gctgggtttg aaaacacaca catgtgtaaa      60
gatgtttatc ttccgggaac tgatccaaga ggagctgtta ttaaaagcac aaaatggcca      120
aatggcagcg tcattactgt aagtctgaac ggtggaacag ccaaagttcg cagcaaagta      180
atgcaatatg ctaatgaatg gtctaagtat gctaacatta cttttaaat tttaccagc      240
ggaacagcac aaatccgggt tacctttaca caaggagcag gatcttattc ttatttagga      300
acacaagctc ttaatcgccc ttctaactct gaaacaatga acttcggttg gtttaatgat      360
tcaacaacag atacagagtt cagcagaaca acgattcatg aatttggaca tgctctaggt      420
atgatacagc agcaccagca tccttttagct aatatccctt gggataaaga aaaagtgtat      480
acctattatg gaggttatcc taactattgg tcaagagcac aggtagacag taacctgttt      540
gcaaaatatt ctactacaca aacgcaatat agtgcttatg atacacaatc tatcatgcat      600
tatagcatta gtagcagctt gacaacaaac ggattcagtg ttggcagcaa tactgttctt      660
tctactactg ataagcagtt tattgcatca gtatatccaa aataa      705

```

```

<210> 138
<211> 234
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample.

```

```

<400> 138
Met Lys Ala Val Pro Gln Ala Asp Ile Pro Ala Gly Phe Glu Asn Thr
1      5      10      15
His Met Cys Lys Asp Val Tyr Leu Pro Gly Thr Asp Pro Arg Gly Ala
20      25      30
Val Ile Lys Ser Thr Lys Trp Pro Asn Gly Ser Val Ile Thr Val Ser
35      40      45
Leu Asn Gly Gly Thr Ala Lys Val Arg Ser Lys Val Met Gln Tyr Ala
50      55      60
Asn Glu Trp Ser Lys Tyr Ala Asn Ile Thr Phe Lys Phe Ile Thr Ser
65      70      75      80
Gly Thr Ala Gln Ile Arg Val Thr Phe Thr Gln Gly Ala Gly Ser Tyr
85      90      95
Ser Tyr Leu Gly Thr Gln Ala Leu Asn Arg Pro Ser Asn Ser Glu Thr
100      105      110
Met Asn Phe Gly Trp Phe Asn Asp Ser Thr Thr Asp Thr Glu Phe Ser
115      120      125
Arg Thr Thr Ile His Glu Phe Gly His Ala Leu Gly Met Ile His Glu
130      135      140
His Gln His Pro Leu Ala Asn Ile Pro Trp Asp Lys Glu Lys Val Tyr
145      150      155      160
Thr Tyr Tyr Gly Gly Tyr Pro Asn Tyr Trp Ser Arg Ala Gln Val Asp
165      170      175
Ser Asn Leu Phe Ala Lys Tyr Ser Thr Thr Gln Thr Gln Tyr Ser Ala
180      185      190
Tyr Asp Thr Gln Ser Ile Met His Tyr Ser Ile Ser Ser Ser Leu Thr
195      200      205
Thr Asn Gly Phe Ser Val Gly Ser Asn Thr Val Leu Ser Thr Thr Asp
210      215      220
Lys Gln Phe Ile Ala Ser Val Tyr Pro Lys
225      230

```

```

<210> 139
<211> 1428
<212> DNA
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample.

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<400> 139
atggaaatgt caggaatgaa gcccgtcgac gcaaacaaga cccacaagcg catccggatc      60
gcagccggca ccgtggcgct cgccctgatg gcaacgggtt ccgtcgcgct ggctgccggc      120
ccgcaggccc gggcgggaa cgggacgtgg aaagtcagcc aggccttcgg caagcagcgc      180
accggccgca tcgtcggcgg catcggcgcg gtgggcgacc gttcggtcac ggtgcgcacc      240
tcgggctgcg gcggcacgat catcgccgac agctgggtgc tgaccgccgc gcattgcggc      300

```

10336256.txt

```

agccagagca ccgtctgggc aggctcgaac aacaccggca gccagacggc ctattccgtc 360
gcgcagtaca tccagcaccc caactacagc ccgaactcct ccgcaggcag ttacagcaac 420
gacttcgccc tgctccgcat caacggcacg ttcccggccc acctgatccg cgcgaaactg 480
cccagcgcgg cgatcatgca ggccatcgcc aagccaggcg atccggtgac cacgctgggc 540
tggggccgga cctcggaagg cggcagcagc accaccagcc tgcgcgaagt gaccgtcccg 600
gtcgtgtccg atgcaacctg cgccgcgtcc tacaacggca gttccgctgc cggcggcctc 660
aagctcaatc cggccgtgtc gatctgcgcc ggcttcgcag cgggcggcca ggatgcctgc 720
caggggcgaca gcgggcgccc gctgatcgcg ccctacaacg gctcgatcta cagcatcggc 780
gtcgtgagct acggactggg ctgcgcgcgg ccgaactatt acggcgtgta ttcggaaacg 840
gtcgccgtgc tggactggat caacggccac atcggcaacg gcggtggcag cggcaccgtc 900
atcaccgacg tcgttcttgt cgcgtcgaac ggctcgaccg cgccggcccg ccccgcgggc 960
tactcgctgg tcggttactg ggacgtcgac aagggcgggc cccagggcac gtacggcacc 1020
accggaagct tcatgaccgc gctgtacgtg cggcggcagc ttccttcgga aaccagcacc 1080
tgcgtcggcg ggatcggcct gtacacctcg gccggaagca ccgttcccgg cagcatcgcg 1140
cccaactgga cctatcgcgg catgtgggac atggacaagg gcggcggggg cggcaacctc 1200
aacagccagt ggcaggaata catgatgggc ctgtacacca ggccggcctc gactggccag 1260
ggcgccctgcc tcaccgatgt cgccctctac gcctcgaacg gctcgacgcc tgtcacgccc 1320
tcgggcttca gccatggcgt ctggtgggac gtggacgcgg cgggcgcgtt cggcaccag 1380
ggttcacgcg gttcctacgt ggccacgctg tccacgaaga gcgagtga 1428

```

<210> 140
 <211> 475
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(38)

<400> 140
 Met Glu Met Ser Gly Met Lys Pro Val Asp Ala Asn Lys Thr His Lys
 1 5 10 15
 Arg Ile Arg Ile Ala Ala Gly Thr Val Ala Leu Ala Leu Met Ala Thr
 20 25 30
 Gly Ser Val Ala Leu Ala Ala Gly Pro Gln Ala Arg Ala Gly Asn Gly
 35 40 45
 Thr Trp Lys Val Ser Gln Ala Phe Gly Lys Gln Arg Thr Gly Arg Ile
 50 55 60
 Val Gly Gly Ile Gly Ala Val Gly Asp Arg Ser Phe Thr Val Arg Thr
 65 70 75 80
 Ser Gly Cys Gly Gly Thr Ile Ile Ala Asp Ser Trp Val Leu Thr Ala
 85 90 95
 Ala His Cys Gly Ser Gln Ser Thr Val Trp Ala Gly Ser Asn Asn Thr
 100 105 110
 Gly Ser Gln Thr Ala Tyr Ser Val Ala Gln Tyr Ile Gln His Pro Asn
 115 120 125
 Tyr Ser Pro Asn Ser Ser Ala Gly Ser Tyr Ser Asn Asp Phe Ala Leu
 130 135 140
 Leu Arg Ile Asn Gly Thr Phe Pro Ala His Leu Ile Arg Ala Lys Leu
 145 150 155 160
 Pro Asp Ala Ala Ile Met Gln Ala Ile Ala Lys Pro Gly Asp Pro Val
 165 170 175
 Thr Thr Leu Gly Trp Gly Arg Thr Ser Glu Gly Gly Ser Ser Thr Thr
 180 185 190
 Ser Leu Arg Glu Val Thr Val Pro Val Val Ser Asp Ala Thr Cys Ala
 195 200 205
 Ala Ser Tyr Asn Gly Ser Ser Ala Ala Gly Gly Leu Lys Leu Asn Pro
 210 215 220
 Ala Val Ser Ile Cys Ala Gly Leu Ala Ala Gly Gln Asp Ala Cys
 225 230 235 240
 Gln Gly Asp Ser Gly Gly Pro Leu Ile Ala Pro Tyr Asn Gly Ser Ile
 245 250 255
 Tyr Ser Ile Gly Val Val Ser Tyr Gly Leu Gly Cys Ala Arg Pro Asn
 260 265 270
 Tyr Tyr Gly Val Tyr Ser Glu Thr Val Ala Val Leu Asp Trp Ile Asn
 275 280 285

10336256.txt

Gly	His	Ile	Gly	Asn	Gly	Gly	Gly	Ser	Gly	Thr	Val	Ile	Thr	Asp	Val
Val	290	Leu	Val	Ala	Ser	Asn	295	Gly	Ser	Thr	Ala	Pro	300	Ala	Gly
305						310									320
Tyr	Ser	Leu	Val	Gly	Tyr	Trp	Asp	Val	Asp	Lys	Gly	Gly	Ala	Gln	Gly
				325					330					335	
Thr	Tyr	Gly	Thr	Thr	Gly	Ser	Phe	Met	Thr	Ala	Leu	Tyr	Val	Arg	Arg
			340					345					350		
Gln	Leu	Pro	Ser	Glu	Thr	Ser	Thr	Cys	Val	Gly	Gly	Ile	Gly	Leu	Tyr
		355					360					365			
Thr	Ser	Ala	Gly	Ser	Thr	Val	Pro	Gly	Ser	Ile	Ala	Pro	Asn	Trp	Thr
	370					375					380				
Tyr	Arg	Gly	Met	Trp	Asp	Met	Asp	Lys	Gly	Gly	Val	Gly	Asn	Leu	
385					390					395				400	
Asn	Ser	Gln	Trp	Gln	Glu	Tyr	Met	Met	Gly	Leu	Tyr	Thr	Arg	Pro	Ala
				405					410					415	
Ser	Thr	Gly	Gln	Gly	Ala	Cys	Leu	Thr	Asp	Val	Ala	Leu	Tyr	Ala	Ser
			420					425					430		
Asn	Gly	Ser	Thr	Pro	Val	Thr	Pro	Ser	Gly	Phe	Ser	Gln	Val	Gly	Trp
		435					440					445			
Trp	Asp	Val	Asp	Ala	Gly	Gly	Ala	Phe	Gly	Thr	Gln	Gly	Ser	Ser	Gly
	450					455					460				
Ser	Tyr	Val	Ala	Thr	Leu	Ser	Thr	Lys	Ser	Glu					
465					470					475					

<210> 141
 <211> 1755
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<400> 141																			
gtgaaaaaga	aagttgtatt	attggggctg	tctatgggtc	tattaagtaa	tcctgctatt														60
ggaacgggtat	gggcagaagg	agctgcgaat	cctgtatttt	ttcagaatga	gaatgaagaa														120
tcgaccacgt	ttacttcaac	tacctcggat	caattgcaaa	taaataaaaat	gaaggcatcc														180
ccctttgatg	tgatggcata	tgcaaagaga	tggaagaaga	agggtacaccg	taatcctgag														240
agcaacaaaag	tagaattcat	ttcagggcaa	tttaaacccta	aaaatcctta	taatttcaac														300
actggttggtc	aggaattcgt	aggtgcaaac	tcggatggtt	ttaaagtaac	aacggaagac														360
accatacagg	taatgaaaga	agaaatgact	cccttgggag	attatgtaat	tcgtaccag														420
cagttcttca	gaggagtgcc	cgtatatggt	tcgacacaag	tattaaactt	aaatcaaaaa														480
ggagtggtaa	cagcatgggtc	cggagggatt	gtttcagaac	tgaacaagca	agaaaaccta														540
aataaagcaa	agaatcctag	tcaacaggca	gcgattcaaa	aagccgaaca	tgacctagg														600
tttatccctg	agtattatat	tccaccggct	gtcgaactcg	taattttacat	gaaagaagag														660
attgcgcatt	acgcttacca	tgtaaattcta	aattttctga	atccacaacc	gggaaattgg														720
gattacttta	tagatgcaaa	tgatggaacc	atttttaata	aagtcaatcg	tatccatcaa														780
gtgcaagtgg	cgcgaaatat	ggctcgtatt	aaccaaattg	gatttggaat	aggagtgcac														840
ggagataaaa	aacaagtaaa	tacagtattt	tctaattcgt	attactattt	gcaagataat														900
actagaggta	agggcattta	tacatacgat	gccaaaaatt	caaaccggct	cccgggcacg														960
ctatggagaa	acgcggataa	tcagtttact	gcaaagtatg	atgggtccgc	tgtagacgca														1020
cattattacg	caggagtgtg	atacgattac	tacaaaaata	agtttaatcg	taacagctat														1080
gatggagcag	gagcgccaat	aaaatcaact	gttcattatg	ggaaatcgta	tacgaacgcg														1140
ttttggaatt	cctatcaaat	ggtttatgga	gatgggggacg	ggtctaccta	tccatttcta														1200
ggagcattgg	atgtagtagg	acatgagttg	acgcatgctg	taacggaaaa	aacggcaaat														1260
tttaatttacg	aaaatgagtc	tggtgcttta	aatgaagcaa	tgtccgatat	ttttgggaca														1320
tttaattgagt	actacaataa	tcagaatcct	gattgggaaa	tgggtgagga	cttaagtttt														1380
aatagacagg	gatttcgttc	attagctgat	ccgacaaaaat	atgggtgatcc	ggaccattat														1440
tccaaaagat	accgtgggtc	aaaccaaagc	tatttagttc	atacaaacag	cgggaattata														1500
aacaaggctg	cttatcttat	cagtgaaggc	ggaaccact	atggcgttac	cgtgaatgga														1560
atcggcaaag	agaaactggg	aaatattttt	tacagggcat	taacacagta	tcttacagag														1620
tcagctacat	ttagccaaat	gagggcagca	gctttacaag	ccgcgacgga	tttatatgga														1680
gcagcaagtg	ctgaagttat	aagcgtgggc	aaagcttttg	atgcagtagg	agtcaattct														1740
atagacttgt	cctaa																		1755

<210> 142
 <211> 584
 <212> PRT

10336256.txt

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(25)

<400> 142

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Phe Phe Gln Asn Glu Asn Glu Glu Ser Thr Thr Phe Thr Ser Thr Thr
 35      40      45
Ser Asp Gln Leu Gln Ile Asn Lys Met Lys Ala Ser Pro Phe Asp Val
 50      55      60
Met Ala Tyr Ala Lys Arg Trp Lys Arg Lys Val His Arg Asn Pro Glu
 65      70      75      80
Ser Asn Lys Val Glu Phe Ile Ser Gly Gln Phe Lys Pro Lys Asn Pro
 85      90      95
Tyr Asn Phe Asn Thr Val Val Gln Glu Phe Val Gly Ala Asn Ser Asp
100      105      110
Val Phe Lys Val Thr Thr Glu Asp Thr Ile Gln Val Met Lys Glu Glu
115      120      125
Met Thr Pro Leu Gly Asp Tyr Val Ile Arg Thr Gln Gln Phe Phe Arg
130      135      140
Gly Val Pro Val Tyr Gly Ser Thr Gln Val Leu Asn Leu Asn Gln Lys
145      150      155      160
Gly Val Val Thr Ala Trp Ser Gly Gly Ile Val Ser Glu Leu Asn Lys
165      170      175
Gln Glu Asn Leu Asn Lys Ala Lys Asn Leu Ser Gln Gln Ala Ala Ile
180      185      190
Gln Lys Ala Glu His Asp Leu Gly Phe Ile Pro Glu Tyr Tyr Ile Pro
195      200      205
Pro Ala Val Glu Leu Val Ile Tyr Met Lys Glu Glu Ile Ala His Tyr
210      215      220
Ala Tyr His Val Asn Leu Asn Phe Leu Asn Pro Gln Pro Gly Asn Trp
225      230      235      240
Asp Tyr Phe Ile Asp Ala Asn Asp Gly Thr Ile Leu Asn Lys Val Asn
245      250      255
Arg Ile His Gln Val Gln Val Ala Arg Asn Met Val Asp Ser Asn Gln
260      265      270
Ile Gly Phe Gly Ile Gly Val His Gly Asp Lys Lys Gln Val Asn Thr
275      280      285
Val Phe Ser Asn Ser Tyr Tyr Tyr Leu Gln Asp Asn Thr Arg Gly Lys
290      295      300
Gly Ile Tyr Thr Tyr Asp Ala Lys Asn Ser Asn Arg Leu Pro Gly Thr
305      310      315      320
Leu Trp Arg Asn Ala Asp Asn Gln Phe Thr Ala Lys Tyr Asp Gly Pro
325      330      335
Ala Val Asp Ala His Tyr Tyr Ala Gly Val Val Tyr Asp Tyr Tyr Lys
340      345      350
Asn Lys Phe Asn Arg Asn Ser Tyr Asp Gly Ala Gly Ala Pro Ile Lys
355      360      365
Ser Thr Val His Tyr Gly Lys Ser Tyr Thr Asn Ala Phe Trp Asn Ser
370      375      380
Tyr Gln Met Val Tyr Gly Asp Gly Asp Gly Ser Thr Tyr Pro Phe Ser
385      390      395      400
Gly Ala Leu Asp Val Val Gly His Glu Leu Thr His Ala Val Thr Glu
405      410      415
Lys Thr Ala Asn Leu Ile Tyr Glu Asn Glu Ser Gly Ala Leu Asn Glu
420      425      430
Ala Met Ser Asp Ile Phe Gly Thr Leu Ile Glu Tyr Tyr Asn Asn Gln
435      440      445
Asn Pro Asp Trp Glu Met Gly Glu Asp Leu Ser Phe Asn Arg Gln Gly
450      455      460
Phe Arg Ser Leu Ala Asp Pro Thr Lys Tyr Gly Asp Pro Asp His Tyr

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465 470 475 480
 Ser Lys Arg Tyr Arg Gly Ser Asn Gln Ser Tyr Leu Val His Thr Asn
 485 490 495
 Ser Gly Ile Ile Asn Lys Ala Ala Tyr Leu Ile Ser Glu Gly Gly Thr
 500 505 510
 His Tyr Gly Val Thr Val Asn Gly Ile Gly Lys Glu Lys Leu Gly Asn
 515 520 525
 Ile Phe Tyr Arg Ala Leu Thr Gln Tyr Leu Thr Glu Ser Ala Thr Phe
 530 535 540
 Ser Gln Met Arg Ala Ala Ala Leu Gln Ala Ala Thr Asp Leu Tyr Gly
 545 550 555 560
 Ala Ala Ser Ala Glu Val Ile Ser Val Gly Lys Ala Phe Asp Ala Val
 565 570 575
 Gly Val Asn Ser Ile Asp Leu Ser
 580

<210> 143

<211> 2541

<212> DNA

<213> Unknown

<220>

<223> obtained from an environmental sample.

<400> 143

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gtccccgtac	gcgaccggcc	cccgtaccc	gcctccacgg	acgcgtgcg	gcgtgactac	240
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accgtcacca	cgcagtactg	a				2541

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<210> 144
 <211> 846
 <212> PRT
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(35)

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 35 40 45
 Ala Thr Arg Asp Pro Ala His Val Gln Lys Ser Arg Val Pro Val Arg
 50 55 60
 Asp Arg Pro Pro Leu Pro Ala Ser Thr Asp Ala Leu Arg Arg Asp Tyr
 65 70 75 80
 Asp Glu Ser Ala Gln Ala Gln Pro Arg Thr His Pro Arg Pro Ser Ala
 85 90 95
 Glu Arg Ala Ala Thr Ala Ala Ala Ala Cys Asp Val Thr Asp Phe
 100 105 110
 Thr Thr Arg Ser Gly Ser Glu Leu Val Arg Ala Ile Thr Ser Ser Thr
 115 120 125
 Thr Asp Cys Val Asn Thr Leu Phe Thr Leu Thr Gly Thr Asp Ala Asn
 130 135 140
 Ala Ala Phe Arg Glu Ser Gln Met Thr Thr Val Ala Tyr Ala Leu Arg
 145 150 155 160
 Asp Asn Ala Arg Ala Tyr Pro Gly Asp Asn Ser Thr Gly Thr Ala Gln
 165 170 175
 Leu Val Leu Tyr Leu Arg Ala Gly Tyr Val Gln Trp Tyr His Pro
 180 185 190
 Ser Asp Val Gly Ser Tyr Gly Pro Ala Leu Lys Thr Ala Ile Gln Ser
 195 200 205
 Gly Leu Asp Ala Phe Phe Gly Asn Ala Arg Ala Phe Thr Val Ala Asp
 210 215 220
 Ala Asn Gly Glu Val Leu Ser Glu Ala Val Thr Leu Ile Asp Ser Ala
 225 230 235 240
 Gln Glu Asn Asp Arg Tyr Leu Ser Val Val Lys Arg Leu Leu Asn Asp
 245 250 255
 Tyr Asn Ala Thr Tyr Asp Ala Ser Trp Trp Met Leu Asn Ala Val Asn
 260 265 270
 Asn Val Phe Thr Val Leu Phe Arg Ala His Gln Val Pro Ala Phe Val
 275 280 285
 Thr Ala Val Glu Ala Asp Arg Ser Val Leu Glu Thr Leu Arg Ser Phe
 290 295 300
 Ala Val Asn His Leu Asp Leu Leu Gly Thr Lys Asn Ala Phe Leu Thr
 305 310 315 320
 Ala Asn Ala Gly Arg Glu Leu Gly Arg Phe Leu Gln His Asp Ser Leu
 325 330 335
 Arg Gly Ala Val Arg Pro Leu Ala Lys Asp Leu Leu Gly Arg Ser Ser
 340 345 350
 Met Thr Gly Pro Thr Ala Arg Leu Trp Val Gly Val Ala Glu Met Ala
 355 360 365
 Asp Ala Tyr Asp Lys Ala Asn Cys Ser Tyr Tyr Gly Thr Cys Asp Leu
 370 375 380
 Ser Arg Arg Leu Gln Asp Val Val Leu Pro Val Ser His Thr Cys Ser
 385 390 395 400
 Ala ser Ile Lys Ile Arg Ala Gln Glu Met Thr Ala Glu Gln Leu Ala
 405 410 415
 Asp ser Cys Ala Ser Leu Ala Gly Gln Asp Ala Phe Phe His Asp Ile
 420 425 430
 Ala Lys Asp Gly Asp Arg Pro Val Ala Asp Asp Asn Asn Thr Thr Leu

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435 440 445
 Glu Val Val Val Phe Asp Ser Ser Ser Asp Tyr Gln Thr Phe Ala Gly
 450 455 460
 Val Ile Phe Gly Ile Asp Thr Asn Asn Gly Gly Met Tyr Leu Glu Gly
 465 470 475 480
 Asp Pro Ala Lys Ala Ser Asn Gln Pro Arg Phe Ile Ala Tyr Glu Ala
 485 490 495
 Glu Trp Val Arg Pro Arg Phe Glu Ile Trp Asn Leu Asn His Glu Tyr
 500 505 510
 Thr His Tyr Leu Asp Gly Arg Phe Asp Met Tyr Gly Asp Phe Glu Ala
 515 520 525
 Gly Met Thr Thr Pro Thr Val Trp Trp Val Glu Gly Phe Ala Glu Tyr
 530 535 540
 Val Ser Tyr Ser Tyr Arg Lys Leu Thr Tyr Glu Ala Ala Val Ala Glu
 545 550 555 560
 Ala Ala Lys Lys Thr Tyr Ala Leu Arg Thr Leu Phe Asp Thr Ala Tyr
 565 570 575
 Ser His Asp Thr Arg Ile Tyr Arg Trp Gly Tyr Leu Gly Val Arg
 580 585 590
 Tyr Met Leu Glu Arg His Pro Asp Asp Ile Ala Thr Leu Leu Gly His
 595 600 605
 Tyr Arg Thr Gly Ala Trp Asp Ala Ala Arg Thr Leu Leu Thr Gly Thr
 610 615 620
 Ile Gly Ser Arg Tyr Asp Ala Asp Trp Gln Thr Trp Leu Ala Ala Cys
 625 630 635 640
 Ala Ser Gly Ala Cys Ser Asp Gly Gly Ala Asn Lys Pro Pro Ala Ala
 645 650 655 660
 Ser Phe Thr Val Thr Ala Asn Ala Leu Ser Ala Gln Phe Thr Asp Thr
 660 665 670
 Ser Ala Asp Pro Asp Gly Arg Val Val Ser Arg Arg Trp Asp Phe Gly
 675 680 685
 Asp Gly Gly Ser Ser Thr Glu Ala Asn Pro Ser His Val Tyr Thr Ser
 690 695 700
 Gly Gly Thr Tyr Thr Val Thr Leu Thr Ala Thr Asp Asp Asp Gly Ala
 705 710 715 720
 Thr Gly Thr Ala Thr Arg Gln Val Thr Val Ser Ala Gly Gly Gly Ser
 725 730 735
 Leu Pro Glu Cys Ser Ser Ala Asp Thr Arg Gln Leu Asp Lys Asn Cys
 740 745 750
 Lys Arg Gly Asn Val Ser Ala Met Ser Gly Asn Tyr Ala Tyr Phe Tyr
 755 760 765
 Ile Leu Ile Pro Glu Gly Val Arg Arg Leu Thr Val Thr Ser Ser Gly
 770 775 780
 Gly Thr Gly Asn Ala Asp Leu Tyr Tyr Tyr Trp Lys Gln Trp Ala Thr
 785 790 795 800
 Thr Thr Ala His Asn Tyr Arg Ser Thr Thr Ala Gly Asn Glu Glu Thr
 805 810 815
 Leu Val Ile Asp Tyr Pro Pro Ala Gly Tyr Asn Tyr Ile Ser Leu His
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 Ala Val Glu Asp Phe Ser Gly Val Thr Val Thr Thr Gln Tyr
 835 840 845

<210> 145
 <211> 4772
 <212> DNA
 <213> Unknown

<220>
 <223> obtained from an environmental sample.

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 gatggggctc cagacgcaac ccctcaggtc cggttctctt tcgatgaact gcattctgat 180
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10336256.txt

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ggcatcgggt	gtgctggttt	aagcctgaga	gtattgaagc	agcctcaggc	tttatttgtc	4680
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<210> 146
 <211> 2397
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

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atctccgtcg	ccgccgtcac	gaacaaccac	gtcttcgcgg	aggcgctggc	cgtagccgcg	180
ccggggggccc	cgccggtgct	gacctcgatc	gccctccagg	gcgcccggcg	ctccgatccg	240
cccgcgcgct	ggagcgcgcg	cgagcaaacc	ctcgtcgacg	tccgctcgat	cgtagccacc	300
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10336256.txt

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 Arg Thr Thr Phe Tyr Pro Leu Asp Gly Thr Ser Met Ala Thr Pro His
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 Pro Gln Glu Val Lys Ser Ala Leu Met Ser Thr Gly Val Pro Ala Trp
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 Thr Trp Asp Val Glu Leu Arg Pro Gln Ser Thr Ser Ala Gly Ala Ser
 370 375 380
 Leu Asp Val Gln Ser Ser Leu Asp Leu Ala Pro Gly Gly Thr Leu Tyr
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 Leu Val Arg Gln Tyr Arg Tyr Pro Thr Tyr Pro Phe Gly Pro Pro Pro
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 Thr Val Arg Val Thr Asp Pro Ala Val Asn Val Gly Val Ser Val Ile
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 Ala Ala Gly Pro Asn Ala Leu Val Asp Pro Trp Met Leu Ser Ala Leu
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 Phe Pro Arg Arg Gln Gln Gln Leu Tyr Val Val Val Asp Ser Gly Ser

10336256.txt

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625      630      635      640
Val Gly Ala Ala Ala Tyr Asp Pro Val Ser Gly Leu Ala Leu Phe Pro
      645      650      655
Leu Pro Pro Asp Val Pro Ala Leu Ser Thr Gly Thr Thr Ser Ala Glu
      660      665      670
Leu Leu Ala Ser Asp Phe Gln Glu Ala Lys Asn Val Asp Thr Pro Gly
      675      680      685
Gly Glu Ile Leu Pro Asn Thr Arg Phe Val Gln Ser Arg Ile Arg Val
      690      695      700
Val Asp Gly Pro Ala Leu Thr Trp Leu Ala Pro Ala Gly Ser Cys
705      710      715      720
Ala Gly Lys Ser Pro Glu Leu Leu Val Thr Ala Gly Ser Thr Lys Arg
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      740      745      750
Arg Thr Gly Pro Ile Gly Leu Tyr Ser Ala Thr Trp Arg Thr Ala Gly
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Ile Ala Gly Thr Ala Ser Ala Ala Val Phe Asp Leu Pro Val Val Ile
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Lys Ser Thr Tyr Ser Ser Val Lys Phe Asp Ile Gly Thr Pro Pro Lys
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gaa cac cag cta ctg ttc gat acc ggc tcg tca acc ctc tgg acc gtt      376
Glu His Gln Leu Leu Phe Asp Thr Gly Ser Ser Thr Leu Trp Thr Val
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agc act gac tgc aca caa gac tcg tgt cca gaa gga agc acg gag ctg      424
Ser Thr Asp Cys Thr Gln Asp Ser Cys Pro Glu Gly Ser Thr Glu Leu
              60              65              70

tat aaa cga cgg tac tac aat gca tcg gca tca tcc acg gcc gtc gat      472
Tyr Lys Arg Arg Tyr Tyr Asn Ala Ser Ala Ser Ser Thr Ala Val Asp
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10336256.txt

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<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

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 245 250 255
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acg ctg cta tgg gat ggc aag cta gac aaa ccc cga ttc ggc cta tac	Thr Leu Leu Trp Asp Gly Lys Leu Asp Lys Pro Arg Phe Gly Leu Tyr	165	170	175	528
tat ggc aca aac cta gga gac gag ggc cct cag gac ggt gta ctg agc	Tyr Gly Thr Asn Leu Gly Asp Glu Gly Pro Gln Asp Gly Val Leu Ser	180	185	190	576
att ggc gac agt cac gag gac aag ttt gtt gat ggc cag gtg gtt tat	Ile Gly Asp Ser His Glu Asp Lys Phe Val Asp Gly Gln Val Val Tyr	195	200	205	624
gct cct ctg cag aag gtc aac aac gag tat gat cta tgg cgc aca ccg	Ala Pro Leu Gln Lys Val Asn Asn Glu Tyr Asp Leu Trp Arg Thr Pro	210	215	220	672
ttg aag gct gtc aac cta ctg gtc gcc aag aac ccg tcc aac cca aac	Leu Lys Ala Val Asn Leu Leu Val Ala Lys Asn Pro Ser Asn Pro Asn	225	230	235	720
cac aca gtc gag acg cac att ggc aaa ctg ccc acg acg cag ttt tct	His Thr Val Glu Thr His Ile Gly Lys Leu Pro Thr Thr Gln Phe Ser	245	250	255	768
ggc aat gcc ata gag tca ccc aat gtg act ttg tca acg ttc ggc gac	Gly Asn Ala Ile Glu Ser Pro Asn Val Thr Leu Ser Thr Phe Gly Asp	260	265	270	816
ggc act gcc att ttc gac acg gga gct ggc ggc ctt tcc ctg cca gaa	Gly Thr Ala Ile Phe Asp Thr Gly Ala Gly Gly Leu Ser Leu Pro Glu				864

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275					280					285						
gat	atg	att	gat	tcc	ata	tac	tac	aat	ctc	ggc	tgg	gat	tac	caa	agt	912
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	290					295					300					
ctg	ctc	aac	ggc	aag	cag	cgc	ttt	aca	tgc	gag	gcc	atg	aac	gca	tcc	960
Leu	Leu	Asn	Gly	Lys	Gln	Arg	Phe	Thr	Cys	Glu	Ala	Met	Asn	Ala	Ser	
305					310					315					320	
tgg	gcc	att	tct	cta	atc	ctt	ggt	gaa	ggt	gcg	ccc	gag	aac	gat	gtc	1008
Trp	Ala	Ile	Ser	Leu	Ile	Leu	Gly	Glu	Gly	Ala	Pro	Glu	Asn	Asp	Val	
				325					330					335		
gta	gtt	agc	att	cgc	ggc	gat	gaa	tta	ctc	aag	cct	gga	gct	caa	tgt	1056
Val	Val	Ser	Ile	Arg	Gly	Asp	Glu	Leu	Leu	Lys	Pro	Gly	Ala	Gln	Cys	
			340					345					350			
atg	cca	ccg	ttt	gac	cct	tcc	aac	gca	cct	tca	ttt	gcg	ctt	gtt	ggc	1104
Met	Pro	Pro	Phe	Asp	Pro	Ser	Asn	Ala	Pro	Ser	Phe	Ala	Leu	Val	Gly	
		355					360					365				
act	acc	tta	ctc	cag	agg	tac	tac	act	ata	tgg	gac	ttt	ggt	gcg	gac	1152
Thr	Thr	Leu	Leu	Gln	Arg	Tyr	Tyr	Thr	Ile	Trp	Asp	Phe	Gly	Ala	Asp	
	370					375					380					
aag	gtg	gcc	gag	tac	aag	cct	cgg	ctt	gga	ttt	ggt	agg	ctc	aag	aag	1200
Lys	Val	Ala	Glu	Tyr	Lys	Pro	Arg	Leu	Gly	Phe	Gly	Arg	Leu	Lys	Lys	
385					390					395					400	
cag	ttt	gac	tgg	aag	tat	cag	tca									1224
Gln	Phe	Asp	Trp	Lys	Tyr	Gln	Ser									
				405												

<210> 151

<211> 408

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> DOMAIN

<222> (5)...(389)

<223> Eukaryotic aspartyl protease

<400> 151

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Ala	Ala	Val	Phe	Asp	Leu	Pro	Val	Val	Ile	Lys	Ser	Thr	Tyr	Ser	Ser
			20					25					30		
Val	Lys	Phe	Asp	Ile	Gly	Thr	Pro	Lys	Glu	His	Gln	Leu	Leu	Phe	
		35					40				45				
Asp	Thr	Gly	Ser	Ser	Thr	Leu	Trp	Thr	Val	Ser	Thr	Asp	Cys	Thr	Gln
	50					55					60				
Asp	Ser	Cys	Pro	Glu	Gly	Ser	Thr	Glu	Leu	Tyr	Lys	Arg	Arg	Tyr	Tyr
65					70				75					80	
Asn	Ala	Ser	Ala	Ser	Ser	Thr	Ala	Val	Asp	Val	Gly	Ile	Pro	Ala	Thr
				85					90					95	
Ile	Pro	Tyr	Leu	Gly	Gly	Asn	Val	Glu	Gly	Glu	Ile	Tyr	Gln	Asp	Val
			100					105					110		
Phe	Ser	Ala	Leu	Asp	Gly	Ser	Val	Glu	Trp	Asn	Gln	Ser	Phe	Ile	Ala
		115					120				125				
Val	Asn	Lys	Ser	Ser	Trp	Leu	Trp	Ile	Thr	Ala	Asp	Gly	Phe	Leu	Gly
	130					135				140					
Leu	Gly	Phe	Ser	Thr	Ile	Ala	Glu	Pro	Asn	Thr	Ser	Thr	Leu	Val	Glu
	145				150				155					160	
Thr	Leu	Leu	Trp	Asp	Gly	Lys	Leu	Asp	Lys	Pro	Arg	Phe	Gly	Leu	Tyr
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Tyr Gly Thr Asn Leu Gly Asp Glu Gly Pro Gln Asp Gly Val Leu Ser
 180 185 190
 Ile Gly Asp Ser His Glu Asp Lys Phe Val Asp Gly Gln Val Val Tyr
 195 200 205
 Ala Pro Leu Gln Lys Val Asn Asn Glu Tyr Asp Leu Trp Arg Thr Pro
 210 215 220
 Leu Lys Ala Val Asn Leu Val Ala Lys Asn Pro Ser Asn Pro Asn
 225 230 235 240
 His Thr Val Glu Thr His Ile Gly Lys Leu Pro Thr Thr Gln Phe Ser
 245 250 255
 Gly Asn Ala Ile Glu Ser Pro Asn Val Thr Leu Ser Thr Phe Gly Asp
 260 265 270
 Gly Thr Ala Ile Phe Asp Thr Gly Ala Gly Gly Leu Ser Leu Pro Glu
 275 280 285
 Asp Met Ile Asp Ser Ile Tyr Tyr Asn Leu Gly Trp Asp Tyr Gln Ser
 290 295 300
 Leu Leu Asn Gly Lys Gln Arg Phe Thr Cys Glu Ala Met Asn Ala Ser
 305 310 315 320
 Trp Ala Ile Ser Leu Ile Leu Gly Glu Gly Ala Pro Glu Asn Asp Val
 325 330 335
 Val Val Ser Ile Arg Gly Asp Glu Leu Lys Pro Gly Ala Gln Cys
 340 345 350
 Met Pro Pro Phe Asp Pro Ser Asn Ala Pro Ser Phe Ala Leu Val Gly
 355 360 365
 Thr Thr Leu Leu Gln Arg Tyr Tyr Thr Ile Trp Asp Phe Gly Ala Asp
 370 375 380
 Lys Val Ala Glu Tyr Lys Pro Arg Leu Gly Phe Gly Arg Leu Lys Lys
 385 390 395 400
 Gln Phe Asp Trp Lys Tyr Gln Ser
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<210> 152

<211> 3002

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (257)...(304)

<223> Exon

<221> CDS

<222> (363)...(428)

<223> Exon

<221> CDS

<222> (588)...(725)

<223> Exon

<221> CDS

<222> (774)...(950)

<223> Exon

<221> CDS

<222> (1001)...(2290)

<223> Exon

<400> 152

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gttggtttgt	ttgcgggtgt	tatcacacaa	gtgcaaacct	tgatacttc	caccggtgcc	120
tgagcagtat	gtagggagat	tctgaaaccc	tctagagggc	atgttcgacc	tacgtgatga	180
aagatcaagc	tgagtagacg	ttggcggggc	ctttgcaaac	ggccagttgc	gcgtgttggt	240
tgctactagt	caagca atg	ggc cga gca	agc cgt aac	ttg cca tca	tac cct	292
	Met	Gly	Arg	Ala	Ser	Arg
	1		5			10
				Asn	Leu	Pro
				Ser	Tyr	Pro

cgc ctt cct aac caggtataga gctgggttcc agttttccaa cctaatatcg
 Arg Leu Pro Asn

344

15

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aaa	gtg	tac	atc	acc	ggc	gag	tca	tac	gct	ggg	cgc	tac	gtc	ccc	tac	1303
Lys	Val	Tyr	Ile	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Arg	Tyr	Val	Pro	Tyr	
	230					235					240					
att	gcc	gac	gcc	atg	ctg	agc	aag	aac	gac	tca	aca	tac	tac	gac	gtc	1351
Ile	Ala	Asp	Ala	Met	Leu	Ser	Lys	Asn	Asp	Ser	Thr	Tyr	Tyr	Asp	Val	
245					250					255					260	
aag	ggc	gtc	atg	ttt	tac	gac	ccc	agc	gta	gcc	gaa	gac	ggc	ctc	cta	1399
Lys	Gly	Val	Met	Phe	Tyr	Asp	Pro	Ser	Val	Ala	Glu	Asp	Gly	Leu	Leu	
				265					270					275		
acc	gac	gtc	cct	gcc	gtc	gcc	tac	gtc	gac	gaa	tgg	gcc	ggt	ctc	ttc	1447
Thr	Asp	Val	Pro	Ala	Val	Ala	Tyr	Val	Asp	Glu	Trp	Ala	Gly	Leu	Phe	
			280					285					290			
aac	ttc	aac	cag	agc	ttc	atg	gac	gac	atc	cac	gcc	cgc	gcc	gac	gcc	1495
Asn	Phe	Asn	Gln	Ser	Phe	Met	Asp	Asp	Ile	His	Ala	Arg	Ala	Asp	Ala	
		295					300					305				
tgc	ggc	tac	acc	gag	tac	atg	gaa	aaa	tac	ctc	act	ttc	ccc	ccg	acc	1543
Cys	Gly	Tyr	Thr	Glu	Tyr	Met	Glu	Lys	Tyr	Leu	Thr	Phe	Pro	Pro	Thr	
	310					315					320					
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Ser	Lys	Phe	Pro	Thr	Pro	Ala	Asn	Asn	Ser	Asp	Thr	Glu	Gly	Cys	Ser	
325					330					335					340	
ctt	tgg	caa	gac	att	ttc	gac	gcc	gtt	atc	tac	aca	aac	ccc	tgc	ttc	1639
Leu	Trp	Gln	Asp	Ile	Phe	Asp	Ala	Val	Ile	Tyr	Thr	Asn	Pro	Cys	Phe	
				345				350						355		
gac	gtc	tac	gca	atc	gca	acc	acc	tgc	cct	ctc	ctc	tgg	gac	ccc	ctc	1687
Asp	Val	Tyr	Ala	Ile	Ala	Thr	Thr	Cys	Pro	Leu	Leu	Trp	Asp	Pro	Leu	
			360					365					370			
ggc	ttc	ccc	ggc	tcc	ttc	gac	tac	ctg	cct	cca	cgc	acc	gaa	atc	tac	1735
Gly	Phe	Pro	Gly	Ser	Phe	Asp	Tyr	Leu	Pro	Pro	Arg	Thr	Glu	Ile	Tyr	
		375					380					385				
ttt	aac	cgc	agc	gac	gtt	cag	gcc	gcc	atc	aac	gcg	ccc	atc	cag	ccc	1783
Phe	Asn	Arg	Ser	Asp	Val	Gln	Ala	Ala	Ile	Asn	Ala	Pro	Ile	Gln	Pro	
	390					395					400					
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Trp	Ala	Glu	Cys	Ser	Asn	Gly	Val	Leu	Asp	Thr	Asp	Thr	Ser	Pro	Pro	
405					410					415					420	
tcg	tcc	tgg	gaa	gtc	atc	ccc	cgc	atc	atc	gac	gcc	ctc	gac	cgc	aca	1879
Ser	Ser	Trp	Glu	Val	Ile	Pro	Arg	Ile	Ile	Asp	Ala	Leu	Asp	Arg	Thr	
				425					430					435		
atc	att	gcc	cac	ggc	gaa	ctc	gac	tac	gtc	ctg	ctg	cac	aac	ggc	acc	1927
Ile	Ile	Ala	His	Gly	Glu	Leu	Asp	Tyr	Val	Leu	Leu	His	Asn	Gly	Thr	
			440					445					450			
ctg	atg	gcc	atc	cag	aac	atg	acg	tgg	ggc	ggc	ctt	cag	ggc	ttc	cag	1975
Leu	Met	Ala	Ile	Gln	Asn	Met	Thr	Trp	Gly	Gly	Leu	Gln	Gly	Phe	Gln	
		455					460					465				
aac	ccg	ccc	act	gat	gac	ttc	tac	gtc	ccc	tac	cac	gac	gat	ctg	agc	2023
Asn	Pro	Pro	Thr	Asp	Asp	Phe	Tyr	Val	Pro	Tyr	His	Asp	Asp	Leu	Ser	
	470					475					480					
ctg	acg	agt	ctg	agc	gca	aag	gga	ttg	atg	ggc	aag	acg	att	acc	gag	2071
Leu	Thr	Ser	Leu	Ser	Ala	Lys	Gly	Leu	Met	Gly	Lys	Thr	Ile	Thr	Glu	
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Arg Lys Leu Thr Phe Val Gln Gln Ala Met Ser Gly His Met Val Pro
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cag tac cag ccc agc agt gcg tac agg cag ttg gag ttt ttg ctc ggc      2167
Gln Tyr Gln Pro Ser Ser Ala Tyr Arg Gln Leu Glu Phe Leu Leu Gly
520                               525                               530

agg gtc gag agt ctg aca tcg aga gag ggt ttt acg acg ctg ccg aag      2215
Arg Val Glu Ser Leu Thr Ser Arg Glu Gly Phe Thr Thr Leu Pro Lys
535                               540                               545

agt gcg cag agt aat ggc acg agt att gga gag aag agg gat ttg ggt      2263
Ser Ala Gln Ser Asn Gly Thr Ser Ile Gly Glu Lys Arg Asp Leu Gly
550                               555                               560

gtt atg agg gag ttt aag agg tgg gtt tgagcgagct ttatctactt      2310
Val Met Arg Glu Phe Lys Arg Trp Val
565                               570

ctttctctat agaaggaaaa gaaaaaaaaag aaggagattg agtaatgttg tcgtaatgtc      2370
gatatgtaag ataatgaaaa aacaaaaacat acgtgcaaat catcccgccca cattctcgac      2430
ttctttcttg ccatccatcg ccaacatccc ctctgcctc tccttcactg cctctggcac      2490
ctccgcaaac atcttgccga tagcctccac cgtcgtgttc cccccgctaa agacaacacc      2550
aacattccat ccctcctccc cagcctccct ctgcaccaat gccctaaact cctcgttaaa      2610
cagcacaacc gcgagcccaa cgaccgcaga gggctctaca aaacacttca tcctctcaag      2670
aaccaggcgc attgccttct taatctggtc ttcagtcacc gcaaacaagc cggccacata      2730
ctctggcttc gagatgatac tccaggtgtg ctctccaagc ggcgtagcga agccatctgc      2790
aatcgtaagc gtcttgacag atgtgacgcg ctacccgcg gcaacacccc tgcgtgcatc      2850
gtcaccgccc tggaaactcg gttccgcgcc gaacacgcgg atgcccgtagc cgtgcagtgc      2910
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<211> 16

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 153

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Met Gly Arg Ala Ser Arg Asn Leu Pro Ser Tyr Pro Arg Leu Pro Asn
1                               5                               10                               15

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<210> 154

<211> 22

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 154

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Gln Leu Asp Met Cys Arg Val Val Gly Arg Val Cys Leu Asn Asp Val
1                               5                               10                               15
Ser Leu Ala Arg Cys Ala
20

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<210> 155

<211> 46

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 155

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Ala Ser Val Ser Ala Arg Ser Ala Arg Ser Val Gly Arg Lys Val Glu
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Phe Pro Arg Pro Arg Ile Gly Ile Pro Ala Gln Asn Val His Pro His
20                               25                               30
Lys Arg Gln Ala Thr Gln Ile Ile Asn Thr Glu Ala Ser Lys
35                               40                               45

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<210> 156

<211> 59

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<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 156

Ala Phe Ala Val Asn Gly Thr Ala Gly Ala Ile Pro Glu Val Tyr Phe
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 Asp Ile Gly Glu Ser Tyr Ala Gly Leu Leu Pro Ile Ser Lys Ala Ala
 20 25 30
 Asn Glu Thr Arg Glu Leu Tyr Phe Trp Phe Phe Pro Ser Glu Asn Pro
 35 40 45
 Asp Ala Ser Asp Glu Ile Thr Ile Trp Leu Asn
 50 55

<210> 157

<211> 430

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 157

Gly Gly Pro Gly Cys Ser Ser Leu Glu Gly Phe Leu Gln Glu Asn Gly
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 Pro Ile Ser Trp Gln Tyr Gly Ser Gly Pro Gly Pro Val Tyr Asn Pro
 20 25 30
 Trp Asn Trp Ala Asn Leu Thr Asn Met Val Trp Val Glu Gln Pro Val
 35 40 45
 Gly Thr Gly Phe Ser Gln Gly Thr Pro Thr Ala Thr Asn Gln Glu Glu
 50 55 60
 Thr Ala Ala Glu Phe Leu Gly Phe Phe Lys Asn Phe Val Asp Thr Phe
 65 70 75 80
 Gly Leu Gln Asn Arg Lys Val Tyr Ile Thr Gly Glu Ser Tyr Ala Gly
 85 90 95
 Arg Tyr Val Pro Tyr Ile Ala Asp Ala Met Leu Ser Lys Asn Asp Ser
 100 105 110
 Thr Tyr Tyr Asp Val Lys Gly Val Met Phe Tyr Asp Pro Ser Val Ala
 115 120 125
 Glu Asp Gly Leu Leu Thr Asp Val Pro Ala Val Ala Tyr Val Asp Glu
 130 135 140
 Trp Ala Gly Leu Phe Asn Phe Asn Gln Ser Phe Met Asp Asp Ile His
 145 150 155 160
 Ala Arg Ala Asp Ala Cys Gly Tyr Thr Glu Tyr Met Glu Lys Tyr Leu
 165 170 175
 Thr Phe Pro Pro Thr Ser Lys Phe Pro Thr Pro Ala Asn Asn Ser Asp
 180 185 190
 Thr Glu Gly Cys Ser Leu Trp Gln Asp Ile Phe Asp Ala Val Ile Tyr
 195 200 205
 Thr Asn Pro Cys Phe Asp Val Tyr Ala Ile Ala Thr Thr Cys Pro Leu
 210 215 220
 Leu Trp Asp Pro Leu Gly Phe Pro Gly Ser Phe Asp Tyr Leu Pro Pro
 225 230 235 240
 Arg Thr Glu Ile Tyr Phe Asn Arg Ser Asp Val Gln Ala Ala Ile Asn
 245 250 255
 Ala Pro Ile Gln Pro Trp Ala Glu Cys Ser Asn Gly Val Leu Asp Thr
 260 265 270
 Asp Thr Ser Pro Pro Ser Ser Trp Glu Val Ile Pro Arg Ile Ile Asp
 275 280 285
 Ala Leu Asp Arg Thr Ile Ile Ala His Gly Glu Leu Asp Tyr Val Leu
 290 295 300
 Leu His Asn Gly Thr Leu Met Ala Ile Gln Asn Met Thr Trp Gly Gly
 305 310 315 320
 Leu Gln Gly Phe Gln Asn Pro Pro Thr Asp Asp Phe Tyr Val Pro Tyr
 325 330 335
 His Asp Asp Leu Ser Leu Thr Ser Leu Ala Lys Gly Leu Met Gly
 340 345 350
 Lys Thr Ile Thr Glu Arg Lys Leu Thr Phe Val Gln Gln Ala Met Ser
 355 360 365
 Gly His Met Val Pro Gln Tyr Gln Pro Ser Ser Ala Tyr Arg Gln Leu
 370 375 380
 Glu Phe Leu Leu Gly Arg Val Glu Ser Leu Thr Ser Arg Glu Gly Phe

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385 Thr Thr Leu Pro Lys 390 Ser Ala Gln Ser 395 Gly Thr Ser Ile Gly 400
 Thr Thr Leu Pro Lys 405 Ser Ala Gln Ser 410 Gly Thr Ser Ile Gly 415
 Lys Arg Asp Leu 420 Val Met Arg Glu 425 Phe Lys Arg Trp Val 430

<210> 158

<211> 1719

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1719)

<400> 158

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cag tta gat atg tgc cgc gtc gtt ggc agg gta tgc ctg aat gat gtc	96
Gln Leu Asp Met 20 Cys Arg Val Val Gly 25 Arg Val Cys Leu 30 Asn Asp Val	
agc ctc gcg cgc tgc gcc gcc agt gtc tct gct cgg agc gct cgt tcc	144
Ser Leu Ala 35 Arg Cys Ala Ala Ser 40 Val Ser Ala Arg Ser 45 Ala Arg Ser	
gtt ggc agg aag gtg gaa ttc cct cgc cct cgc atc ggc ata ccg gcg	192
Val Gly 50 Arg Lys Val Glu 55 Phe 55 Pro Arg Pro Arg Ile 60 Gly Ile Pro Ala	
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Gln Asn Val His Pro His 70 Lys Arg Gln Ala Thr 75 Gln Ile Ile Asn Thr 80	
gaa gcc tcc aag gcc ttt gct gtg aac ggc act gct gga gct att ccc	288
Glu Ala Ser Lys 85 Phe Ala Val Asn Gly 90 Thr Ala Gly Ala Ile 95 Ile Pro	
gaa gtc tac ttc gac att ggc gag tca tac gct ggt ctt ctc ccc att	336
Glu Val Tyr 100 Asp Ile Gly Glu Ser 105 Tyr Ala Gly Leu 110 Leu Pro Ile	
agc aaa gct gcc aat gag act cgg gag ctc tac ttt tgg ttc ttt cct	384
Ser Lys Ala 115 Ala Asn Glu Thr Arg 120 Glu Leu Tyr Phe Trp 125 Phe Phe Pro	
tcg gag aac cca gat gct agc gac gaa atc acc atc tgg ttg aac ggt	432
Ser Glu Asn Pro Asp Ala Ser 135 Asp Glu Ile Thr Ile 140 Trp Leu Asn Gly	
ggt ccc ggc tgc tct tct ctc gaa gga ttt ctt cag gaa aac gga ccc	480
Gly Pro Gly Cys Ser 150 Leu Glu Gly Phe 155 Gln Glu Asn Gly Pro 160	
atc tca tgg caa tac ggc agc ggc cca ggt ccc gtc tac aac cca tgg	528
Ile Ser Trp Gln Tyr 165 Gly Ser Gly Pro 170 Pro Val Tyr Asn Pro 175 Trp	
aac tgg gcg aac ctc acc aac atg gtt tgg gtc gaa cag ccc gtc ggc	576
Asn Trp Ala 180 Leu Thr Asn Met Val 185 Trp Val Glu Gln Pro 190 Val Val Gly	
act ggc ttc tct cag gga acg ccg act gct act aat caa gaa gag act	624
Thr Gly Phe 195 Ser Gln Gly Thr Pro 200 Thr Ala Thr Asn Gln 205 Glu Glu Thr	

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gcc Ala 210	gag Ala 210	gag Glu	ttc Phe	ctc Leu	ggt Gly	ttt Phe 215	ttc Phe	aag Lys	aac Asn	ttt Phe	gtt Val 220	gac Asp	act Thr	ttt Phe	ggt Gly	672
ctg Leu 225	cag Gln	aac Asn	cgc Arg	aaa Lys	gtg Val 230	tac Tyr	atc Ile	acc Thr	ggc Gly	gag Glu 235	tca Ser	tac Tyr	gct Ala	ggg Gly	cgc Arg 240	720
tac Tyr	gtc Val	ccc Pro	tac Tyr	att Ile 245	gcc Ala	gac Asp	gcc Ala	atg Met	ctg Leu 250	agc Ser	aag Lys	aac Asn	gac Asp	tca Ser 255	aca Thr	768
tac Tyr	tac Tyr	gac Asp	gtc Val 260	aag Lys	ggc Gly	gtc Val	atg Met	ttt Phe 265	tac Tyr	gac Asp	ccc Pro	agc Ser	gta Val 270	gcc Ala	gaa Glu	816
gac Asp	ggc Gly	ctc Leu 275	cta Leu	acc Thr	gac Asp	gtc Val	cct Pro 280	gcc Ala	gtc Val	gcc Ala	tac Tyr	gtc Val 285	gac Asp	gaa Glu	tgg Trp	864
gcc Ala 290	ggt Gly	ctc Leu	ttc Phe	aac Asn	ttc Phe 295	aac Asn	cag Gln	agc Ser	ttc Phe	atg Met	gac Asp 300	gac Asp	atc Ile	cac His	gcc Ala	912
cgc Arg 305	gcc Ala	gac Asp	gcc Ala	tgc Cys	ggc Gly 310	tac Tyr	acc Thr	gag Glu	tac Tyr	atg Met 315	gaa Glu	aaa Lys	tac Tyr	ctc Leu	act Thr 320	960
ttc Phe	ccc Pro	ccg Pro	acc Thr	agc Ser 325	aaa Lys	ttc Phe	ccc Pro	acc Thr	ccg Pro 330	gcc Ala	aac Asn	aac Asn	tcc Ser	gac Asp 335	aca Thr	1008
gaa Glu	ggc Gly	tgc Cys	tcc Ser 340	ctt Leu	tgg Trp	caa Gln	gac Asp	att Ile 345	ttc Phe	gac Asp	gcc Ala	gtt Val	atc Ile 350	tac Tyr	aca Thr	1056
aac Asn	ccc Pro	tgc Cys 355	ttc Phe	gac Asp	gtc Val	tac Tyr	gca Ala 360	atc Ile	gca Ala	acc Thr	acc Thr	tgc Cys 365	cct Pro	ctc Leu	ctc Leu	1104
tgg Trp 370	gac Asp	ccc Pro	ctc Leu	ggc Gly	ttc Phe	ccc Pro 375	ggc Gly	tcc Ser	ttc Phe	gac Asp	tac Tyr 380	ctg Leu	cct Pro	cca Pro	cgc Arg	1152
acc Thr 385	gaa Glu	atc Ile	tac Tyr	ttt Phe	aac Asn 390	cgc Arg	agc Ser	gac Asp	gtt Val	cag Gln 395	gcc Ala	gcc Ala	atc Ile	aac Asn	gag Ala 400	1200
ccc Pro	atc Ile	cag Gln	ccc Pro	tgg Trp 405	gcc Ala	gag Glu	tgc Cys	tcc Ser	aac Asn 410	ggc Gly	gtc Val	ctc Leu	gac Asp	aca Thr 415	gat Asp	1248
acc Thr	tgc Ser	ccc Pro	ccg Pro	tgc Ser	tcc Ser	tgg Trp	gaa Glu	gtc Val 425	atc Ile	ccc Pro	cgc Arg	atc Ile	atc Ile 430	gac Asp	gcc Ala	1296
ctc Leu	gac Asp	cgc Arg 435	aca Thr	atc Ile	att Ile	gcc Ala	cac His 440	ggc Gly	gaa Glu	ctc Leu	gac Asp	tac Tyr 445	gtc Val	ctg Leu	ctg Leu	1344
cac His	aac Asn 450	ggc Gly	acc Thr	ctg Leu	atg Met	gcc Ala 455	atc Ile	cag Gln	aac Asn	atg Met	acg Thr 460	tgg Trp	ggc Gly	ggc Gly	ctt Leu	1392
cag Gln 465	ggc Gly	ttc Phe	cag Gln	aac Asn	ccg Pro 470	ccc Pro	act Thr	gat Asp	gac Asp	ttc Phe 475	tac Tyr	gtc Val	ccc Pro	tac Tyr	cac His 480	1440

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gac	gat	ctg	agc	ctg	acg	agt	ctg	agc	gca	aag	gga	ttg	atg	ggc	aag	1488
Asp	Asp	Leu	Ser	Leu	Thr	Ser	Leu	Ser	Ala	Lys	Gly	Leu	Met	Gly	Lys	
			485						490					495		
acg	att	acc	gag	cgc	aag	ctt	acg	ttt	gtg	cag	cag	gcg	atg	agt	ggg	1536
Thr	Ile	Thr	Glu	Arg	Lys	Leu	Thr	Phe	Val	Gln	Gln	Ala	Met	Ser	Gly	
			500					505					510			
cac	atg	gtg	ccg	cag	tac	cag	ccc	agc	agt	gcg	tac	agg	cag	ttg	gag	1584
His	Met	Val	Pro	Gln	Tyr	Gln	Pro	Ser	Ser	Ala	Tyr	Arg	Gln	Leu	Glu	
		515					520					525				
ttt	ttg	ctc	ggc	agg	gtc	gag	agt	ctg	aca	tcg	aga	gag	ggt	ttt	acg	1632
Phe	Leu	Leu	Gly	Arg	Val	Glu	Ser	Leu	Thr	Ser	Arg	Glu	Gly	Phe	Thr	
	530					535					540					
acg	ctg	ccg	aag	agt	gcg	cag	agt	aat	ggc	acg	agt	att	gga	gag	aag	1680
Thr	Leu	Pro	Lys	Ser	Ala	Gln	Ser	Asn	Gly	Thr	Ser	Ile	Gly	Glu	Lys	
	545				550					555					560	
agg	gat	ttg	ggt	gtt	atg	agg	gag	ttt	aag	agg	tgg	gtt				1719
Arg	Asp	Leu	Gly	Val	Met	Arg	Glu	Phe	Lys	Arg	Trp	Val				
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<210> 159

<211> 573

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> DOMAIN

<222> (96)...(532)

<223> Serine carboxypeptidase

<400> 159

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Gln	Leu	Asp	Met	Cys	Arg	Val	Val	Gly	Arg	Val	Cys	Leu	Asn	Asp	Val	
			20					25					30			
Ser	Leu	Ala	Arg	Cys	Ala	Ala	Ser	Val	Ser	Ala	Arg	Ser	Ala	Arg	Ser	
		35					40					45				
Val	Gly	Arg	Lys	Val	Glu	Phe	Pro	Arg	Pro	Arg	Ile	Gly	Ile	Pro	Ala	
	50					55					60					
Gln	Asn	Val	His	Pro	His	Lys	Arg	Gln	Ala	Thr	Gln	Ile	Ile	Asn	Thr	
	65				70					75				80		
Glu	Ala	Ser	Lys	Ala	Phe	Ala	Val	Asn	Gly	Thr	Ala	Gly	Ala	Ile	Pro	
			85						90					95		
Glu	Val	Tyr	Phe	Asp	Ile	Gly	Glu	Ser	Tyr	Ala	Gly	Leu	Leu	Pro	Ile	
			100					105					110			
Ser	Lys	Ala	Ala	Asn	Glu	Thr	Arg	Glu	Leu	Tyr	Phe	Trp	Phe	Phe	Pro	
		115					120					125				
Ser	Glu	Asn	Pro	Asp	Ala	Ser	Asp	Glu	Ile	Thr	Ile	Trp	Leu	Asn	Gly	
	130					135					140					
Gly	Pro	Gly	Cys	Ser	Ser	Leu	Glu	Gly	Phe	Leu	Gln	Glu	Asn	Gly	Pro	
	145				150					155				160		
Ile	Ser	Trp	Gln	Tyr	Gly	Ser	Gly	Pro	Gly	Pro	Val	Tyr	Asn	Pro	Trp	
			165						170					175		
Asn	Trp	Ala	Asn	Leu	Thr	Asn	Met	Val	Trp	Val	Glu	Gln	Pro	Val	Gly	
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Thr	Gly	Phe	Ser	Gln	Gly	Thr	Pro	Thr	Ala	Thr	Asn	Gln	Glu	Glu	Thr	
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Ala	Ala	Glu	Phe	Leu	Gly	Phe	Phe	Lys	Asn	Phe	Val	Asp	Thr	Phe	Gly	
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Leu	Gln	Asn	Arg	Lys	Val	Tyr	Ile	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Arg	
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Tyr	Val	Pro	Tyr	Ile	Ala	Asp	Ala	Met	Leu	Ser	Lys	Asn	Asp	Ser	Thr	
				245					250					255		

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Tyr Tyr Asp Val Lys Gly Val Met Phe Tyr Asp Pro Ser Val Ala Glu
 260 265 270
 Asp Gly Leu Leu Thr Asp Val Pro Ala Val Ala Tyr Val Asp Glu Trp
 275 280 285
 Ala Gly Leu Phe Asn Phe Asn Gln Ser Phe Met Asp Asp Ile His Ala
 290 295 300
 Arg Ala Asp Ala Cys Gly Tyr Thr Glu Tyr Met Glu Lys Tyr Leu Thr
 305 310 315 320
 Phe Pro Pro Thr Ser Lys Phe Pro Thr Pro Ala Asn Asn Ser Asp Thr
 325 330 335
 Glu Gly Cys Ser Leu Trp Gln Asp Ile Phe Asp Ala Val Ile Tyr Thr
 340 345 350
 Asn Pro Cys Phe Asp Val Tyr Ala Ile Ala Thr Thr Cys Pro Leu Leu
 355 360 365
 Trp Asp Pro Leu Gly Phe Pro Gly Ser Phe Asp Tyr Leu Pro Pro Arg
 370 375 380
 Thr Glu Ile Tyr Phe Asn Arg Ser Asp Val Gln Ala Ala Ile Asn Ala
 385 390 395 400
 Pro Ile Gln Pro Trp Ala Glu Cys Ser Asn Gly Val Leu Asp Thr Asp
 405 410 415
 Thr Ser Pro Pro Ser Ser Trp Glu Val Ile Pro Arg Ile Ile Asp Ala
 420 425 430
 Leu Asp Arg Thr Ile Ile Ala His Gly Glu Leu Asp Tyr Val Leu Leu
 435 440 445
 His Asn Gly Thr Leu Met Ala Ile Gln Asn Met Thr Trp Gly Gly Leu
 450 455 460
 Gln Gly Phe Gln Asn Pro Thr Asp Asp Phe Tyr Val Pro Tyr His
 465 470 475 480
 Asp Asp Leu Ser Leu Thr Ser Leu Ser Ala Lys Gly Leu Met Gly Lys
 485 490 495
 Thr Ile Thr Glu Arg Lys Leu Thr Phe Val Gln Gln Ala Met Ser Gly
 500 505 510
 His Met Val Pro Gln Tyr Gln Pro Ser Ser Ala Tyr Arg Gln Leu Glu
 515 520 525
 Phe Leu Leu Gly Arg Val Glu Ser Leu Thr Ser Arg Glu Gly Phe Thr
 530 535 540
 Thr Leu Pro Lys Ser Ala Gln Ser Asn Gly Thr Ser Ile Gly Glu Lys
 545 550 555 560
 Arg Asp Leu Gly Val Met Arg Glu Phe Lys Arg Trp Val
 565 570

<210> 160

<211> 3407

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1001)...(1156)

<223> Exon

<221> CDS

<222> (1277)...(2023)

<223> Exon

<221> CDS

<222> (2177)...(2407)

<223> Exon

<221> misc_feature

<222> (1)...(3407)

<223> n = A,T,C or G

<400> 160

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tcacttatac	ccacttttat	tcattttgcat	gtagcgcggg	agtttgctga	tgaaagagaa	180
agggtttttt	gtcttggtat	tttcttgctg	tgacgaaagt	tttttgttac	ctcactccaa	240

10336256.txt

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aaagactatc atgtttgaaa ttatcatggt gagagaaaaat tcacatgttg caggtaggca 300
ggcatatggt ggcttacata ctatactaga gcacaaaaaa agaaggatag taagcgaaat 360
attcaagttg aaagggtcatg ttacgataac tcccccttg gacttattac ctattagtca 420
ctcagtcaag cttcttccct ttctctccac cttcttcttc ctcccccttc ccgtcagcaa 480
aacaatatga atgtactttg atttaccac tttcgggtcc tctcgccgc catcatctt 540
tctttgtacg tcagacctgc ctcttggtggt acacatgcgt cacggtacac catgccggt 600
taggaaagcg acaagatgga tatgcggtac ccaagacttg cttggcggtt tatcctggat 660
ccccgcgcag catgtttatt ggctaagatg gctggtgaag ctataatagg catgatgcgg 720
atgctgaaaa catgtgtgtt tatgtatctt ttttttgggt gagtggaccg ggtattgttg 780
gctttgtggg gattgtggac ggggatgggg tgggtaacgg tgagggtgagg ggggttacta 840
tagtataaat tggagttgat tattttgctt cttgtttgat ttcttttact tcaacttctt 900
ctatcctcgc ttctttttct cgccttttgt aagaacaag gccgccgtgt tttttttctc 960
agtcaagatt tcaaaaggga caaaggaaa agaggacaag atg aag tcg ctt ggt 1015
                                         Met Lys Ser Leu Gly
                                         1 5

ctt ctc gca act gtt tgc gct act gct gcg ctg gcc aag gga ccc gag 1063
Leu Leu Ala Thr Val Cys Ala Thr Ala Ala Leu Ala Lys Gly Pro Glu
                                         10 15 20

cga gtt agc aat gcg gcg agg agt att acg att gaa gtt gcg ccg ggg 1111
Arg Val Ser Asn Ala Ala Arg Ser Ile Thr Ile Glu Val Ala Pro Gly
                                         25 30 35

gag acg cgc cag att act gag gat gag agg tgg gat att gct act 1156
Glu Thr Arg Gln Ile Thr Glu Asp Glu Arg Trp Asp Ile Ala Thr
                                         40 45 50

gtgagtttgt ggtggttgtt gaaacacttg tctattatcc ctccctttct tccccacgga 1216
aacacctttt ttttaaaact acagctcctt tcgttttatt tttactaaact ataacaccag 1276
ggc ggc ggt tgt gga agc cac ttc ttc gac att acg gat tcg ttc gcc 1324
Gly Gly Gly Cys Gly Ser His Phe Phe Asp Ile Thr Asp Ser Phe Ala
                                         55 60 65

gaa ccc ata gcc gtc acg cgc gcg gcc gcc tac cca tcc acc ttc caa 1372
Glu Pro Ile Ala Val Thr Arg Ala Ala Ala Tyr Pro Ser Thr Phe Gln
                                         70 75 80

tac agc acc aac atc cgg cgc ctc ttc ccc tcg ctc agc tgg gcc aac 1420
Tyr Ser Thr Asn Ile Arg Arg Leu Phe Pro Ser 95 Leu Ser Trp Ala Asn
                                         85 90 100

atc aag aaa aac ctc gag caa tac tcg acc ttc cac acg cgc ttc tca 1468
Ile Lys Lys Asn Leu Glu Gln Tyr Ser Thr Phe His Thr Arg Phe Ser
                                         105 110 115

gaa acc caa tct gcc gcc gac gct gcc cag tgg ctc ctc gcc caa gtc 1516
Glu Thr Gln Ser Gly Ala Asp Ala Ala Gln Trp Leu Leu Ala Gln Val
                                         120 125 130

caa gcc gtg gtc aag caa gcc aac aaa tcg ggc gtc aca gcc tct gcc 1564
Gln Ala Val Val Lys Gln Ala Asn Lys Ser Gly Val Thr Ala Ser Ala
                                         135 140 145

ttc ccc cac tcg ctc tgg ccg caa aac tca atc ata gcc cgc atc caa 1612
Phe Pro His Ser Leu Trp Pro Gln Asn Ser Ile Ile Ala Arg Ile Gln
                                         150 155 160

ggc cgc tcc aac cgc act gtc gtc gta ggc gcc cac ctc gac tcc atc 1660
Gly Arg Ser Asn Arg Thr Val Val Val Gly Ala His Leu Asp Ser Ile
                                         165 170 175 180

aac tcg gcc aac cgc ctc acc ggc cgc gcc ccg ggc gtc gac gac gac 1708
Asn Ser Ala Asn Arg Leu Thr Gly Arg Ala Pro Gly Val Asp Asp Asp
                                         185 190 195

ggc agc ggc tcc atg ctt ctt ctc gag gcc ctg cgc gtg ctg ctc acc 1756
Gly Ser Gly Ser Met Leu Leu Leu Glu Ala Leu Arg Val Leu Leu Thr

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200	205	210	
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ttc cac tgg tat gcc gct gaa gag ggc ggt ctc cgc ggg agc caa gac	Phe His Trp Tyr Ala Ala Glu Glu Gly Gly Leu Arg Gly Ser Gln Asp	1852	
atc ttc acg cag tac aag aac gca gga aga gag atc tgg gct atg ctg	Ile Phe Thr Gln Tyr Lys Asn Ala Gly Arg Glu Ile Trp Ala Met Leu	1900	
cag cag gat atg gtg ggg tac aca aag ggg acg ctg gat gcg ggc aag	Gln Gln Asp Met Val Gly Tyr Thr Lys Gly Thr Leu Asp Ala Gly Lys	1948	
ccc gag agt ttt ggg ctg att acg gat ttt acg gat gcc gtc ttg aat	Pro Glu Ser Phe Gly Leu Ile Thr Asp Phe Thr Asp Ala Val Leu Asn	1996	
cag tat ttg gta aaa gtg att ggt gag gtatgtaaat ttttttggtt	Gln Tyr Leu Val Lys Val Ile Gly Glu	2043	
cctttttcccc ttctctctnnn nnnnnnnnnn nnnnnnnccc ccccccccc cctccgtag	acctttttccc ctctttttgc tgcaaaggga gggagacaag aaagaagaat acacaatgct	2103	
gatgttgatc cag tac acc gat atc acc tat gtc aac agc acg tgc ggt	Tyr Thr Asp Ile Thr Tyr Val Asn Ser Thr Cys Gly	2163	
	305 310	2212	
tat gca tgc tca gac cac ggt tcc gcc atg cgc agt gga tac cct gcc	Tyr Ala Cys Ser Asp His Gly Ser Ala Met Arg Ser Gly Tyr Pro Ala	2260	
tgc ttt gtc ttt gag tct gac ttc cgg tac cgc aat ccg tat atc cat	Ser Phe Val Phe Glu Ser Asp Phe Arg Tyr Arg Asn Pro Tyr Ile His	2308	
act ccg aac gat acc atg gag cac atg gac cct aac cac gtg ttg caa	Thr Pro Asn Asp Thr Met Glu His Met Asp Pro Asn His Val Leu Gln	2356	
cat gga cgc ttg gtg ctg ggc tat ttg tat gaa ctt ggg ttt agc aag	His Gly Arg Leu Val Leu Gly Tyr Leu Tyr Glu Leu Gly Phe Ser Lys	2404	
gcc taaggggggtt ctttacaat gggctctcac aatgtagttg tgcgcgggtt	Ala	2457	
gttgtgtaaa tgtgaatatg gatatgacat tttcttttga tgggttatgt acacatatat	gaaaaaattc agatatgatt ttgtctcttg tattgtttgc ctgtcatctc aaagaccacg	2517	
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gaaagtgtat gacgagaaaa cttgggtgaga caaggctcat ttgaattttg acatcgtgag	gcacgctgag caaatgaact tggataatgg attaacgtct gacacgaagc aagattaaca	2637	
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tacacaagaa gagcaataat cagtataatg aaatctttga aaaaagaaat gtgagtatgt	gtggggaggg ggggaggggg gggtaaagaa aacgtgaggt aataaagtct tgggcacaaa	2877	
tcttgacagga tagatggaaa cgctaaattg cagaaatctg gaaatgaaag agaaaacagga	tatcaagaag aatagaaaat tggcttcttt ttggctgcag atgctccctg	2937	
		2997	
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		3237	
		3297	
		3357	
		3407	

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<210> 161
 <211> 52
 <212> PRT
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 161
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 Ala Lys Gly Pro Glu Arg Val Ser Asn Ala Ala Arg Ser Ile Thr Ile
 20 25 30
 Glu Val Ala Pro Gly Glu Thr Arg Gln Ile Thr Glu Asp Glu Arg Trp
 35 40 45
 Asp Ile Ala Thr
 50

<210> 162
 <211> 249
 <212> PRT
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 162
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 1 5 10 15
 Glu Pro Ile Ala Val Thr Arg Ala Ala Tyr Pro Ser Thr Phe Gln
 20 25 30
 Tyr Ser Thr Asn Ile Arg Arg Leu Phe Pro Ser Leu Ser Trp Ala Asn
 35 40 45
 Ile Lys Lys Asn Leu Glu Gln Tyr Ser Thr Phe His Thr Arg Phe Ser
 50 55 60
 Glu Thr Gln Ser Gly Ala Asp Ala Ala Gln Trp Leu Leu Ala Gln Val
 65 70 75 80
 Gln Ala Val Val Lys Gln Ala Asn Lys Ser Gly Val Thr Ala Ser Ala
 85 90 95
 Phe Pro His Ser Leu Trp Pro Gln Asn Ser Ile Ile Ala Arg Ile Gln
 100 105 110
 Gly Arg Ser Asn Arg Thr Val Val Val Gly Ala His Leu Asp Ser Ile
 115 120 125
 Asn Ser Ala Asn Arg Leu Thr Gly Arg Ala Pro Gly Val Asp Asp Asp
 130 135 140
 Gly Ser Gly Ser Met Leu Leu Leu Glu Ala Leu Arg Val Leu Leu Thr
 145 150 155 160
 Asp Ser Ala Phe Ala Gly Ser Asn Asn Leu Leu Glu Asn Thr Ile Glu
 165 170 175
 Phe His Trp Tyr Ala Ala Glu Glu Gly Leu Arg Gly Ser Gln Asp
 180 185 190
 Ile Phe Thr Gln Tyr Lys Asn Ala Gly Arg Glu Ile Trp Ala Met Leu
 195 200 205
 Gln Gln Asp Met Val Gly Tyr Thr Lys Gly Thr Leu Asp Ala Gly Lys
 210 215 220
 Pro Glu Ser Phe Gly Leu Ile Thr Asp Phe Thr Asp Ala Val Leu Asn
 225 230 235 240
 Gln Tyr Leu Val Lys Val Ile Gly Glu
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<210> 163
 <211> 77
 <212> PRT
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

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 Asp His Gly Ser Ala Met Arg Ser Gly Tyr Pro Ala Ser Phe Val Phe
 20 25 30
 Glu Ser Asp Phe Arg Tyr Arg Asn Pro Tyr Ile His Thr Pro Asn Asp
 35 40 45
 Thr Met Glu His Met Asp Pro Asn His Val Leu Gln His Gly Arg Leu

10336256.txt

50 55 60
Val Leu Gly Tyr Leu Tyr Glu Leu Gly Phe Ser Lys Ala
65 70 75

<210> 164
<211> 1134
<212> DNA
<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>
<221> CDS
<222> (1)...(1134)

<400> 164

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gcc aag gga ccc gag cga gtt agc aat gcg gcg agg agt att acg att	96
Ala Lys Gly Pro Glu Arg Val Ser Asn Ala Ala Arg Ser Ile Thr Ile	
20 25 30	
gaa gtt gcg ccg ggg gag acg cgc cag att act gag gat gag agg tgg	144
Glu Val Ala Pro Gly Glu Thr Arg Gln Ile Thr Glu Asp Glu Arg Trp	
35 40 45	
gat att gct act ggc ggc ggt tgt gga agc cac ttc ttc gac att acg	192
Asp Ile Ala Thr Gly Gly Gly Cys Gly Ser His Phe Phe Asp Ile Thr	
50 55 60	
gat tcg ttc gcc gaa ccc ata gcc gtc acg cgc gcg gcc gcc tac cca	240
Asp Ser Phe Ala Glu Pro Ile Ala Val Thr Arg Ala Ala Ala Tyr Pro	
65 70 75 80	
tcc acc ttc caa tac agc acc aac atc cgg cgc ctc ttc ccc tcg ctc	288
Ser Thr Phe Gln Tyr Ser Thr Asn Ile Arg Arg Leu Phe Pro Ser Leu	
85 90 95	
agc tgg gcc aac atc aag aaa aac ctc gag caa tac tcg acc ttc cac	336
Ser Trp Ala Asn Ile Lys Lys Asn Leu Glu Gln Tyr Ser Thr Phe His	
100 105 110	
acg cgc ttc tca gaa acc caa tct ggc gcc gac gct gcc cag tgg ctc	384
Thr Arg Phe Ser Glu Thr Gln Ser Gly Ala Asp Ala Ala Gln Trp Leu	
115 120 125	
ctc gcc caa gtc caa gcc gtg gtc aag caa gcc aac aaa tcg ggc gtc	432
Leu Ala Gln Val Gln Ala Val Val Lys Gln Ala Asn Lys Ser Gly Val	
130 135 140	
aca gcc tct gcc ttc ccc cac tcg ctc tgg ccg caa aac tca atc ata	480
Thr Ala Ser Ala Phe Pro His Ser Leu Trp Pro Gln Asn Ser Ile Ile	
145 150 155 160	
gcc cgc atc caa ggc cgc tcc aac cgc act gtc gtc gta ggc gcc cac	528
Ala Arg Ile Gln Gly Arg Ser Asn Arg Thr Val Val Val Gly Ala His	
165 170 175	
ctc gac tcc atc aac tcg gcc aac cgc ctc acc ggc cgc gcc ccg ggc	576
Leu Asp Ser Ile Asn Ser Ala Asn Arg Leu Thr Gly Arg Ala Pro Gly	
180 185 190	
gtc gac gac gac ggc agc ggc tcc atg ctt ctt ctc gag gcc ctg cgc	624
Val Asp Asp Asp Gly Ser Gly Ser Met Leu Leu Leu Glu Ala Leu Arg	
195 200 205	
gtg ctg ctc acc gac tcg gcc ttt gca ggc tcc aac aac ctt ctc gag	672
Val Leu Leu Thr Asp Ser Ala Phe Ala Gly Ser Asn Asn Leu Leu Glu	

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220

210	215		
aac acg att gag ttc cac tgg tat gcc gct gaa gag ggc ggt ctc cgc Asn Thr Ile Glu Phe His Trp Tyr Ala Ala Glu Glu Gly Gly Leu Arg 225 230 235 240			720
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tgg gct atg ctg cag cag gat atg gtg ggg tac aca aag ggg acg ctg Trp Ala Met Leu Gln Gln Asp Met Val Gly Tyr Thr Lys Gly Thr Leu 260 265 270			816
gat gcg ggc aag ccc gag agt ttt ggg ctg att acg gat ttt acg gat Asp Ala Gly Lys Pro Glu Ser Phe Gly Leu Ile Thr Asp Phe Thr Asp 275 280 285			864
gcc gtc ttg aat cag tat ttg gta aaa gtg att ggt gag tac acc gat Ala Val Leu Asn Gln Tyr Leu Val Lys Val Ile Gly Glu Tyr Thr Asp 290 295 300			912
atc acc tat gtc aac agc acg tgc ggt tat gca tgc tca gac cac ggt Ile Thr Tyr Val Asn Ser Thr Cys Gly Tyr Ala Cys Ser Asp His Gly 305 310 315 320			960
tcc gcc atg cgc agt gga tac cct gcc tcg ttt gtc ttt gag tct gac Ser Ala Met Arg Ser Gly Tyr Pro Ala Ser Phe Val Phe Glu Ser Asp 325 330 335			1008
ttc cgg tac cgc aat ccg tat atc cat act ccg aac gat acc atg gag Phe Arg Tyr Arg Asn Pro Tyr Ile His Thr Pro Asn Asp Thr Met Glu 340 345 350			1056
cac atg gac cct aac cac gtg ttg caa cat gga cgc ttg gtg ctg ggc His Met Asp Pro Asn His Val Leu Gln His Gly Arg Leu Val Leu Gly 355 360 365			1104
tat ttg tat gaa ctt ggg ttt agc aag gcc Tyr Leu Tyr Glu Leu Gly Phe Ser Lys Ala 370 375			1134

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<211> 378

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> SIGNAL

<222> (1)...(17)

<221> DOMAIN

<222> (128)...(378)

<223> Peptidase family M28

<400> 165

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20 25 30
Glu Val Ala Pro Gly Glu Thr Arg Gln Ile Thr Glu Asp Glu Arg Trp
35 40 45
Asp Ile Ala Thr Gly Gly Gly Cys Gly Ser His Phe Phe Asp Ile Thr
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Asp Ser Phe Ala Glu Pro Ile Ala Val Thr Arg Ala Ala Ala Tyr Pro
65 70 75 80
Ser Thr Phe Gln Tyr Ser Thr Asn Ile Arg Arg Leu Phe Pro Ser Leu

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Ser Trp Ala Asn Ile Lys Lys Asn Leu Glu Gln Tyr Ser Thr Phe His
 85 90 95
 100 105 110
 Thr Arg Phe Ser Glu Thr Gln Ser Gly Ala Asp Ala Ala Gln Trp Leu
 115 120 125
 Leu Ala Gln Val Gln Ala Val Val Lys Gln Ala Asn Lys Ser Gly Val
 130 135 140
 Thr Ala Ser Ala Phe Pro His Ser Leu Trp Pro Gln Asn Ser Ile Ile
 145 150 155 160
 Ala Arg Ile Gln Gly Arg Ser Asn Arg Thr Val Val Val Gly Ala His
 165 170 175
 Leu Asp Ser Ile Asn Ser Ala Asn Arg Leu Thr Gly Arg Ala Pro Gly
 180 185 190
 Val Asp Asp Gly Ser Gly Ser Met Leu Leu Leu Glu Ala Leu Arg
 195 200 205
 Val Leu Leu Thr Asp Ser Ala Phe Ala Gly Ser Asn Asn Leu Leu Glu
 210 215 220
 Asn Thr Ile Glu Phe His Trp Tyr Ala Ala Glu Glu Gly Gly Leu Arg
 225 230 235 240
 Gly Ser Gln Asp Ile Phe Thr Gln Tyr Lys Asn Ala Gly Arg Glu Ile
 245 250 255
 Trp Ala Met Leu Gln Gln Asp Met Val Gly Tyr Thr Lys Gly Thr Leu
 260 265 270
 Asp Ala Gly Lys Pro Glu Ser Phe Gly Leu Ile Thr Asp Phe Thr Asp
 275 280 285
 Ala Val Leu Asn Gln Tyr Leu Val Lys Val Ile Gly Glu Tyr Thr Asp
 290 295 300
 Ile Thr Tyr Val Asn Ser Thr Cys Gly Tyr Ala Cys Ser Asp His Gly
 305 310 315 320
 Ser Ala Met Arg Ser Gly Tyr Pro Ala Ser Phe Val Phe Glu Ser Asp
 325 330 335
 Phe Arg Tyr Arg Asn Pro Tyr Ile His Thr Pro Asn Asp Thr Met Glu
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 His Met Asp Pro Asn His Val Leu Gln His Gly Arg Leu Val Leu Gly
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<210> 166

<211> 4437

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1834)...(1854)

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<222> (1932)...(2114)

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<222> (3204)...(3437)

<223> Exon

<400> 166

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caatgcctcg	gcagccgtct	tcgacctgcc	cgttgtcatc	aagagcacat	acagcagcgt	300
aagtttcgac	atcggcacgc	ccccgaaaga	acaccagcta	ctgttcgata	ccggctcgtc	360
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 atggccttgg atcactgcag acgggttttct gggccttggc ttctctacca tcgcagagcc 660
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 Met Ile Gln Ala Leu Leu Gln
 1 5

gtacgtctag ccttgcaatt gctgcctttg ctctaaaac tacctccctt ttcattcacc 1914
 actaacgcat actacag cgc ctg gcc cgc tgg ctc gac cgg ccg caa ttc 1964
 Arg Leu Ala Arg Trp Leu Asp Arg Pro Gln Phe
 10 15

cca tgg aag cgc ctg gtt gtc ggc ttc tcc ctc gca gaa ttt gcc ctc 2012
 Pro Trp Lys Arg Leu Val Val Gly Phe Ser Leu Ala Glu Phe Ala Leu
 20 25 30

gaa aac tgg ctt ctc ttc cgc cag tat cgt gtc ctc caa cgc acc tct 2060
 Glu Asn Trp Leu Leu Phe Arg Gln Tyr Arg Val Leu Gln Arg Thr Ser
 35 40 45 50

atc ccc aag gct ctt gac aag gaa att gaa aag gaa acg ttt gac aag 2108
 Ile Pro Lys Ala Leu Asp Lys Glu Ile Glu Lys Glu Thr Phe Asp Lys
 55 60 65

tct cag gtgcgcctcc cctcgccgcc ccactgaggc cagacatggc gccaatcgtg 2164
 Ser Gln

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 Gln Tyr Gly Arg Ala Lys Ala Arg Phe
 70 75

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 Ser Phe Ile Ser Gly Val Phe Asn Gln Leu Lys His Leu Ala Ser Leu
 80 85 90

tac ttc aac cta tac ccg ttt gtc tgg acc gcc gcc ggc act gtc ctc 2312
 Tyr Phe Asn Leu Tyr Pro Phe Val Trp Thr Ala Ala Gly Thr Val Leu
 95 100 105

gcc cgc tat gcg ccc gcc cgc ttt tcg ggc gag ata tcg cag tcg ctc 2360
 Ala Arg Tyr Ala Pro Ala Arg Phe Ser Gly Glu Ile Ser Gln Ser Leu
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 Leu Phe Met Tyr Met Leu Gly Trp Ile Asp Leu Val Ala Ser Leu Gly
 130 135 140

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aag atg acg gtc aag ctc tgg ctc acg gat atg gtc aag ggc cag gcg	2504
Lys Met Thr Val Lys Leu Trp Leu Thr Asp Met Val Lys Gly Gln Ala	
160 165 170	
ctc gcc att gca ttt ggt att ccg att gga agc gcc ttc ctg gcc att	2552
Leu Ala Ile Ala Phe Gly Ile Pro Ile Gly Ser Ala Phe Leu Ala Ile	
175 180 185	
atc aat aag acg ggg cag ggc ttt ttc tac tac ctg tgg atg ttc atg	2600
Ile Asn Lys Thr Gly Gln Gly Phe Phe Tyr Tyr Leu Trp Met Phe Met	
190 195 200 205	
cta gtt gtg cag att acc ggc atg act gtc tac ccg atc ctc att gtg	2648
Leu Val Val Gln Ile Thr Gly Met Thr Val Tyr Pro Ile Leu Ile Val	
210 215 220	
ccc ctg ttc aac aag ctg gag ccg ctc aag ccc ggc aaa ctc aag gag	2696
Pro Leu Phe Asn Lys Leu Glu Pro Leu Lys Pro Gly Lys Leu Lys Glu	
225 230 235	
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Ser Val Glu Ala Leu Ala Ser Lys Leu Asn Phe Pro Leu Ser Glu Leu	
240 245 250	
cag gtc att gac ggc agc aag cgc agt gct cac agc aat gcc tac ttc	2792
Gln Val Ile Asp Gly Ser Lys Arg Ser Ala His Ser Asn Ala Tyr Phe	
255 260 265	
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Thr Gly Leu Pro Trp Ile Gly Lys Lys Lys Ile Val Ile Tyr Asp Thr	
270 275 280 285	
ctg ctg gaa aag agc acg gag aag gag gtc gag gct gta ctg gca cac	2888
Leu Leu Glu Lys Ser Thr Glu Lys Glu Val Glu Ala Val Leu Ala His	
290 295 300	
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Glu Leu Gly His Trp Lys Met Asn His Thr Ser Arg Leu Leu Phe Ile	
305 310 315	
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Ser Gln Ala His Leu Phe Tyr Ile Phe Ala Leu Phe Ser Val Phe Ile	
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Asn Asn Arg Ser Leu Tyr Ala Asp Phe Gly Phe His Arg Glu Gln Pro	
335 340 345	
acc att gtt ggt ttc atg ctc ttc aac gag att ctg tcg ccc acg gac	3080
Thr Ile Val Gly Phe Met Leu Phe Asn Glu Ile Leu Ser Pro Thr Asp	
350 355 360 365	
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Ser Ile Val Lys Leu Leu Leu Asn Ile Trp Thr Arg Ser Met Glu Tyr	
370 375 380	
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Glu Ala	
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385 390	

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 Glu Leu Gly Ala Ser Leu Ile Lys Leu Gln Ile Gln Asn Leu Ser Ser
 395 400 405 410

atg gat gcc gac tgg ttc tac tcg agc ttc cac cac tcg cac ccc att 3332
 Met Asp Ala Asp Trp Phe Tyr Ser Ser Phe His His Ser His Pro Ile
 415 420 425

ttg acg gag cgt ctc aag gct atg aaa tgg act ggt gag aag aag att 3380
 Leu Thr Glu Arg Leu Lys Ala Met Lys Trp Thr Gly Glu Lys Lys Ile
 430 435 440

gtg gtt gac aag gcg gcc gac gag gac aag gct gta aag gca gcg gat 3428
 Val Val Asp Lys Ala Ala Asp Glu Asp Lys Ala Val Lys Ala Ala Asp
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cgg gag ctg taggcgctgg tgggtggtgg tgggtgctgt gagtgtgcga 3477
 Arg Glu Leu
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<210> 167

<211> 7

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 167

Met Ile Gln Ala Leu Leu Gln
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<210> 168

<211> 61

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 168

Arg Leu Ala Arg Trp Leu Asp Arg Pro Gln Phe Pro Trp Lys Arg Leu
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 Val Val Gly Phe Ser Leu Ala Glu Phe Ala Leu Glu Asn Trp Leu Leu
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 Phe Arg Gln Tyr Arg Val Leu Gln Arg Thr Ser Ile Pro Lys Ala Leu
 35 40 45
 Asp Lys Glu Ile Glu Lys Glu Thr Phe Asp Lys Ser Gln
 50 55 60

<210> 169

<211> 315

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 169

Gln Tyr Gly Arg Ala Lys Ala Arg Phe Ser Phe Ile Ser Gly Val Phe

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Asn Gln Leu Lys His Leu Ala Ser Leu Tyr Phe Asn Leu Tyr Pro Phe
20
Val Trp Thr Ala Ala Gly Thr Val 25 Leu Ala Arg Tyr Ala Pro Ala Arg
35
Phe Ser Gly Glu Ile Ser Gln Ser Leu Leu Phe Met Tyr Met Leu Gly
50
Trp Ile Asp Leu Val Ala Ser Leu Gly Phe Ser Tyr Tyr His Ser Phe
65
Val Leu Glu Glu Lys Phe Gly Phe Asn Lys Met Thr Val Lys Leu Trp
85
Leu Thr Asp Met Val Lys Gly Gln Ala Leu Ala Ile Ala Phe Gly Ile
100
Pro Ile Gly Ser Ala Phe Leu Ala Ile Ile Asn Lys Thr Gly Gln Gly
115
Phe Phe Tyr Tyr Leu Trp Met Phe Met Leu Val Val Gln Ile Thr Gly
130
Met Thr Val Tyr Pro Ile Leu Ile Val Pro Leu Phe Asn Lys Leu Glu
145
Pro Leu Lys Pro Gly Lys Leu Lys Glu Ser Val Glu Ala Leu Ala Ser
165
Lys Leu Asn Phe Pro Leu Ser Glu Leu Gln Val Ile Asp Gly Ser Lys
180
Arg Ser Ala His Ser Asn Ala Tyr Phe Thr Gly Leu Pro Trp Ile Gly
195
Lys Lys Lys Ile Val Ile Tyr Asp Thr Leu Leu Glu Lys Ser Thr Glu
210
Lys Glu Val Glu Ala Val Leu Ala His Glu Leu Gly His Trp Lys Met
225
Asn His Thr Ser Arg Leu Leu Phe Ile Ser Gln Ala His Leu Phe Tyr
245
Ile Phe Ala Leu Phe Ser Val Phe Ile Asn Asn Arg Ser Leu Tyr Ala
260
Asp Phe Gly Phe His Arg Glu Gln Pro Thr Ile Val Gly Phe Met Leu
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Phe Asn Glu Ile Leu Ser Pro Thr Asp Ser Ile Val Lys Leu Leu Leu
290
Asn Ile Trp Thr Arg Ser Met Glu Tyr Glu Ala
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315

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<210> 170

<211> 78

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 170

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Leu Ile Lys Leu Gln Ile Gln Asn Leu Ser Ser Met Asp Ala Asp Trp
20
Phe Tyr Ser Ser Phe His His Ser His Pro Ile Leu Thr Glu Arg Leu
35
Lys Ala Met Lys Trp Thr Gly Glu Lys Lys Ile Val Val Asp Lys Ala
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Ala Asp Glu Asp Lys Ala Val Lys Ala Ala Asp Arg Glu Leu
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70
75

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<210> 171

<211> 1383

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1383)

<400> 171

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Gln	Phe	Pro	Trp	Lys	Arg	Leu	Val	Val	Gly	Phe	Ser	Leu	Ala	Glu	Phe		
			20					25					30				
gcc	ctc	gaa	aac	tgg	ctt	ctc	ttc	cgc	cag	tat	cgt	gtc	ctc	caa	cgc		144
Ala	Leu	Glu	Asn	Trp	Leu	Leu	Phe	Arg	Gln	Tyr	Arg	Val	Leu	Gln	Arg		
			35				40					45					
acc	tct	atc	ccc	aag	gct	ctt	gac	aag	gaa	att	gaa	aag	gaa	acg	ttt		192
Thr	Ser	Ile	Pro	Lys	Ala	Leu	Asp	Lys	Glu	Ile	Glu	Lys	Glu	Thr	Phe		
			50			55					60						
gac	aag	tct	cag	caa	tat	ggt	cgc	gcc	aaa	gca	agg	ttc	agc	ttc	atc		240
Asp	Lys	Ser	Gln	Gln	Tyr	Gly	Arg	Ala	Lys	Ala	Arg	Phe	Ser	Phe	Ile		
					70				75						80		
tcc	ggt	gtc	ttc	aac	cag	ctc	aag	cac	cta	gcc	tct	ctc	tac	ttc	aac		288
Ser	Gly	Val	Phe	Asn	Gln	Leu	Lys	His	Leu	Ala	Ser	Leu	Tyr	Phe	Asn		
				85					90					95			
cta	tac	ccg	ttt	gtc	tgg	acc	gcc	gcc	ggc	act	gtc	ctc	gcc	cgc	tat		336
Leu	Tyr	Pro	Phe	Val	Trp	Thr	Ala	Ala	Gly	Thr	Val	Leu	Ala	Arg	Tyr		
			100					105					110				
gcg	ccc	gcc	cgc	ttt	tcg	ggc	gag	ata	tcg	cag	tcg	ctc	ttg	ttc	atg		384
Ala	Pro	Ala	Arg	Phe	Ser	Gly	Glu	Ile	Ser	Gln	Ser	Leu	Leu	Phe	Met		
			115				120					125					
tac	atg	ctc	ggc	tgg	atc	gac	ttg	gtc	gcc	agt	ctc	ggt	ttc	tcg	tac		432
Tyr	Met	Leu	Gly	Trp	Ile	Asp	Leu	Val	Ala	Ser	Leu	Gly	Phe	Ser	Tyr		
						135					140						
tac	cac	agc	ttc	gtc	ctg	gaa	gaa	aag	ttt	ggc	ttc	aat	aag	atg	acg		480
Tyr	His	Ser	Phe	Val	Leu	Glu	Glu	Lys	Phe	Gly	Phe	Asn	Lys	Met	Thr		
					150				155						160		
gtc	aag	ctc	tgg	ctc	acg	gat	atg	gtc	aag	ggc	cag	gcg	ctc	gcc	att		528
Val	Lys	Leu	Trp	Leu	Thr	Asp	Met	Val	Lys	Gly	Gln	Ala	Leu	Ala	Ile		
				165					170					175			
gca	ttt	ggt	att	ccg	att	gga	agc	gcc	ttc	ctg	gcc	att	atc	aat	aag		576
Ala	Phe	Gly	Ile	Pro	Ile	Gly	Ser	Ala	Phe	Leu	Ala	Ile	Ile	Asn	Lys		
				180				185					190				
acg	ggg	cag	ggc	ttt	ttc	tac	tac	ctg	tgg	atg	ttc	atg	cta	gtt	gtg		624
Thr	Gly	Gln	Gly	Phe	Phe	Tyr	Tyr	Leu	Trp	Met	Phe	Met	Leu	Val	Val		
				195			200					205					
cag	att	acc	ggc	atg	act	gtc	tac	ccg	atc	ctc	att	gtg	ccc	ctg	ttc		672
Gln	Ile	Thr	Gly	Met	Thr	Val	Tyr	Pro	Ile	Leu	Ile	Val	Pro	Leu	Phe		
						215					220						
aac	aag	ctg	gag	ccg	ctc	aag	ccc	ggc	aaa	ctc	aag	gag	tca	gtc	gag		720
Asn	Lys	Leu	Glu	Pro	Leu	Lys	Pro	Gly	Lys	Leu	Lys	Glu	Ser	Val	Glu		
					230				235						240		
gca	ctt	gct	tcc	aag	ctc	aac	ttt	cct	ctt	tcg	gag	ctg	cag	gtc	att		768
Ala	Leu	Ala	Ser	Lys	Leu	Asn	Phe	Pro	Leu	Ser	Glu	Leu	Gln	Val	Ile		
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gac	ggc	agc	aag	cgc	agt	gct	cac	agc	aat	gcc	tac	ttc	acg	ggc	cta		816
Asp	Gly	Ser	Lys	Arg	Ser	Ala	His	Ser	Asn	Ala	Tyr	Phe	Thr	Gly	Leu		
			260					265					270				
ccc	tgg	att	ggc	aag	aag	aag	att	gtc	atc	tac	gac	aca	ctg	ctg	gaa		864

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 275 280 285

aag agc acg gag aag gag gtc gag gct gta ctg gca cac gag ctc ggt 912
 Lys Ser Thr Glu Lys Glu Val Glu Ala Val Leu Ala His Glu Leu Gly
 290 295 300

cac tgg aag atg aac cac acg tcg cga ctt ctc ttt att agc caa gcg 960
 His Trp Lys Met Asn His Thr Ser Arg Leu Leu Phe Ile Ser Gln Ala
 305 310 315 320

cat cta ttc tac att ttt gcc ctt ttc tcc gtc ttc atc aac aac cgg 1008
 His Leu Phe Tyr Ile Phe Ala Leu Phe Ser Val Phe Ile Asn Asn Arg
 325 330 335

tcg ctg tac gca gac ttt ggc ttc cac cgg gag cag ccg acc att gtt 1056
 Ser Leu Tyr Ala Asp Phe Phe His Arg Glu Gln Pro Thr Ile Val
 340 345

ggt ttc atg ctc ttc aac gag att ctg tcg ccc acg gac tcg atc gtc 1104
 Gly Phe Met Leu Phe Asn Glu Ile Leu Ser Pro Thr Asp Ser Ile Val
 355 360 365

aag ctt ctc ctt aac atc tgg acc cgc agc atg gag tac gaa gca gat 1152
 Lys Leu Leu Leu Asn Ile Trp Thr Arg Ser Met Glu Tyr Glu Ala Asp
 370 375 380

gct ttt gct gtc aaa ctt gga tat gcg cgc gag cta ggc gca tcg tta 1200
 Ala Phe Ala Val Lys Leu Gly Tyr Ala Arg Glu Leu Gly Ala Ser Leu
 385 390 395 400

atc aag ctg cag att cag aac cta tcg agc atg gat gcc gac tgg ttc 1248
 Ile Lys Leu Gln Ile Gln Asn Leu Ser Ser Met Asp Ala Asp Trp Phe
 405 410 415

tac tcg agc ttc cac cac tcg cac ccc att ttg acg gag cgt ctc aag 1296
 Tyr Ser Ser Phe His His Ser His Pro Ile Leu Thr Glu Arg Leu Lys
 420 425 430

gct atg aaa tgg act ggt gag aag aag att gtg gtt gac aag gcg gcc 1344
 Ala Met Lys Trp Thr Gly Glu Lys Lys Ile Val Val Asp Lys Ala Ala
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gac gag gac aag gct gta aag gca gcg gat cgg gag ctg 1383
 Asp Glu Asp Lys Ala Val Lys Ala Ala Asp Arg Glu Leu
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<210> 172

<211> 461

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> DOMAIN

<222> (239)...(439)

<223> Peptidase family M48

<400> 172

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 Ala Leu Glu Asn Trp Leu Leu Phe Arg Gln Tyr Arg Val Leu Gln Arg
 35 40 45
 Thr Ser Ile Pro Lys Ala Leu Asp Lys Glu Ile Glu Lys Glu Thr Phe
 50 55 60
 Asp Lys Ser Gln Gln Tyr Gly Arg Ala Lys Ala Arg Phe Ser Phe Ile

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65      70      75      80
Ser Gly Val Phe Asn Gln Leu Lys His Leu Ala Ser Leu Tyr Phe Asn
85      90      95
Leu Tyr Pro Phe Val Trp Thr Ala Ala Gly Thr Val Leu Ala Arg Tyr
100     105
Ala Pro Ala Arg Phe Ser Gly Glu Ile Ser Gln Ser Leu Leu Phe Met
115     120     125
Tyr Met Leu Gly Trp Ile Asp Leu Val Ala Ser Leu Gly Phe Ser Tyr
130     135     140
Tyr His Ser Phe Val Leu Glu Glu Lys Phe Gly Phe Asn Lys Met Thr
145     150     155     160
Val Lys Leu Trp Leu Thr Asp Met Val Lys Gly Gln Ala Leu Ala Ile
165     170     175
Ala Phe Gly Ile Pro Ile Gly Ser Ala Phe Leu Ala Ile Ile Asn Lys
180     185     190
Thr Gly Gln Gly Phe Phe Tyr Tyr Leu Trp Met Phe Met Leu Val Val
195     200     205
Gln Ile Thr Gly Met Thr Val Tyr Pro Ile Leu Ile Val Pro Leu Phe
210     215     220
Asn Lys Leu Glu Pro Leu Lys Pro Gly Lys Leu Lys Glu Ser Val Glu
225     230     235     240
Ala Leu Ala Ser Lys Leu Asn Phe Pro Leu Ser Glu Leu Gln Val Ile
245     250     255
Asp Gly Ser Lys Arg Ser Ala His Ser Asn Ala Tyr Phe Thr Gly Leu
260     265     270
Pro Trp Ile Gly Lys Lys Lys Ile Val Ile Tyr Asp Thr Leu Leu Glu
275     280     285
Lys Ser Thr Glu Lys Glu Val Glu Ala Val Leu Ala His Glu Leu Gly
290     295     300
His Trp Lys Met Asn His Thr Ser Arg Leu Leu Phe Ile Ser Gln Ala
305     310     315     320
His Leu Phe Tyr Ile Phe Ala Leu Phe Ser Val Phe Ile Asn Asn Arg
325     330     335
Ser Leu Tyr Ala Asp Phe Gly Phe His Arg Glu Gln Pro Thr Ile Val
340     345     350
Gly Phe Met Leu Phe Asn Glu Ile Leu Ser Pro Thr Asp Ser Ile Val
355     360     365
Lys Leu Leu Leu Asn Ile Trp Thr Arg Ser Met Glu Tyr Glu Ala Asp
370     375     380
Ala Phe Ala Val Lys Leu Gly Tyr Ala Arg Glu Leu Gly Ala Ser Leu
385     390     395     400
Ile Lys Leu Gln Ile Gln Asn Leu Ser Ser Met Asp Ala Asp Trp Phe
405     410     415
Tyr Ser Ser Phe His His Ser His Pro Ile Leu Thr Glu Arg Leu Lys
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<210> 173

<211> 3237

<212> DNA

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1440)...(1808) .

<223> Exon

<221> CDS

<222> (1862)...(2044)

<223> Exon

<221> CDS

<222> (2096)...(2211)

<223> Exon

10336256.txt

<221> CDS
 <222> (2263) ... (2353)
 <223> Exon

<221> CDS
 <222> (2448) ... (3011)
 <223> Exon

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 tgctttattc gaatccgggg cgctcggcagc catgctcggc aataatccag aaaccctgtt 180
 tcacaacgtg ctcttatcgg atagttgcgt ttaatatgag gaagaaattg aggaagaagg 240
 acaagagggt ggatgatgaa gtatagttct tatcgtgact tggctgcgac aaagacggct 300
 aggaactgtt cgattcagct gcgttttccc tctatatattc attcccgtct tggatttgaa 360
 gcttcgatag ggagtgtctag ctgcttactc ttatagccca gtctttccaa actgggatatg 420
 gaaatggaag gggtattcag ttggaggctc gttttatgtt aattcgagga tcacgtgatg 480
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 acctaaggct acattctcgt agcttttagat gcgcatataa ccgaacacgc tagtagcttc 600
 atgagttccg tttccgaaac ggaacctgaa ttggggaaat agaacgcaga atgtagcttg 660
 caattcgcgc aaccgaacaa gctttccagc cctgttttgt agatggagcg gacggaaaac 720
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 gggtgttgcc tttgtacaca agtcggcact tagtcccatt attagaccgt ggcaagttgc 960
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 tatccacgac tatcccgtgt atccagcgga catgtataat gtcaccgtgc gcctgtagta 1260
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 ttccatggac tgcggtcttg ccaagcaaac gcatagtgaa agggatataa agtgaggttc 1380
 gggcaagagt tataaacttc cctcttacac ccgcccgtt gggtgctcgt cagggtcatc 1439
 atg aag ttt gta ttc aac ctt gcc tgg ctg tgc ctt gct gct ggc gcg 1487
 Met Lys Phe Val Phe Asn Leu Ala Trp Leu Ser Leu Ala Ala Gly Ala
 1 5 10 15
 act att cgc agc tcg cag cca gtt acc tac gat ggc tac cag gtc cac 1535
 Thr Ile Arg Ser Ser Gln Pro Val Thr Tyr Asp Gly Tyr Gln Val His
 20 25 30
 cgc atc cgg gcc att ggt caa cag ggc gtg atg gca aag cgt gca atg 1583
 Arg Ile Arg Ala Ile Gly Gln Gln Gly Val Met Ala Lys Arg Ala Met
 35 40 45
 tcg tcc att cct cac gag acg ctc aat gaa gct cga ggt tcc tgg gac 1631
 Ser Ser Ile Pro His Glu Thr Leu Asn Glu Ala Arg Gly Ser Trp Asp
 50 55 60
 gtg ctc att gca cca gac caa ctc gat gca ttc agc cgc ctc ggg ctg 1679
 Val Leu Ile Ala Pro Asp Gln Leu Asp Ala Phe Ser Arg Leu Gly Leu
 65 70 75 80
 aag tcg cga acc ctg cac aag gac ttg gcc tac tcc att gct cgc gag 1727
 Lys Ser Arg Thr Leu His Lys Asp Leu Ala Tyr Ser Ile Ala Arg Glu
 85 90 95
 cgt caa gtc agg aat gtt tgg aag agg caa tca aac ggc tct gat gat 1775
 Arg Gln Val Arg Asn Val Trp Lys Arg Gln Ser Asn Gly Ser Asp Asp
 100 105 110
 gct tgg ttt gac agc tat cac ccc tat gaa gat gtaagtgcatt gtttatcagt 1828
 Ala Trp Phe Asp Ser Tyr His Pro Tyr Glu Asp
 115 120
 ctcgaggaaa gaatcatgct aacatcattg aag cac atc act tgg tgg aag gat 1882
 His Ile Thr Trp Trp Lys Asp
 125 130

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ctc cag gcc act ttc ccc gag cag tca aac tgg acg agt agc gga acg 1930
 Leu Gln Ala Thr Phe Pro Glu Gln Ser Asn Trp Thr Ser Ser Gly Thr
 135 140 145

tcc tac gag gga cgc gac ctg ttc ggt gtg cat ctc tgg gga gca ggt 1978
 Ser Tyr Glu Gly Arg Asp Leu Phe Gly Val His Leu Trp Gly Ala Gly
 150 155 160

ggc cct gga aag cct gca gtc atc tac cac ggt act gta cat gcc cgt 2026
 Gly Pro Gly Lys Pro Ala Val Ile Tyr His Gly Thr Val His Ala Arg
 165 170 175

gaa tgg atc gtc gct ccc gtttagtaaac ccaaaaaggc agttctcctt 2074
 Glu Trp Ile Val Ala Pro

atcataacta acactttata g acc att gag tac atc aca aaa cag ctc att 2125
 Thr Ile Glu Tyr Ile Thr Lys Gln Leu Ile
 185 190

gat gga tac aag gcc gga gac aac gac aca aag gca atc ttg gac aaa 2173
 Asp Gly Tyr Lys Ala Gly Asp Asn Asp Thr Lys Ala Ile Leu Asp Lys
 195 200 205 210

tac gac ttc tac atc ttt ccc ttt gtg aac ccg gat gg taagctgcga 2221
 Tyr Asp Phe Tyr Ile Phe Pro Phe Val Asn Pro Asp Gly
 215 220

ctccactgcat tgcgttgacc aattcactca cacgtgacag g t ttc gtc ttc tcc 2275
 Phe Val Phe Ser
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cag acc gac gac cgt ctc tgg cgc aag aac cgc cag ccc cca ccc gcc 2323
 Gln Thr Asp Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro Pro Ala
 230 235 240

aac caa aac caa acc tgc ttc ggc cgc gat gtaagcactc cccaacttcc 2373
 Asn Gln Asn Gln Thr Cys Phe Gly Arg Asp
 245 250

cccaaacttc gtattccaat ttcaatctca attctcaatt ccaattccag tcccactaac 2433
 catatcttgt aaag atc aac cgc aac tgg gaa aca aac tgg gac gcc gac 2483
 Ile Asn Arg Asn Trp Glu Thr Asn Trp Asp Ala Asp
 255 260 265

ccc cgc ggc gcc tgc cca gac gcc tgc tca caa gtg tac cgc ggc gag 2531
 Pro Arg Gly Ala Ser Pro Asp Ala Cys Ser Gln Val Tyr Arg Gly Glu
 270 275 280

aaa ccc cgc gac gcg ccc gaa aac gag agc atg gac aac ttc atc cgc 2579
 Lys Pro Arg Asp Ala Pro Glu Asn Glu Ser Met Asp Asn Phe Ile Arg
 285 290 295

aaa gtc cgc gac gag caa ggc att acg ctc tac att gac tgg cac agc 2627
 Lys Val Arg Asp Glu Gln Gly Ile Thr Leu Tyr Ile Asp Trp His Ser
 300 305 310

tac tcg cag ctc atc ctc ttc ccc ttt ggc cac aaa gaa acg ctc tac 2675
 Tyr Ser Gln Leu Ile Leu Phe Pro Phe Gly His Lys Glu Thr Leu Tyr
 315 320 325

gcc ccc gaa ctc ggc atg tgg acc aag acg gcc tcg ctg atg agc gag 2723
 Ala Pro Glu Leu Gly Met Trp Thr Lys Thr Ala Ser Leu Met Ser Glu
 330 335 340 345

tac att cgc gat tcg tca agg aac gat act acg tat ctg ttt ggt ccg 2771
 Tyr Ile Arg Asp Ser Ser Arg Asn Asp Thr Thr Tyr Leu Phe Gly Pro

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350	355	360	
agc gga gcg acg ctg tac ccc acg acg ggt gcg tcg att gat cat gtt	370		2819
Ser Gly Ala Thr Leu Tyr Pro Thr Thr Gly Ala Ser Ile Asp His Val			
	365	375	
tat acg att ggt agg gcc aag ttc tcg ttt aca atc gag ttg ccg gat			2867
Tyr Thr Ile Gly Arg Ala Lys Phe Ser Phe Thr Ile Glu Leu Pro Asp	385	390	
	380		
acc ggt gac ttt ggg ttt gtg ctg ccg cca gag agg atc agg cct gcg			2915
Thr Gly Asp Phe Gly Phe Val Leu Pro Pro Glu Arg Ile Arg Pro Ala	400	405	
	395		
att gag gag cag tgg gtg gga cag cag gtc ctg ctg gcg ctc ttg gac			2963
Ile Glu Glu Gln Trp Val Gly Gln Gln Val Leu Leu Ala Leu Leu Asp	415	420	
	410	425	
gag ccg ttt ttt gac ggt gtg ggc cct gcg att ggg act agt acg tgg			3011
Glu Pro Phe Phe Asp Gly Val Gly Pro Ala Ile Gly Thr Ser Thr Trp	430	435	
	440		
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tagaaagata agaaagttaga gcgagaaaag agtcaggcca tactgtgttg aaagttcatg			3131
cttggccttca agcgttgatg tgaaaagtcg gcttcacttg gccttgcattg aaactaacgt			3191
cagtgatatg agtgagagca gccgcgccat tctccatgcc ctcaat			3237

<210> 174

<211> 123

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 174

Met Lys Phe Val Phe Asn Leu Ala Trp Leu Ser Leu Ala Ala Gly Ala	5	10	15
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Arg Ile Arg Ala Ile Gly Gln Gln Gly Val Met Ala Lys Arg Ala Met			
	35	40	45
Ser Ser Ile Pro His Glu Thr Leu Asn Glu Ala Arg Gly Ser Trp Asp			
	50	55	60
Val Leu Ile Ala Pro Asp Gln Leu Asp Ala Phe Ser Arg Leu Gly Leu			
	65	70	75
Lys Ser Arg Thr Leu His Lys Asp Leu Ala Tyr Ser Ile Ala Arg Glu			
	80	85	90
Arg Gln Val Arg Asn Val Trp Lys Arg Gln Ser Asn Gly Ser Asp Asp			
	95	100	105
Ala Trp Phe Asp Ser Tyr His Pro Tyr Glu Asp			
	110	115	120

<210> 175

<211> 61

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 175

His Ile Thr Trp Trp Lys Asp Leu Gln Ala Thr Phe Pro Glu Gln Ser	5	10	15
Asn Trp Thr Ser Ser Gly Thr Ser Tyr Glu Gly Arg Asp Leu Phe Gly			
	20	25	30
Val His Leu Trp Gly Ala Gly Gly Pro Gly Lys Pro Ala Val Ile Tyr			
	35	40	45
His Gly Thr Val His Ala Arg Glu Trp Ile Val Ala Pro			
	50	55	60

<210> 176

<211> 39

<212> PRT

10336256.txt

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 176

Thr Ile Glu Tyr Ile Thr Lys Gln Leu Ile Asp Gly Tyr Lys Ala Gly
 1 5 10 15
 Asp Asn Asp Thr Lys Ala Ile Leu Asp Lys Tyr Asp Phe Tyr Ile Phe
 20 25 30
 Pro Phe Val Asn Pro Asp Gly
 35

<210> 177

<211> 30

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 177

Phe Val Phe Ser Gln Thr Asp Asp Arg Leu Trp Arg Lys Asn Arg Gln
 1 5 10 15
 Pro Pro Pro Ala Asn Gln Asn Gln Thr Cys Phe Gly Arg Asp
 20 25 30

<210> 178

<211> 188

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 178

Ile Asn Arg Asn Trp Glu Thr Asn Trp Asp Ala Asp Pro Arg Gly Ala
 1 5 10 15
 Ser Pro Asp Ala Cys Ser Gln Val Tyr Arg Gly Glu Lys Pro Arg Asp
 20 25 30
 Ala Pro Glu Asn Glu Ser Met Asp Asn Phe Ile Arg Lys Val Arg Asp
 35 40 45
 Glu Gln Gly Ile Thr Leu Tyr Ile Asp Trp His Ser Tyr Ser Gln Leu
 50 55 60
 Ile Leu Phe Pro Phe Gly His Lys Glu Thr Leu Tyr Ala Pro Glu Leu
 65 70 75 80
 Gly Met Trp Thr Lys Thr Ala Ser Leu Met Ser Glu Tyr Ile Arg Asp
 85 90 95
 Ser Ser Arg Asn Asp Thr Thr Tyr Leu Phe Gly Pro Ser Gly Ala Thr
 100 105 110
 Leu Tyr Pro Thr Thr Gly Ala Ser Ile Asp His Val Tyr Thr Ile Gly
 115 120 125
 Arg Ala Lys Phe Ser Phe Thr Ile Glu Leu Pro Asp Thr Gly Asp Phe
 130 135 140
 Gly Phe Val Leu Pro Pro Glu Arg Ile Arg Pro Ala Ile Glu Glu Gln
 145 150 155 160
 Trp Val Gly Gln Gln Val Leu Leu Ala Leu Leu Asp Glu Pro Phe Phe
 165 170 175
 Asp Gly Val Gly Pro Ala Ile Gly Thr Ser Thr Trp
 180 185

<210> 179

<211> 1323

<212> DNA

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1323)

<400> 179

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 Met Lys Phe Val Phe Asn Leu Ala Trp Leu Ser Leu Ala Ala Gly Ala
 1 5 10 15

48

act att cgc agc tcg cag cca gtt acc tac gat ggc tac cag gtc cac
 Thr Ile Arg Ser Ser Gln Pro Val Thr Tyr Asp Gly Tyr Gln Val His
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20								25				30				
cgc	atc	cgg	gcc	att	ggt	caa	cag	ggc	gtg	atg	gca	aag	cgt	gca	atg	144
Arg	Ile	Arg	Ala	Ile	Gly	Gln	Gln	Gly	Val	Met	Ala	Lys	Arg	Ala	Met	
		35					40					45				
tcg	tcc	att	cct	cac	gag	acg	ctc	aat	gaa	gct	cga	ggg	tcc	tgg	gac	192
Ser	Ser	Ile	Pro	His	Glu	Thr	Leu	Asn	Glu	Ala	Arg	Gly	Ser	Trp	Asp	
	50					55					60					
gtg	ctc	att	gca	cca	gac	caa	ctc	gat	gca	ttc	agc	cgc	ctc	ggg	ctg	240
Val	Leu	Ile	Ala	Pro	Asp	Gln	Leu	Asp	Ala	Phe	Ser	Arg	Leu	Gly	Leu	
65					70					75					80	
aag	tcg	cga	acc	ctg	cac	aag	gac	ttg	gcc	tac	tcc	att	gct	cgc	gag	288
Lys	Ser	Arg	Thr	Leu	His	Lys	Asp	Leu	Ala	Tyr	Ser	Ile	Ala	Arg	Glu	
				85					90					95		
cgt	caa	gtc	agg	aat	gtt	tgg	aag	agg	caa	tca	aac	ggc	tct	gat	gat	336
Arg	Gln	Val	Arg	Asn	Val	Trp	Lys	Arg	Gln	Ser	Asn	Gly	Ser	Asp	Asp	
			100				105						110			
gct	tgg	ttt	gac	agc	tat	cac	ccc	tat	gaa	gat	cac	atc	act	tgg	tgg	384
Ala	Trp	Phe	Asp	Ser	Tyr	His	Pro	Tyr	Glu	Asp	His	Ile	Thr	Trp	Trp	
		115					120					125				
aag	gat	ctc	cag	gcc	act	ttc	ccc	gag	cag	tca	aac	tgg	acg	agt	agc	432
Lys	Asp	Leu	Gln	Ala	Thr	Phe	Pro	Glu	Gln	Ser	Asn	Trp	Thr	Ser	Ser	
	130					135					140					
gga	acg	tcc	tac	gag	gga	cgc	gac	ctg	ttc	ggg	gtg	cat	ctc	tgg	gga	480
Gly	Thr	Ser	Tyr	Glu	Gly	Arg	Asp	Leu	Phe	Gly	Val	His	Leu	Trp	Gly	
145				150					155						160	
gca	ggg	ggc	cct	gga	aag	cct	gca	gtc	atc	tac	cac	ggg	act	gta	cat	528
Ala	Gly	Gly	Pro	Gly	Lys	Pro	Ala	Val	Ile	Tyr	His	Gly	Thr	Val	His	
				165					170					175		
gcc	cgt	gaa	tgg	atc	gtc	gct	ccc	acc	att	gag	tac	atc	aca	aaa	cag	576
Ala	Arg	Glu	Trp	Ile	Val	Ala	Pro	Thr	Ile	Glu	Tyr	Ile	Thr	Lys	Gln	
			180				185						190			
ctc	att	gat	gga	tac	aag	gcc	gga	gac	aac	gac	aca	aag	gca	atc	ttg	624
Leu	Ile	Asp	Gly	Tyr	Lys	Ala	Gly	Asp	Asn	Asp	Thr	Lys	Ala	Ile	Leu	
		195					200					205				
gac	aaa	tac	gac	ttc	tac	atc	ttt	ccc	ttt	gtg	aac	ccg	gat	ggg	ttc	672
Asp	Lys	Tyr	Asp	Phe	Tyr	Ile	Phe	Pro	Phe	Val	Asn	Pro	Asp	Gly	Phe	
	210					215					220					
gtc	ttc	tcc	cag	acc	gac	gac	cgt	ctc	tgg	cgc	aag	aac	cgc	cag	ccc	720
Val	Phe	Ser	Gln	Thr	Asp	Asp	Arg	Leu	Trp	Arg	Lys	Asn	Arg	Gln	Pro	
225				230					235						240	
cca	ccc	gcc	aac	caa	aac	caa	acc	tgc	ttc	ggc	cgc	gat	atc	aac	cgc	768
Pro	Pro	Ala	Asn	Gln	Asn	Gln	Thr	Cys	Phe	Gly	Arg	Asp	Ile	Asn	Arg	
				245				250						255		
aac	tgg	gaa	aca	aac	tgg	gac	gcc	gac	ccc	cgc	ggc	gcc	tcg	cca	gac	816
Asn	Trp	Glu	Thr	Asn	Trp	Asp	Ala	Asp	Pro	Arg	Gly	Ala	Ser	Pro	Asp	
			260				265						270			
gcc	tgc	tca	caa	gtg	tac	cgc	ggc	gag	aaa	ccc	cgc	gac	gcg	ccc	gaa	864
Ala	Cys	Ser	Gln	Val	Tyr	Arg	Gly	Glu	Lys	Pro	Arg	Asp	Ala	Pro	Glu	
		275					280					285				
aac	gag	agc	atg	gac	aac	ttc	atc	cgc	aaa	gtc	cgc	gac	gag	caa	ggc	912
Asn	Glu	Ser	Met	Asp	Asn	Phe	Ile	Arg	Lys	Val	Arg	Asp	Glu	Gln	Gly	

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Thr	Ile	Arg	Ser	Ser	Gln	Pro	Val	Thr	Tyr	Asp	Gly	Tyr	Gln	Val	His	
			20					25					30			
Arg	Ile	Arg	Ala	Ile	Gly	Gln	Gln	Gly	Val	Met	Ala	Lys	Arg	Ala	Met	
		35					40					45				
Ser	Ser	Ile	Pro	His	Glu	Thr	Leu	Asn	Glu	Ala	Arg	Gly	Ser	Trp	Asp	
	50					55					60					
Val	Leu	Ile	Ala	Pro	Asp	Gln	Leu	Asp	Ala	Phe	Ser	Arg	Leu	Gly	Leu	
65					70					75					80	
Lys	Ser	Arg	Thr	Leu	His	Lys	Asp	Leu	Ala	Tyr	Ser	Ile	Ala	Arg	Glu	
				85					90					95		
Arg	Gln	Val	Arg	Asn	Val	Trp	Lys	Arg	Gln	Ser	Asn	Gly	Ser	Asp	Asp	
			100					105					110			
Ala	Trp	Phe	Asp	Ser	Tyr	His	Pro	Tyr	Glu	Asp	His	Ile	Thr	Trp	Trp	

10336256.txt

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115      120      125
Lys Asp Leu Gln Ala Thr Phe Pro Glu Gln Ser Asn Trp Thr Ser Ser
130      135      140
Gly Thr Ser Tyr Glu Gly Arg Asp Leu Phe Gly Val His Leu Trp Gly
145      150      155
Ala Gly Gly Pro Gly Lys Pro Ala Val Ile Tyr His Gly Thr Val His
160      165      170
Ala Arg Glu Trp Ile Val Ala Pro Thr Ile Glu Tyr Ile Thr Lys Gln
175      180      185
Leu Ile Asp Gly Tyr Lys Ala Gly Asp Asn Asp Thr Lys Ala Ile Leu
190      195      200
Asp Lys Tyr Asp Phe Tyr Ile Phe Pro Phe Val Asn Pro Asp Gly Phe
205      210      215
Val Phe Ser Gln Thr Asp Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro
220      225      230
Pro Pro Ala Asn Gln Asn Gln Thr Cys Phe Gly Arg Asp Ile Asn Arg
235      240      245
Asn Trp Glu Thr Asn Trp Asp Ala Asp Pro Arg Gly Ala Ser Pro Asp
250      255      260
Ala Cys Ser Gln Val Tyr Arg Gly Glu Lys Pro Arg Asp Ala Pro Glu
265      270      275
Asn Glu Ser Met Asp Asn Phe Ile Arg Lys Val Arg Asp Glu Gln Gly
280      285      290
Ile Thr Leu Tyr Ile Asp Trp His Ser Tyr Ser Gln Leu Ile Leu Phe
295      300      305
Pro Phe Gly His Lys Glu Thr Leu Tyr Ala Pro Glu Leu Gly Met Trp
310      315      320
Thr Lys Thr Ala Ser Leu Met Ser Glu Tyr Ile Arg Asp Ser Ser Arg
325      330      335
Asn Asp Thr Thr Tyr Leu Phe Gly Pro Ser Gly Ala Thr Leu Tyr Pro
340      345      350
Thr Thr Gly Ala Ser Ile Asp His Val Tyr Thr Ile Gly Arg Ala Lys
355      360      365
Phe Ser Phe Thr Ile Glu Leu Pro Asp Thr Gly Asp Phe Gly Phe Val
370      375      380
Leu Pro Pro Glu Arg Ile Arg Pro Ala Ile Glu Glu Gln Trp Val Gly
385      390      395
Gln Gln Val Leu Ala Leu Leu Asp Glu Pro Phe Phe Asp Gly Val
400      405      410
Gly Pro Ala Ile Gly Thr Ser Thr Trp
415      420      425
430      435      440

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<210> 181

<211> 3266

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (7)...(114)

<223> Exon

<221> CDS

<222> (856)...(1134)

<223> Exon

<221> CDS

<222> (1185)...(1337)

<223> Exon

<221> CDS

<222> (1442)...(1786)

<223> Exon

<221> CDS

<222> (1838)...(2266)

<223> Exon

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<400> 181
gtgtgc atg tgg cac gcg gcg gtt gtg tct gcg aat gga ggc gca gag 48
Met Trp His Ala Ala Val Val Ser Ala Asn Gly Gly Ala Glu
1 5 10

ggc ttg ggt ggt ggg gga cga ggc acg gtc agg gat gtt ttt ttg gag 96
Gly Leu Gly Gly Gly Gly Arg Gly Thr Val Arg Asp Val Phe Leu Glu
15 20 25 30

gtg gca gct gct gtc ggg taagttgcac agcgtgaggt ttcaggggtgg 144
Val Ala Ala Ala Val Gly
35

gactgggtggg attgacgggt cttttaggaa caaaggaaaa tcgtggctgg attgatttgt 204
cgagttgatt ttcgatgggt ggggggaacg atgttctgga ttattctttg ttccttctat 264
gatacgtata ttgggaagca atgatacgggt atttgtgtag cgggtcaggc ggttttactc 324
tgccgcagcc acagataggt tgtgccgcat ctgcacgtgt ccgttgaact tgccaatcga 384
tatcacttgt ttgtggtcat ggtttaccct cttttcgtgc actgtagata cctcacatgt 444
tggaagatag cttttgccgc tctatctaaa gcttcggact attttaatga tatcaagtct 504
tttgcaaccc aagaaggatt aagagcaca ggcggtacta tgaagtctta ttccagcagt 564
cccactgtca ccaacatgcc acgccgtttt ggtccgcctt gaaagaaaca ctgcagcaga 624
tacggcttaa gacattggcc caagtaagggt tgcactgcac acgtacgac ctaatacttg 684
actctcacgg actacgtgct tgagtgccag agaaactgtc cccctttagt caacagcgac 744
ccgtacaaca tgtatattta tcagtagcgc tgccttccaa ggaggtaaatt cagagcttgc 804
aatattgttc actcccttac tttgctaaaa ctcaacgtac tgtcattcag c aaa cct 861
Lys Pro

cga aag att ctt act gca ata atg tac ttc att ctg cta tcc ttg ctt 909
Arg Lys Ile Leu Thr Ala Ile Met Tyr Phe Ile Leu Leu Ser Leu Leu
40 45 50

gct tca ctt gta acc gct aca cca tta gtc aaa gca ccc ggt agc aag 957
Ala Ser Leu Val Thr Ala Thr Pro Leu Val Lys Ala Pro Gly Ser Lys
55 60 65 70

gcc att gcc aac aag tgg att gtc aaa ctc aag gac aac gtc gcc acg 1005
Ala Ile Ala Asn Lys Trp Ile Val Lys Leu Lys Asp Asn Val Ala Thr
75 80 85

atg gcc gct gat ggc gtg aaa gca gct att tcc aca aag ccc gat tac 1053
Met Ala Ala Asp Gly Val Lys Ala Ala Ile Ser Thr Lys Pro Asp Tyr
90 95 100

cag tat tcg atg cct ggc ttc cga ggc ttc gca gga act cta tcc gac 1101
Gln Tyr Ser Met Pro Gly Phe Arg Gly Phe Ala Gly Thr Leu Ser Asp
105 110 115

gat gag gta gca ctg ttg caa gct tca gat caa gtaaggcatt tgcagcacaa 1154
Asp Glu Val Ala Leu Leu Gln Ala Ser Asp Gln
120 125

gtccgaaagc ccctttgttg atttgtgtag att gag tat atc cag caa gat gct 1208
Ile Glu Tyr Ile Gln Gln Asp Ala
130 135

gaa gtt tac acg acg gca att atc gaa cag tcg aat gcc acg tgg gga 1256
Glu Val Tyr Thr Thr Ala Ile Ile Glu Gln Ser Asn Ala Thr Trp Gly
140 145 150

ata tcc cgt atc tcg cat aca aag cca agt gaa acg gcg tat ctc tat 1304
Ile Ser Arg Ile Ser His Thr Lys Pro Ser Glu Thr Ala Tyr Leu Tyr
155 160 165

gat tcc agt gca gga gag gga acg tgt gcg tat gtttttatct gccgccagac 1357
Asp Ser Ser Ala Gly Glu Gly Thr Cys Ala Tyr
170 175 180

10336256.txt

gttctctgtg tatcactgac gaaatgtgaa gctatgtgat tgatacagga gtcgatgtta 1417
 cgcaccccgga gtttcaagga cgta agt aat gac gct caa atg caa gac ttg 1468
 Ser Asn Asp Ala Gln Met Gln Asp Leu
 185

cag act gac cca gta aca ggc gct tta ttc ctg gca gac ctc act cat 1516
 Gln Thr Asp Pro Val Thr Gly Ala Leu Phe Leu Ala Asp Leu Thr His
 190 195 200 205

gaa ggt aat ttt ata gac ggg tat ggt cat gga acg cac gtc gct gga 1564
 Glu Gly Asn Phe Ile Asp Gly Tyr Gly His Gly Thr His Val Ala Gly
 210 215 220

aca att ggg tct gcc act tgg gga gta gca aag aaa act acc atc ttt 1612
 Thr Ile Gly Ser Ala Thr Trp Gly Val Ala Lys Lys Thr Thr Ile Phe
 225 230 235

gct gtg cga gta ctc gac tcc aat ggc tgg ggt aca aac gct gat gtg 1660
 Ala Val Arg Val Leu Asp Ser Asn Gly Trp Gly Thr Asn Ala Asp Val
 240 245 250

att gcg ggc ctg gag ttg atc ttg cga gat gca aga gag cgt agg ggg 1708
 Ile Ala Gly Leu Glu Leu Ile Leu Arg Asp Ala Arg Glu Arg Arg Gly
 255 260 265

acg gat cag tgt cgc aat ggc ttt gtt gtc aat atc agc ctg gga agt 1756
 Thr Asp Gln Cys Arg Asn Gly Phe Val Val Asn Ile Ser Leu Gly Ser
 270 275 280 285

gaa aag ctt cca gct ttg aat gat gct gta agtagctctt gtcaagtttt 1806
 Glu Lys Leu Pro Ala Leu Asn Asp Ala Val
 290 295

cttgtctgaa cgctgattta gatgtaaggt c gca gct atg gtt gca gag gat 1858
 Ala Ala Met Val Ala Glu Asp
 300

atc ttt cta gga gtt gca gca ggt aac gat ggt gtg cca gct gat gac 1906
 Ile Phe Leu Gly Val Ala Ala Gly Asn Asp Gly Val Pro Ala Asp Asp
 305 310 315

ttc tct ccg gga tcc gag cct tcg gtc tgc act gta gga gca acg gca 1954
 Phe Ser Pro Gly Ser Glu Pro Ser Val Cys Thr Val Gly Ala Thr Ala
 320 325 330

gcg aat gat aca ctt gcc caa tgg tcc aat cat ggt tct cgg atc gac 2002
 Ala Asn Asp Thr Leu Ala Gln Trp Ser Asn His Gly Ser Arg Ile Asp
 335 340 345 350

att cta gct ccc ggc cta gac atc act agc act ctt ccc aat ggt gtg 2050
 Ile Leu Ala Pro Gly Leu Asp Ile Thr Ser Thr Leu Pro Asn Gly Val
 355 360 365

gtt gcc tcg ttt tcg ggt aca agt atg gca gct ccg cat gtt gtt ggc 2098
 Val Ala Ser Phe Ser Gly Thr Ser Met Ala Ala Pro His Val Val Gly
 370 375 380

ctt gca gcg tat ttg ctt gga ctc ggg tca cca gca aag gat ctc tgt 2146
 Leu Ala Ala Tyr Leu Leu Gly Leu Gly Ser Pro Ala Lys Asp Leu Cys
 385 390 395

ggt aca atc gct gcc ttg gcg atc aaa aat gcg atc gat caa gat acg 2194
 Gly Thr Ile Ala Ala Leu Ala Ile Lys Asn Ala Ile Asp Gln Asp Thr
 400 405 410

ctt cca aaa gga aca cca aac cta ttg gcg ttc aat ggc gca gac gcc 2242
 Leu Pro Lys Gly Thr Pro Asn Leu Leu Ala Phe Asn Gly Ala Asp Ala
 415 420 425 430

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agc cag aag cgt atg agg cat tca tgaagtgttt gggagacgtg aagaagtaca 2296
 Ser Gln Lys Arg Met Arg His Ser
 435

agggtatttcg gaattcgcca cggcgatttg ggatattcct tgtgtatgta tgcaggtgtc 2356
 aatatcatcg ccattgccat gagcatccct ccaatacgca tccctgtccg atggataatt 2416
 ctggaagaca ctgactcac agccacaatg ctatatggcc gatggccgct tggccataaa 2476
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 gggcctgtca gcgacaaacg gcctatcaca gtccagcaat aaattctccg aactccatgg 2596
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 agtggcacca tcagcgtgta tagaccagat gcctcaagaa caacggaaac agttgggccc 3016
 cactagcagc ctgatgtccc cagccgtcgc tcagatcctt gaaggactag gagatgacca 3076
 ctcgagtagc agcgacgaag actctgacct atcagacgat caagagaagg gacatcccaa 3136
 gtcgcagtct aagaaggatg tcagcgccca gaagatacag cagaagaaac aaaagctcaa 3196
 ctgagctcaa gcacctcggc catcctctct ctccccgaac agaagcagaa gtcgctccag 3256
 gtcagcaacc 3266

<210> 182

<211> 36

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 182

Met Trp His Ala Ala Val Val Ser Ala Asn Gly Gly Ala Glu Gly Leu
 1 5 10 15
 Gly Gly Gly Gly Arg Gly Thr Val Arg Asp Val Phe Leu Glu Val Ala
 20 25 30
 Ala Ala Val Gly
 35

<210> 183

<211> 93

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 183

Lys Pro Arg Lys Ile Leu Thr Ala Ile Met Tyr Phe Ile Leu Leu Ser
 1 5 10 15
 Leu Leu Ala Ser Leu Val Thr Ala Thr Pro Leu Val Lys Ala Pro Gly
 20 25 30
 Ser Lys Ala Ile Ala Asn Lys Trp Ile Val Lys Leu Lys Asp Asn Val
 35 40 45
 Ala Thr Met Ala Ala Asp Gly Val Lys Ala Ala Ile Ser Thr Lys Pro
 50 55 60
 Asp Tyr Gln Tyr Ser Met Pro Gly Phe Arg Gly Phe Ala Gly Thr Leu
 65 70 75 80
 Ser Asp Asp Glu Val Ala Leu Leu Gln Ala Ser Asp Gln
 85 90

<210> 184

<211> 51

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 184

Ile Glu Tyr Ile Gln Gln Asp Ala Glu Val Tyr Thr Thr Ala Ile Ile
 1 5 10 15
 Glu Gln Ser Asn Ala Thr Trp Gly Ile Ser Arg Ile Ser His Thr Lys
 20 25 30
 Pro ser Glu Thr Ala Tyr Leu Tyr Asp Ser Ser Ala Gly Glu Gly Thr
 35 40 45
 Cys Ala Tyr

10336256.txt

50

<210> 185
 <211> 115
 <212> PRT
 <213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 185
 Ser Asn Asp Ala Gln Met Gln Asp Leu Gln Thr Asp Pro Val Thr Gly
 1 5 10 15
 Ala Leu Phe Leu Ala Asp Leu Thr His Glu Gly Asn Phe Ile Asp Gly
 20 25 30
 Tyr Gly His Gly Thr His Val Ala Gly Thr Ile Gly Ser Ala Thr Trp
 35 40 45
 Gly Val Ala Lys Lys Thr Thr Ile Phe Ala Val Arg Val Leu Asp Ser
 50 55 60
 Asn Gly Trp Gly Thr Asn Ala Asp Val Ile Ala Gly Leu Glu Leu Ile
 65 70 75 80
 Leu Arg Asp Ala Arg Glu Arg Arg Gly Thr Asp Gln Cys Arg Asn Gly
 85 90 95
 Phe Val Val Asn Ile Ser Leu Gly Ser Glu Lys Leu Pro Ala Leu Asn
 100 105 110
 Asp Ala Val
 115

<210> 186
 <211> 143
 <212> PRT
 <213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 186
 Ala Ala Met Val Ala Glu Asp Ile Phe Leu Gly Val Ala Ala Gly Asn
 1 5 10 15
 Asp Gly Val Pro Ala Asp Asp Phe Ser Pro Gly Ser Glu Pro Ser Val
 20 25 30
 Cys Thr Val Gly Ala Thr Ala Ala Asn Asp Thr Leu Ala Gln Trp Ser
 35 40 45
 Asn His Gly Ser Arg Ile Asp Ile Leu Ala Pro Gly Leu Asp Ile Thr
 50 55 60
 Ser Thr Leu Pro Asn Gly Val Val Ala Ser Phe Ser Gly Thr Ser Met
 65 70 75 80
 Ala Ala Pro His Val Val Gly Leu Ala Ala Tyr Leu Leu Gly Leu Gly
 85 90 95
 Ser Pro Ala Lys Asp Leu Cys Gly Thr Ile Ala Ala Leu Ala Ile Lys
 100 105 110
 Asn Ala Ile Asp Gln Asp Thr Leu Pro Lys Gly Thr Pro Asn Leu Leu
 115 120 125
 Ala Phe Asn Gly Ala Asp Ala Ser Gln Lys Arg Met Arg His Ser
 130 135 140

<210> 187
 <211> 1314
 <212> DNA
 <213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>
 <221> CDS
 <222> (1)...(1314)

<400> 187
 atg tgg cac gcg gcg gtt gtg tct gcg aat gga ggc gca gag ggc ttg 48
 Met Trp His Ala Val Val Ser Ala Asn Gly Gly Ala Glu Gly Leu 15
 1 5 10
 ggt ggt ggg gga cga ggc acg gtc agg gat gtt ttt ttg gag gtg gca 96
 Gly Gly Gly Gly Arg Gly Thr Val Arg Asp Val Phe Leu Glu Val Ala 20 25 30

10336256.txt

gct gct gtc ggg aaa cct cga aag att ctt act gca ata atg tac ttc Ala Ala Val Gly Lys Pro Arg Lys Ile Leu Thr Ala Ile Met Tyr Phe 35 40 45	144
att ctg cta tcc ttg ctt gct tca ctt gta acc gct aca cca tta gtc Ile Leu Leu Ser Leu Leu Ala Ser Leu Val Thr Ala Thr Pro Leu Val 50 55 60	192
aaa gca ccc ggt agc aag gcc att gcc aac aag tgg att gtc aaa ctc Lys Ala Pro Gly Ser Lys Ala Ile Ala Asn Lys Trp Ile Val Lys Leu 65 70 75 80	240
aag gac aac gtc gcc acg atg gcc gct gat ggc gtg aaa gca gct att Lys Asp Asn Val Ala Thr Met Ala Ala Asp Gly Val Lys Ala Ala Ile 85 90 95	288
tcc aca aag ccc gat tac cag tat tgc atg cct ggc ttc cga ggc ttc Ser Thr Lys Pro Asp Tyr Gln Tyr Ser Met Pro Gly Phe Arg Gly Phe 100 105 110	336
gca gga act cta tcc gac gat gag gta gca ctg ttg caa gct tca gat Ala Gly Thr Leu Ser Asp Asp Glu Val Ala Leu Leu Gln Ala Ser Asp 115 120 125	384
caa att gag tat atc cag caa gat gct gaa gtt tac acg acg gca att Gln Ile Glu Tyr Ile Gln Gln Asp Ala Glu Val Tyr Thr Thr Ala Ile 130 135 140	432
atc gaa cag tgc aat gcc acg tgg gga ata tcc cgt atc tgc cat aca Ile Glu Gln Ser Asn Ala Thr Trp Gly Ile Ser Arg Ile Ser His Thr 145 150 155 160	480
aag cca agt gaa acg gcg tat ctc tat gat tcc agt gca gga gag gga Lys Pro Ser Glu Thr Ala Tyr Leu Tyr Asp Ser Ser Ala Gly Glu Gly 165 170 175	528
acg tgt gcg tat agt aat gac gct caa atg caa gac ttg cag act gac Thr Cys Ala Tyr Ser Asn Asp Ala Gln Met Gln Asp Leu Gln Thr Asp 180 185 190	576
cca gta aca ggc gct tta ttc ctg gca gac ctc act cat gaa ggt aat Pro Val Thr Gly Ala Leu Phe Leu Ala Asp Leu Thr His Glu Gly Asn 195 200 205	624
ttt ata gac ggg tat ggt cat gga acg cac gtc gct gga aca att ggg Phe Ile Asp Gly Tyr Gly His Gly Thr His Val Ala Gly Thr Ile Gly 210 215 220	672
tct gcc act tgg gga gta gca aag aaa act acc atc ttt gct gtg cga Ser Ala Thr Trp Gly Val Ala Lys Lys Thr Thr Ile Phe Ala Val Arg 225 230 235 240	720
gta ctc gac tcc aat gcc tgg ggt aca aac gct gat gtg att gcg gcc Val Leu Asp Ser Asn Gly Trp Gly Thr Asn Ala Asp Val Ile Ala Gly 245 250 255	768
ctg gag ttg atc ttg cga gat gca aga gag cgt agg ggg acg gat cag Leu Glu Leu Ile Leu Arg Asp Ala Arg Glu Arg Arg Gly Thr Asp Gln 260 265 270	816
tgt cgc aat gcc ttt gtt gtc aat atc agc ctg gga agt gaa aag ctt Cys Arg Asn Gly Phe Val Val Asn Ile Ser Leu Gly Ser Glu Lys Leu 275 280 285	864
cca gct ttg aat gat gct gta gca gct atg gtt gca gag gat atc ttt Pro Ala Leu Asn Asp Ala Val Ala Ala Met Val Ala Glu Asp Ile Phe 290 295 300	912

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cta gga gtt gca gca ggt aac gat ggt gtg cca gct gat gac ttc tct 960
 Leu Gly Val Ala Ala Gly Asn Asp Gly Val Pro Ala Asp Asp Phe Ser 320
 305 310 315

ccg gga tcc gag cct tcg gtc tgc act gta gga gca acg gca gcg aat 1008
 Pro Gly Ser Glu Pro Ser Val Cys Thr Val Gly Ala Thr Ala Ala Asn 335
 325 330

gat aca ctt gcc caa tgg tcc aat cat ggt tct cgg atc gac att cta 1056
 Asp Thr Leu Ala Gln Trp Ser Asn His Gly Ser Arg Ile Asp Ile Leu 350
 340 345

gct ccc ggc cta gac atc act agc act ctt ccc aat ggt gtg gtt gcc 1104
 Ala Pro Gly Leu Asp Ile Thr Ser Thr Leu Pro Asn Gly Val Val Ala 365
 355 360

tcg ttt tcg ggt aca agt atg gca gct ccg cat gtt gtt ggc ctt gca 1152
 Ser Phe Ser Gly Thr Ser Met Ala Ala Pro His Val Val Gly Leu Ala 380
 370 375

gcg tat ttg ctt gga ctc ggg tca cca gca aag gat ctc tgt ggt aca 1200
 Ala Tyr Leu Leu Gly Leu Gly Ser Pro Ala Lys Asp Leu Cys Gly Thr 400
 385 390

atc gct gcc ttg gcg atc aaa aat gcg atc gat caa gat acg ctt cca 1248
 Ile Ala Ala Leu Ala Ile Lys Asn Ala Ile Asp Gln Asp Thr Leu Pro 415
 405 410

aaa gga aca cca aac cta ttg gcg ttc aat ggc gca gac gcc agc cag 1296
 Lys Gly Thr Pro Asn Leu Leu Ala Phe Asn Gly Ala Asp Ala Ser Gln 430
 420 425

aag cgt atg agg cat tca 1314
 Lys Arg Met Arg His Ser 435

<210> 188

<211> 438

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> DOMAIN

<222> (156)...(426)

<223> Subtilase family

<221> DOMAIN

<222> (74)...(142)

<223> Subtilisin N-terminal region

<400> 188

Met Trp His Ala Ala Val Val Ser Ala Asn Gly Gly Ala Glu Gly Leu
 1 5 10 15
 Gly Gly Gly Gly Arg Gly Thr Val Arg Asp Val Phe Leu Glu Val Ala
 20 25 30
 Ala Ala Val Gly Lys Pro Arg Lys Ile Leu Thr Ala Ile Met Tyr Phe
 35 40 45
 Ile Leu Leu Ser Leu Leu Ala Ser Leu Val Thr Ala Thr Pro Leu Val
 50 55 60
 Lys Ala Pro Gly Ser Lys Ala Ile Ala Asn Lys Trp Ile Val Lys Leu
 65 70 75 80
 Lys Asp Asn Val Ala Thr Met Ala Ala Asp Gly Val Lys Ala Ala Ile
 85 90 95
 Ser Thr Lys Pro Asp Tyr Gln Tyr Ser Met Pro Gly Phe Arg Gly Phe
 100 105 110
 Ala Gly Thr Leu Ser Asp Asp Glu Val Ala Leu Leu Gln Ala Ser Asp
 115 120 125

10336256.txt

Gln Ile Glu Tyr Ile Gln Gln Asp Ala Glu Val Tyr Thr Thr Ala Ile
 130 135 140
 Ile Glu Gln Ser Asn Ala Thr Trp Gly Ile Ser Arg Ile Ser His Thr
 145 150 155 160
 Lys Pro Ser Glu Thr Ala Tyr Leu Tyr Asp Ser Ser Ala Gly Glu Gly
 165 170 175
 Thr Cys Ala Tyr Ser Asn Asp Ala Gln Met Gln Asp Leu Gln Thr Asp
 180 185 190
 Pro Val Thr Gly Ala Leu Phe Leu Ala Asp Leu Thr His Glu Gly Asn
 195 200 205
 Phe Ile Asp Gly Tyr Gly His Gly Thr His Val Ala Gly Thr Ile Gly
 210 215 220
 Ser Ala Thr Trp Gly Val Ala Lys Lys Thr Thr Ile Phe Ala Val Arg
 225 230 235 240
 Val Leu Asp Ser Asn Gly Trp Gly Thr Asn Ala Asp Val Ile Ala Gly
 245 250 255
 Leu Glu Leu Ile Leu Arg Asp Ala Arg Glu Arg Arg Gly Thr Asp Gln
 260 265 270
 Cys Arg Asn Gly Phe Val Val Asn Ile Ser Leu Gly Ser Glu Lys Leu
 275 280 285
 Pro Ala Leu Asn Asp Ala Val Ala Ala Met Val Ala Glu Asp Ile Phe
 290 295 300
 Leu Gly Val Ala Ala Gly Asn Asp Gly Val Pro Ala Asp Asp Phe Ser
 305 310 315 320
 Pro Gly Ser Glu Pro Ser Val Cys Thr Val Gly Ala Thr Ala Ala Asn
 325 330 335
 Asp Thr Leu Ala Gln Trp Ser Asn His Gly Ser Arg Ile Asp Ile Leu
 340 345 350
 Ala Pro Gly Leu Asp Ile Thr Ser Thr Leu Pro Asn Gly Val Val Ala
 355 360 365
 Ser Phe Ser Gly Thr Ser Met Ala Ala Pro His Val Val Gly Leu Ala
 370 375 380
 Ala Tyr Leu Leu Gly Leu Gly Ser Pro Ala Lys Asp Leu Cys Gly Thr
 385 390 395 400
 Ile Ala Ala Leu Ala Ile Lys Asn Ala Ile Asp Gln Asp Thr Leu Pro
 405 410 415
 Lys Gly Thr Pro Asn Leu Leu Ala Phe Asn Gly Ala Asp Ala Ser Gln
 420 425 430
 Lys Arg Met Arg His Ser
 435

<210> 189

<211> 4101

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1499)...(1597)

<223> Exon

<221> CDS

<222> (1649)...(1967)

<223> Exon

<221> CDS

<222> (2005)...(3104)

<223> Exon

<400> 189

ttgaaacctc	aattctgtct	tgaatactat	ggtgagtcac	tttctgctag	tcactggttt	60
tcgcagtact	gatttttcgt	agctttttcta	gtcatatcat	tgcatgtctc	tcgagatata	120
gatgggatcg	taaacaaaac	cctattttgag	cactttgaat	caatctctac	ttcaaaggag	180
tggcgaaaaa	agagtgatgt	tatgataccc	aacgcaagct	cgcaaagggtg	gagaaacagc	240
agttaatgag	ctcacttagc	gatgtcccat	tgcccagaca	acggcccaaa	agaaaccagg	300
tttttctttc	ttctcgaccg	agctggaatc	atatgggtatt	gagaatttcc	aagggccggc	360
cagtgtcact	agctaccgac	cgatttcgag	ttagaagcgt	tatccgtact	tgaagtcaaa	420
ggtctcaatt	caatactcag	atgtaccagg	agagggaacg	ccgaccggta	gacgacaatg	480

10336256.txt

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tcggcgacta cattctagat ccacggaaac tgatggaagt tatcatgaaa attacgctcc 540
tcgagacatt tcctgttcct acatgcacgg tcagaactcg tgggtgcagc tgtgaagaaa 600
gcaaacatat tcacgtggat cgactgggca acgcatgcat aaagactccg cggaaggaag 660
aagagattct ctaccaacgc ctgacttcgc gatttcgcaa ttgcctatta gtattaggca 720
tacgacacgg tgcccagatt gcgatcggag ggtatacccg atgtgtgcag ccatgaccga 780
cggaattga caataacaga ggatgttggg aggggcgagg gctccacaca aaacaaccct 840
gcatgttttc ggggcgtgca accggaccag gaacagtatg actatgcacc tggttttgca 900
gcagcgcgca tccacgtcaa gcagccctca ggtacacatg atgatgtgta tcagtcacaa 960
aagcttggtc agctcaaaac tggcattgca cctgtaccac acacggcgat gaaaacacag 1020
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agccccatat tgccaccagg acaaccacca agcggcactt ggcaagcttg gcagtccgcc 1140
gcgctgaagc ttaccaaggc ctcttatcac gtcttgacac ggctcgtgtg cttgtttact 1200
gggtccgctc acagcgcta ttggtggatg aagggtcagc ctcggtggtg gatgcgcca 1260
cttggtgga tgtaggagt cgcaaagagc tttgtatgtg ggtttgattg taagctgcat 1320
ttcaggcata cagtgtgtt ggtaggagcg atatttccgg tctctgggcc catttgcagc 1380
tactacgagc tgcaggtggt atggatttag gtaagctagt aaatagcata aattgcacag 1440
catgccctgc caatttgaa acgacactcc ctttgcaaaa aagcaggcaa tagtcgca 1498
atg gca tat ctg aag tca atc gca gca ctt gct gca tgt gct gta gcg 1546
Met Ala Tyr Leu Lys Ser Ile Ala Ala Leu Ala Ala Cys Ala Val Ala
1 5 10 15

ggt gag gca gca gcc ctt cat cct cgc act aac aag acg ctg gtt gat 1594
Val Glu Ala Ala Ala Leu His Pro Arg Thr Asn Lys Thr Leu Val Asp
20 25 30

tcg gtacgagtat acatacattc atttcccagag ttgctctaac acgcattata 1647
Ser

g caa tcg ctc cgt gat acg att gac att gac aac ttg tat gcc aaa gcg 1696
Gln Ser Leu Arg Asp Thr Ile Asp Ile Asp Asn Leu Tyr Ala Lys Ala
35 40 45

gag atc ctt cag gag att gca tac aac aca ccg gga aag aac cgt gtg 1744
Glu Ile Leu Gln Glu Ile Ala Tyr Asn Thr Pro Gly Lys Asn Arg Val
50 55 60 65

att ggt agc cag ggc cat gag gat act gta gaa tac atc aag ggc cag 1792
Ile Gly Ser Gln Gly His Glu Asp Thr Val Glu Tyr Ile Lys Gly Gln
70 75 80

ctc gag gca ttc ccc gac tac tac gat gtg tac act cag gat gtg cct 1840
Leu Glu Ala Phe Pro Asp Tyr Tyr Asp Val Tyr Thr Gln Asp Val Pro
85 90 95

ctc tca atc gga acc act gcc acg ctc cgt gca aac aac aag acg att 1888
Leu Ser Ile Gly Thr Thr Ala Thr Leu Arg Ala Asn Asn Lys Thr Ile
100 105 110

gag gct ttt gca gta act ctg gct ccg ggt ggc aat gta act gga ccg 1936
Glu Ala Phe Ala Val Thr Leu Ala Pro Gly Gly Asn Val Thr Gly Pro
115 120 125

ctc gtt gct att ccc aac ttg ggt tgt gaa g aggtagggttc atgttttcga 1987
Leu Val Ala Ile Pro Asn Leu Gly Cys Glu
130 135

ctatatatac ccaaaga ag ata tca gga agc aag act aac atg gaa aag gcg 2039
Glu Ile Ser Gly Ser Lys Thr Asn Met Glu Lys Ala
140 145 150

gat ttc cca gaa tct ctc gag ggc tct gta gct ctg atc aag cgt ggt 2087
Asp Phe Pro Glu Ser Leu Glu Gly Ser Val Ala Leu Ile Lys Arg Gly
155 160 165

acg tgc tcg tac ggc gag aag gtg cag att gct gct gcc aaa gga gcc 2135
Thr Cys Ser Tyr Gly Glu Lys Val Gln Ile Ala Ala Ala Lys Gly Ala
170 175 180

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10336256.txt

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Leu Gly Val Val Ala Trp Asn Asn Ala Glu Gly Thr 195	
tcg ctc caa gtc ttg tat ccc aag ggc aag ttt gtc cct gta gcc ggc	2231
Ser Leu Gln Val Leu Tyr Pro Lys Gly Lys Phe Val Pro Val Ala Gly 215	
atc acc atg ggc caa gga gaa gcg ctt ctt gcg cag ctc aac gct ggt	2279
Ile Thr Met Gly Gln Gly Glu Ala Leu Leu 225 Ala Gln Leu Asn Ala 230 Gly	
gtc aag atc aat gtc gac atg tca aca gac gcc aag gtg ttc aac act	2327
Val Lys Ile Asn Val Asp Met Ser Thr 240 Asp Ala Lys Val Phe Asn Thr 245	
cgc aac gtg att gcg gag aca aag gct ggc gac cac gac aac gtg atc	2375
Arg Asn Val Ile Ala Glu Thr Lys 255 Ala Gly Asp His Asp Asn Val Ile 260	
cac gtc agc ggc cat tct gac tcg gtc act gct ggc cca ggc atc aac	2423
His Val Ser Gly His Ser Asp Ser Val Thr Ala Gly 275 Pro Gly Ile Asn 265	
gac aat gga tcg ggc act att tcc att ctc gag att gct att caa ctg	2471
Asp Asn Gly Ser Gly Thr 285 Ile Ser Ile Leu Glu Ile Ala Ile Gln Leu 295	
acc aac ttt acc gtc aac aac gcc gtg cgc ttc agc tgg tgg aca gca	2519
Thr Asn Phe Thr Val 300 Asn Asn Ala Val 305 Arg Phe Ser Trp Trp Thr 310 Ala	
gag gag gcc ggt ctt ctc gga gcc gag tac tac gtg cac gag ctg ccc	2567
Glu Glu Ala Gly 315 Leu Leu Gly Ala Glu 320 Tyr Tyr Val His Glu 325 Leu Pro	
caa gct gag aag gac aag atc cgt ctt ttg ctc gac ttt gac atg atg	2615
Gln Ala Glu Lys Asp Lys Ile Arg 335 Leu Leu Leu Asp Phe Asp Met Met 340	
gcc tca ccc aac ttt gcc tac caa atc tat gac ggt gat ggt tcg gca	2663
Ala Ser Pro Asn Phe Ala Tyr 350 Gln Ile Tyr Asp Gly Asp Gly Ser Ala 345	
ttc aac ctg act ggg ccg gtt ggc tca gcc gag gct gag cac gag ttt	2711
Phe Asn Leu Thr Gly Pro Val Gly Ser Ala Glu 370 Ala Glu His Glu Phe 375	
gcc gcc tac ttt gac agc att ggc ctc aac cac act gag att gaa ttc	2759
Ala Ala Tyr Phe Asp Ser Ile Gly Leu Asn His Thr Glu Ile Glu Phe 390	
gac ggc cgg tca gac tac ggc ccg ttc ctt gag gct ggc atc gct tct	2807
Asp Gly Arg Ser 395 Asp Tyr Gly Pro Phe Leu Glu Ala Gly Ile Ala Ser 405	
ggt ggc att gcc ggt gga gcc gag ggt atc aag aca gaa gag gag gcg	2855
Gly Gly Ile Ala Gly Gly Ala Glu Gly Ile Lys Thr Glu Glu Glu Ala 420	
gcc atg ttt ggc gga ggc gcc ggt gtt cct tac gac gtc aac tac cac	2903
Ala Met Phe Gly Gly Gly Ala Gly Val Pro Tyr Asp Val Asn Tyr His 435	
gag gat ggc gat acc gtc aac aac ttg aac ctc gag gcg tgg atc gag	2951
Glu Asp Gly Asp Thr Val Asn Asn Leu Asn Leu Glu Ala Trp Ile Glu 455	

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ttc aca agg gct att gcg cac atg acg gcc aag tat gct gtg tcg tgg 2999
 Phe Thr Arg Ala Ile Ala His Met Thr Ala Lys Tyr Ala Val Ser Trp
 460 465 470

gac agc atc ccg cca agg aac gcg acg gct gcg cag aag cgg tca gag 3047
 Asp Ser Ile Pro Pro Arg Asn Ala Thr Ala Ala Gln Lys Arg Ser Glu
 475 480 485

agg tat gcc gag ttt aag cag gcg ttc cag aag acc aag agg tac cag 3095
 Arg Tyr Ala Glu Phe Lys Gln Ala Phe Gln Lys Thr Lys Arg Tyr Gln
 490 495 500

agg tgg gta tagattgggc tcgatcccgga ggcttttgag tggatgtgag 3144
 Arg Trp Val
 505

cttagacacg actttaatgg tgaatatcaa agaaatcttc aaggcaatgt ttgtgcaagc 3204
 aaaagtggat gaatgtgaga aaacgagttt gtggaattgc acgcatgtca tttgccgttt 3264
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 aaaagtaaga gagagtggcg gagaagggga tagggaccac caaggggtta ctcaagatga 3624
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<210> 190

<211> 33

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 190

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 Val Glu Ala Ala Ala Leu His Pro Arg Thr Asn Lys Thr Leu Val Asp
 20 25 30
 Ser

<210> 191

<211> 106

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 191

Gln Ser Leu Arg Asp Thr Ile Asp Ile Asp Asn Leu Tyr Ala Lys Ala
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 Glu Ile Leu Gln Glu Ile Ala Tyr Asn Thr Pro Gly Lys Asn Arg Val
 20 25 30
 Ile Gly Ser Gln Gly His Glu Asp Thr Val Glu Tyr Ile Lys Gly Gln
 35 40 45
 Leu Glu Ala Phe Pro Asp Tyr Tyr Asp Val Tyr Thr Gln Asp Val Pro
 50 55 60
 Leu Ser Ile Gly Thr Thr Ala Thr Leu Arg Ala Asn Asn Lys Thr Ile
 65 70 75 80
 Glu Ala Phe Ala Val Thr Leu Ala Pro Gly Gly Asn Val Thr Gly Pro
 85 90 95
 Leu Val Ala Ile Pro Asn Leu Gly Cys Glu
 100 105

10336256.txt

<210> 192

<211> 367

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 192

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 20 25 30
 Gly Glu Lys Val Gln Ile Ala Ala Lys Gly Ala Leu Gly Val Val
 35 40 45
 Ala Trp Asn Asn Ala Glu Gly Thr Leu Glu Gly Tyr Ser Leu Gln Val
 50 55 60
 Leu Tyr Pro Lys Gly Lys Phe Val Pro Val Ala Gly Ile Thr Met Gly
 65 70 75 80
 Gln Gly Glu Ala Leu Leu Ala Gln Leu Asn Ala Gly Val Lys Ile Asn
 85 90 95
 Val Asp Met Ser Thr Asp Ala Lys Val Phe Asn Thr Arg Asn Val Ile
 100 105 110
 Ala Glu Thr Lys Ala Gly Asp His Asp Asn Val Ile His Val Ser Gly
 115 120 125
 His Ser Asp Ser Val Thr Ala Gly Pro Gly Ile Asn Asp Asn Gly Ser
 130 135 140
 Gly Thr Ile Ser Ile Leu Glu Ile Ala Ile Gln Leu Thr Asn Phe Thr
 145 150 155 160
 Val Asn Asn Ala Val Arg Phe Ser Trp Trp Thr Ala Glu Glu Ala Gly
 165 170 175
 Leu Leu Gly Ala Glu Tyr Tyr Val His Glu Leu Pro Gln Ala Glu Lys
 180 185 190
 Asp Lys Ile Arg Leu Leu Leu Asp Phe Asp Met Met Ala Ser Pro Asn
 195 200 205
 Phe Ala Tyr Gln Ile Tyr Asp Gly Asp Gly Ser Ala Phe Asn Leu Thr
 210 215 220
 Gly Pro Val Gly Ser Ala Glu Ala Glu His Glu Phe Ala Ala Tyr Phe
 225 230 235 240
 Asp Ser Ile Gly Leu Asn His Thr Glu Ile Glu Phe Asp Gly Arg Ser
 245 250 255
 Asp Tyr Gly Pro Phe Leu Glu Ala Gly Ile Ala Ser Gly Gly Ile Ala
 260 265 270
 Gly Gly Ala Glu Gly Ile Lys Thr Glu Glu Glu Ala Ala Met Phe Gly
 275 280 285
 Gly Gly Ala Gly Val Pro Tyr Asp Val Asn Tyr His Glu Asp Gly Asp
 290 295 300
 Thr Val Asn Asn Leu Asn Leu Glu Ala Trp Ile Glu Phe Thr Arg Ala
 305 310 315 320
 Ile Ala His Met Thr Ala Lys Tyr Ala Val Ser Trp Asp Ser Ile Pro
 325 330 335
 Pro Arg Asn Ala Thr Ala Ala Gln Lys Arg Ser Glu Arg Tyr Ala Glu
 340 345 350
 Phe Lys Gln Ala Phe Gln Lys Thr Lys Arg Tyr Gln Arg Trp Val
 355 360 365

<210> 193

<211> 1518

<212> DNA

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1518)

<400> 193

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 Met Ala Tyr Leu Lys Ser Ile Ala Ala Leu Ala Ala Cys Ala Val Ala
 1 5 10 15

48

gtt gag gca gca gcc ctt cat cct cgc act aac aag acg ctg gtt gat
 Page 180

96

10336256.txt																
Val	Glu	Ala	Ala	Ala	Leu	His	Pro	Arg	Thr	Asn	Lys	Thr	Leu	Val	Asp	
			20					25					30			
tcg	caa	tcg	ctc	cgt	gat	acg	att	gac	att	gac	aac	ttg	tat	gcc	aaa	144
Ser	Gln	Ser	Leu	Arg	Asp	Thr	Ile	Asp	Ile	Asp	Asn	Leu	Tyr	Gln	Lys	
		35					40					45				
gcg	gag	atc	ctt	cag	gag	att	gca	tac	aac	aca	ccg	gga	aag	aac	cgt	192
Ala	Glu	Ile	Leu	Gln	Glu	Ile	Ala	Tyr	Asn	Thr	Pro	Gly	Lys	Asn	Arg	
	50					55					60					
gtg	att	ggt	agc	cag	ggc	cat	gag	gat	act	gta	gaa	tac	atc	aag	ggc	240
Val	Ile	Gly	Ser	Gln	Gly	His	Glu	Asp	Thr	Val	Glu	Tyr	Ile	Lys	Gly	
65					70					75					80	
cag	ctc	gag	gca	ttc	ccc	gac	tac	tac	gat	gtg	tac	act	cag	gat	gtg	288
Gln	Leu	Glu	Ala	Phe	Pro	Asp	Tyr	Tyr	Asp	Val	Tyr	Thr	Gln	Asp	Val	
				85					90					95		
cct	ctc	tca	atc	gga	acc	act	gcc	acg	ctc	cgt	gca	aac	aac	aag	acg	336
Pro	Leu	Ser	Ile	Gly	Thr	Thr	Ala	Thr	Leu	Arg	Ala	Asn	Asn	Lys	Thr	
			100					105					110			
att	gag	gct	ttt	gca	gta	act	ctg	gct	ccg	ggt	ggc	aat	gta	act	gga	384
Ile	Glu	Ala	Phe	Ala	Val	Thr	Leu	Ala	Pro	Gly	Gly	Asn	Val	Thr	Gly	
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ccg	ctc	gtt	gct	att	ccc	aac	ttg	ggt	tgt	gaa	gag	ata	tca	gga	agc	432
Pro	Leu	Val	Ala	Ile	Pro	Asn	Leu	Gly	Cys	Glu	Glu	Ile	Ser	Gly	Ser	
		130				135					140					
aag	act	aac	atg	gaa	aag	gcg	gat	ttc	cca	gaa	tct	ctc	gag	ggc	tct	480
Lys	Thr	Asn	Met	Glu	Lys	Ala	Asp	Phe	Pro	Glu	Ser	Leu	Glu	Gly	Ser	
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gta	gct	ctg	atc	aag	cgt	ggt	acg	tgc	tcg	tac	ggc	gag	aag	gtg	cag	528
Val	Ala	Leu	Ile	Lys	Arg	Gly	Thr	Cys	Ser	Tyr	Gly	Glu	Lys	Val	Gln	
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Ile	Ala	Ala	Ala	Lys	Gly	Ala	Leu	Gly	Val	Val	Ala	Trp	Asn	Asn	Ala	
			180					185					190			
gag	ggc	act	ctt	gag	ggc	tac	tcg	ctc	caa	gtc	ttg	tat	ccc	aag	ggc	624
Glu	Gly	Thr	Leu	Glu	Gly	Tyr	Ser	Leu	Gln	Val	Leu	Tyr	Pro	Lys	Gly	
		195					200					205				
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Lys	Phe	Val	Pro	Val	Ala	Gly	Ile	Thr	Met	Gly	Gln	Gly	Glu	Ala	Leu	
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ctt	gcg	cag	ctc	aac	gct	ggt	gtc	aag	atc	aat	gtc	gac	atg	tca	aca	720
Leu	Ala	Gln	Leu	Asn	Ala	Gly	Val	Lys	Ile	Asn	Val	Asp	Met	Ser	Thr	
225					230					235					240	
gac	gcc	aag	gtg	ttc	aac	act	cgc	aac	gtg	att	gcg	gag	aca	aag	gct	768
Asp	Ala	Lys	Val	Phe	Asn	Thr	Arg	Asn	Val	Ile	Ala	Glu	Thr	Lys	Ala	
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ggc	gac	cac	gac	aac	gtg	atc	cac	gtc	agc	ggc	cat	tct	gac	tcg	gtc	816
Gly	Asp	His	Asp	Asn	Val	Ile	His	Val	Ser	Gly	His	Ser	Asp	Ser	Val	
			260					265					270			
act	gct	ggc	cca	ggc	atc	aac	gac	aat	gga	tcg	ggc	act	att	tcc	att	864
Thr	Ala	Gly	Pro	Gly	Ile	Asn	Asp	Asn	Gly	Ser	Gly	Thr	Ile	Ser	Ile	
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ctc	gag	att	gct	att	caa	ctg	acc	aac	ttt	acc	gtc	aac	aac	gcc	gtg	912

10336256.txt

Leu	Glu	Ile	Ala	Ile	Gln	Leu	Thr	Asn	Phe	Thr	Val	Asn	Asn	Ala	Val		
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Arg	Phe	Ser	Trp	Trp	Thr	Ala	Glu	Glu	Ala	Gly	Leu	Leu	Gly	Ala	Glu	320	
305					310					315							
tac	tac	gtg	cac	gag	ctg	ccc	caa	gct	gag	aag	gac	aag	atc	cgt	ctt	1008	
Tyr	Tyr	Val	His	Glu	Leu	Pro	Gln	Ala	Glu	Lys	Asp	Lys	Ile	Arg	Leu	335	
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Leu	Leu	Asp	Phe	Asp	Met	Met	Ala	Ser	Pro	Asn	Phe	Ala	Tyr	Gln	Ile	350	
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Tyr	Asp	Gly	Asp	Gly	Ser	Ala	Phe	Asn	Leu	Thr	Gly	Pro	Val	Gly	Ser	365	
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Ala	Glu	Ala	Glu	His	Glu	Phe	Ala	Ala	Tyr	Phe	Asp	Ser	Ile	Gly	Leu	370	
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Asn	His	Thr	Glu	Ile	Glu	Phe	Asp	Gly	Arg	Ser	Asp	Tyr	Gly	Pro	Phe	385	
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ctt	gag	gct	ggc	atc	gct	tct	ggt	ggc	att	gcc	ggt	gga	gcc	gag	ggt	1248	
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Pro	Tyr	Asp	Val	Asn	Tyr	His	Glu	Asp	Gly	Asp	Thr	Val	Asn	Asn	Leu	435	
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aac	ctc	gag	gcg	tgg	atc	gag	ttc	aca	agg	gct	att	gcg	cac	atg	acg	1392	
Asn	Leu	Glu	Ala	Trp	Ile	Glu	Phe	Thr	Arg	Ala	Ile	Ala	His	Met	Thr	450	
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gct	gcg	cag	aag	cgg	tca	gag	agg	tat	gcc	gag	ttt	aag	cag	gcg	ttc	1488	
Ala	Ala	Gln	Lys	Arg	Ser	Glu	Arg	Tyr	Ala	Glu	Phe	Lys	Gln	Ala	Phe	485	
				485					490					495			
cag	aag	acc	aag	agg	tac	cag	agg	tgg	gta							1518	
Gln	Lys	Thr	Lys	Arg	Tyr	Gln	Arg	Trp	Val							500	
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<210> 194

<211> 506

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

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<222> (1)...(19)

<221> DOMAIN

<222> (121)...(228)

<223> PA (protease associated) domain

10336256.txt

<221> DOMAIN

<222> (234)...(468)

<223> Peptidase family M28

<400> 194

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Ser Gln Ser Leu Arg Asp Thr Ile Asp Ile Asp Asn Leu Tyr Ala Lys
35      40      45
Ala Glu Ile Leu Gln Glu Ile Ala Tyr Asn Thr Pro Gly Lys Asn Arg
50      55      60
Val Ile Gly Ser Gln Gly His Glu Asp Thr Val Glu Tyr Ile Lys Gly
65      70      75      80
Gln Leu Glu Ala Phe Pro Asp Tyr Tyr Asp Val Tyr Thr Gln Asp Val
85      90      95
Pro Leu Ser Ile Gly Thr Thr Ala Thr Leu Arg Ala Asn Asn Lys Thr
100      105      110
Ile Glu Ala Phe Ala Val Thr Leu Ala Pro Gly Gly Asn Val Thr Gly
115      120      125
Pro Leu Val Ala Ile Pro Asn Leu Gly Cys Glu Glu Ile Ser Gly Ser
130      135      140
Lys Thr Asn Met Glu Lys Ala Asp Phe Pro Glu Ser Leu Glu Gly Ser
145      150      155      160
Val Ala Leu Ile Lys Arg Gly Thr Cys Ser Tyr Gly Glu Lys Val Gln
165      170      175
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Glu Gly Thr Leu Glu Gly Tyr Ser Leu Gln Val Leu Tyr Pro Lys Gly
195      200      205
Lys Phe Val Pro Val Ala Gly Ile Thr Met Gly Gln Gly Glu Ala Leu
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Leu Ala Gln Leu Asn Ala Gly Val Lys Ile Asn Val Asp Met Ser Thr
225      230      235      240
Asp Ala Lys Val Phe Asn Thr Arg Asn Val Ile Ala Glu Thr Lys Ala
245      250      255
Gly Asp His Asp Asn Val Ile His Val Ser Gly His Ser Asp Ser Val
260      265      270
Thr Ala Gly Pro Gly Ile Asn Asp Asn Gly Ser Gly Thr Ile Ser Ile
275      280      285
Leu Glu Ile Ala Ile Gln Leu Thr Asn Phe Thr Val Asn Asn Ala Val
290      295      300
Arg Phe Ser Trp Trp Thr Ala Glu Glu Ala Gly Leu Leu Gly Ala Glu
305      310      315      320
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370      375      380
Asn His Thr Glu Ile Glu Phe Asp Gly Arg Ser Asp Tyr Gly Pro Phe
385      390      395      400
Leu Glu Ala Gly Ile Ala Ser Gly Gly Ile Ala Gly Gly Ala Glu Gly
405      410      415
Ile Lys Thr Glu Glu Glu Ala Ala Met Phe Gly Gly Gly Ala Gly Val
420      425      430
Pro Tyr Asp Val Asn Tyr His Glu Asp Gly Asp Thr Val Asn Asn Leu
435      440      445
Asn Leu Glu Ala Trp Ile Glu Phe Thr Arg Ala Ile Ala His Met Thr
450      455      460
Ala Lys Tyr Ala Val Ser Trp Asp Ser Ile Pro Arg Asn Ala Thr
465      470      475      480
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485      490      495

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10336256.txt

Gln Lys Thr Lys Arg Tyr Gln Arg Trp Val
500 505

<210> 195
 <211> 4182
 <212> DNA
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>
 <221> CDS
 <222> (1001)...(2182)
 <223> Exon

<221> CDS
 <222> (2238)...(2367)
 <223> Exon

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 <222> (2425)...(2549)
 <223> Exon

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ccc gtt cac ttc aag gca ccc agc cct tcc cac ttc ctc gac att gtc 1111
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 55 60 65

gcc cac ctc gaa agg gaa tat gag cac tct ggc gag atc tct ctc cac 1255
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 70 75 80 85

cga cgc gac ctc agc aag agg gct gcc gac gca cca atc ggc act ggt 1303
 Arg Arg Asp Leu Ser Lys Arg Ala Ala Asp Ala Pro Ile Gly Thr Gly
 90 95 100

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375

380

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tgacattcgt atttta gtg gcc gct gta ggt gga cgt tca tac aca tcc atg 2273
Val Ala Ala Val Gly Gly Arg Ser Tyr Thr Ser Met
395 400 405

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Gln Ser Val Gly Leu Tyr Ala Thr Ser Gly Ala Ser Asp Asp Tyr Ala
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gcc agc cgc gtg tac gcc aaa tcc ggt gct aac aag gtc ttt ggc t 2367
Ala Ser Arg Val Tyr Ala Lys Ser Gly Ala Asn Lys Val Phe Gly
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Phe Asn Gln Asn Ile Leu Asp Thr Asn Ala Gly Phe Met Asp Trp Ala
455 460 465 470

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Leu Ala Ala Ile Ala Val Gly Val Asn
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<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

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 35 40 45
 Lys Ala Val Pro His Glu Asp Gly His Phe Glu Leu His Ala Leu Leu
 50 55 60
 Thr Glu Glu Gln Ile Ala His Leu Glu Arg Glu Tyr Glu His Ser Gly
 65 70 75 80
 Glu Ile Ser Leu His Arg Arg Asp Leu Ser Lys Arg Ala Ala Asp Ala
 85 90 95
 Pro Ile Gly Thr Gly Asp Arg Trp Gln Gly Gly Ala Val Thr Pro Ser
 100 105 110
 Gly Leu Gly Thr Lys Ala Ala Gly Ser Thr Val Ser Ser Ile Met Asn
 115 120 125
 Pro Thr Glu Ile Asn Ser Ala Ile Lys Gly Leu Val Asn Gly Tyr Gly
 130 135 140
 Ile Asn Thr Ile Thr Leu Pro Tyr Lys Thr Phe Gln Gly Ala Thr Gln
 145 150 155 160
 Thr Ala Gly Tyr Val Gly Ala Gly Thr Asp Lys Ser Gln Tyr Lys Leu
 165 170 175
 Tyr Leu Ser Ala Gly Met His Ala Arg Glu Arg Gly Gly Pro Asp Gln
 180 185 190
 Leu Ile Tyr Trp Ile Ser Asp Leu Leu Ala Ala Asn Lys Ala Gly Thr
 195 200 205
 Gly Leu Thr Tyr Gly Arg Lys Thr Tyr Thr Asn Ala Gln Val Lys Ser
 210 215 220
 Val Leu Ala Ala Gly Ile Val Phe Phe Pro Leu Val Asn Pro Asp Gly
 225 230 235 240
 Val Ala Tyr Asp Gln Ser Ser Gly Ser Leu Trp Arg Lys Asn Arg Asn
 245 250 255
 Thr Arg Ser Gly Thr Ser Gly Ala Ser Val Gly Val Asp Ile Asn Arg
 260 265 270
 Asn Phe Asp Phe Leu Trp Asn Phe Lys Lys Phe Phe Asp Pro Ser Thr
 275 280 285
 Ser Pro Ala Ser Thr Ser Pro Ser Ser Glu Ala Phe Tyr Gly Thr Ala
 290 295 300
 Ala Ala Ser Glu Pro Glu Thr Lys Asn His Ile Ser Ile Tyr Asp Ser
 305 310 315 320
 Phe Pro Lys Ile Arg Trp Phe Met Asp Ile His Ser Ala Thr Gly Asp
 325 330 335
 Ile Leu Tyr Asn Trp Gly Asp Asp Glu Thr Gln Ser Thr Asn Ser Ala
 340 345 350
 Met Asn Phe Leu Asn Thr Ala Tyr Asp Gly Lys Arg Gly Arg Ile Gly
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 370 375 380
 Lys Ser Val Ala Ser Lys Thr Ala Ala Ala
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<210> 197

<211> 43

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 197

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<210> 198

<211> 42

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

10336256.txt

<400> 198

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 20 25 30
 Ala Leu Ala Ala Ile Ala Val Gly Val Asn
 35 40

<210> 199

<211> 1437

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1437)

<400> 199

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 Leu Gly Ser Leu Leu Pro Val His Phe Lys Ala Pro Ser Pro Ser His
 20 25 30

ttc ctc gac att gtc aac aat ggc aca tac gat ctg ggc tgc cga cca 144
 Phe Leu Asp Ile Val Asn Asn Gly Thr Tyr Asp Leu Gly Cys Arg Pro
 35 40 45

aag gct gta cca cat gag gac ggc cac ttt gag ctt cat gct ctc ctg 192
 Lys Ala Val Pro His Glu Asp Gly His Phe Glu Leu His Ala Leu Leu
 50 55 60

acc gag gag caa att gcc cac ctc gaa agg gaa tat gag cac tct ggg 240
 Thr Glu Glu Gln Ile Ala His Leu Glu Arg Glu Tyr Glu His Ser Gly
 65 70 75 80

gag atc tct ctc cac cga cgc gac ctc agc aag agg gct gcc gac gca 288
 Glu Ile Ser Leu His Arg Arg Asp Leu Ser Lys Arg Ala Ala Asp Ala
 85 90 95

cca atc ggc act ggt gac agg tgg caa ggt ggt gcc gtc aca cct tca 336
 Pro Ile Gly Thr Gly Asp Arg Trp Gln Gly Gly Ala Val Thr Pro Ser
 100 105 110

ggt ctt gga acc aaa gct gcg gga tca aca gtc agc tcc atc atg aac 384
 Gly Leu Gly Thr Lys Ala Ala Gly Ser Thr Val Ser Ser Ile Met Asn
 115 120 125

cct acc gag atc aac tcg gca atc aag ggt ctc gtt aac ggt tat ggt 432
 Pro Thr Glu Ile Asn Ser Ala Ile Lys Gly Leu Val Asn Gly Tyr Gly
 130 135 140

atc aac acc att act ctg cca tac aag act ttc cag ggt gct acg cag 480
 Ile Asn Thr Ile Thr Leu Pro Tyr Lys Thr Phe Gln Gly Ala Thr Gln
 145 150 155 160

acc gct gga tac gtc ggt gct ggt acg gac aag tcg cag tac aag ctc 528
 Thr Ala Gly Tyr Val Gly Ala Gly Thr Asp Lys Ser Gln Tyr Lys Leu
 165 170 175

tac ctc agt gct ggc atg cac gcc cgt gag cga ggt ggt ccc gat cag 576
 Tyr Leu Ser Ala Gly Met His Ala Arg Glu Arg Gly Gly Pro Asp Gln
 180 185 190

ctc att tac tgg atc tcc gac ttg ctt gct gcc aac aag gct gga acc 624
 Page 188

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Val	Leu	Ala	Ala	Gly	Ile	Val	Phe	Phe	Pro	Leu	Val	Asn	Pro	Asp	Gly		
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Val	Ala	Tyr	Asp	Gln	Ser	Ser	Gly	Ser	Leu	Trp	Arg	Lys	Asn	Arg	Asn		
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Thr	Arg	Ser	Gly	Thr	Ser	Gly	Ala	Ser	Val	Gly	Val	Asp	Ile	Asn	Arg		
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Asn	Phe	Asp	Phe	Leu	Trp	Asn	Phe	Lys	Lys	Phe	Phe	Asp	Pro	Ser	Thr		
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Ser	Pro	Ala	Ser	Thr	Ser	Pro	Ser	Ser	Glu	Ala	Phe	Tyr	Gly	Thr	Ala		
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gcc	gca	tct	gag	ccc	gag	acc	aag	aac	cac	atc	agc	atc	tac	gac	agc		960
Ala	Ala	Ser	Glu	Pro	Glu	Thr	Lys	Asn	His	Ile	Ser	Ile	Tyr	Asp	Ser		
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ttc	ccc	aag	atc	agg	tgg	ttc	atg	gat	atc	cac	tct	gct	act	ggt	gac		1008
Phe	Pro	Lys	Ile	Arg	Trp	Phe	Met	Asp	Ile	His	Ser	Ala	Thr	Gly	Asp		
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atc	cta	tac	aac	tgg	ggt	gac	gac	gag	aca	cag	tcc	aca	aac	agc	gct		1056
Ile	Leu	Tyr	Asn	Trp	Gly	Asp	Asp	Glu	Thr	Gln	Ser	Thr	Asn	Ser	Ala		
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Asn	Lys	Val	Phe	Gly	Phe	Thr	Met	Glu	Phe	Gly	Tyr	Ala	Thr	Asn	Phe		
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10336256.txt

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<210> 200

<211> 479

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

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<221> DOMAIN

<222> (124)...(344)

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 35 40 45
 Lys Ala Val Pro His Glu Asp Gly His Phe Glu Leu His Ala Leu Leu
 50 55 60
 Thr Glu Glu Gln Ile Ala His Leu Glu Arg Glu Tyr Glu His Ser Gly
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 Glu Ile Ser Leu His Arg Arg Asp Leu Ser Lys Arg Ala Ala Asp Ala
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 Pro Ile Gly Thr Gly Asp Arg Trp Gln Gly Gly Ala Val Thr Pro Ser
 100 105 110
 Gly Leu Gly Thr Lys Ala Ala Gly Ser Thr Val Ser Ser Ile Met Asn
 115 120 125
 Pro Thr Glu Ile Asn Ser Ala Ile Lys Gly Leu Val Asn Gly Tyr Gly
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 Thr Ala Gly Tyr Val Gly Ala Gly Thr Asp Lys Ser Gln Tyr Lys Leu
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 225 230 235 240
 Val Ala Tyr Asp Gln Ser Ser Gly Ser Leu Trp Arg Lys Asn Arg Asn
 245 250 255
 Thr Arg Ser Gly Thr Ser Gly Ala Ser Val Gly Val Asp Ile Asn Arg
 260 265 270
 Asn Phe Asp Phe Leu Trp Asn Phe Lys Lys Phe Phe Asp Pro Ser Thr
 275 280 285
 Ser Pro Ala Ser Thr Ser Pro Ser Ser Glu Ala Phe Tyr Gly Thr Ala
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 Ala Ala Ser Glu Pro Glu Thr Lys Asn His Ile Ser Ile Tyr Asp Ser
 305 310 315 320
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 Met Asn Phe Leu Asn Thr Ala Tyr Asp Gly Lys Arg Gly Arg Ile Gly
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 Asp Ser Thr Tyr Lys Glu Tyr Met Pro Ser Ala Asp Val Thr Gly Ile
 370 375 380
 Lys Ser Val Ala Ser Lys Thr Ala Ala Ala Val Ala Ala Val Gly Gly
 385 390 395 400

10336256.txt

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 Asn Lys Val Phe Gly Phe Thr Met Glu Phe Gly Tyr Ala Thr Asn Phe
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<211> 3380

<212> DNA

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<220>

<221> CDS

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<222> (1641)...(2380)

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gtgttcatac	gcgtgaaact	tgcaaaacat	cgtagaccgt	agagacgtag	ctcaatgcga	480
cgctcatcaaa	gcaccgatat	cgtctcttga	ggagcatcat	ggtgaaacat	catttgcttc	540
tcaagaaaaa	gaacacgcag	gittccaatg	atctttggaa	tcaagcatga	ggctacagaa	600
tagctatgga	acaggaattt	tgtacggctt	ttcaacggct	ttcgacggga	tcagcaatat	660
acccggggggc	tgagggggag	ttgcataccc	gacctgcctt	gctccttggc	gatgcgtcta	720
gatcaggaag	ctgggggtac	ataagtatac	acaagcctgg	gcatcgctt	ggctagcggg	780
cgaacgcagc	tccacctact	gaatatgatt	ccagtgatgc	aaatgaacac	ggcaatgctg	840
tgcgagctag	catgacagtt	ccatggcgac	attcgattat	tgcaaccgagc	ttcccgcgc	900
gcagataagg	ttagaacagg	gggtccaaagt	catatttaag	aagtgtatat	gatgttgtaa	960
tgacttgtgt	gttgtgtttg	ttaactctcc	gaacttcaaa	atg aga ttg tca aag		1015
				Met Arg Leu Ser Lys		
				1 5		

ttg gtg gtg gcc gct caa ttg gca gca gcg tct cct ttg gca cac gac	1063
Leu Val Val Ala Ala Gln Leu Ala Ala Ala Ser Pro Leu Ala His Asp	
10 15 20	

gct agc tct gtg tct cgc agt gcc aac cca agc tac gat ggc tac caa	1111
Ala Ser Ser Val Ser Arg Ser Ala Asn Pro Ser Tyr Asp Gly Tyr Gln	
25 30 35	

atc tac tcc att acg cca tct tct gcc gaa gaa gct cat gat atc aac	1159
Ile Tyr Ser Ile Thr Pro Ser Ser Ala Glu Glu Ala His Asp Ile Asn	
40 45 50	

aag cgc ttc tcc aac tac cac act cac ccg att cgc aac acc ctg tca	1207
Lys Arg Phe Ser Asn Tyr His Thr His Pro Ile Arg Asn Thr Leu Ser	
55 60 65	

gtt gct att cca ccc gag gag att gac tct ttt cgt gca ctg ggt ttg	1255
Val Ala Ile Pro Pro Glu Glu Ile Asp Ser Phe Arg Ala Leu Gly Leu	

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70	75	80	85	
aac gct cgc ctg gtg aac tcg gat ctg ggc aag tac att cgc tct acc	Asn Ala Arg Leu Val 90	Asn Ser Asp Leu Gly 95	Lys Tyr Ile Arg Ser 100	1303
gac aag gaa gcc gta tac aag cgt gac ttg cat gca acg ggt cag ctc	Asp Lys Glu Ala Val 105	Asp Leu His Ala Thr 110	Gly Gln Leu 115	1351
ccg gac ctg tcg tgg ttc gac act tac cat gct tat tcc gac cac ctt	Pro Asp Leu Ser Trp Phe Asp Thr 125	Tyr His Ala Tyr Ser 130	Asp His Leu 135	1399
cag tac tgg gac gac ctt gtt gcg gcg ttc cct ggt aac tct gag aag	Gln Tyr Trp Asp Asp Leu Val 140	Ala Ala Phe Pro Gly 145	Asn Ser Glu Lys 150	1447
ttt tcg att ggc cag agt tat gag aac cgg aca att tgg gcg ttc cat	Phe Ser Ile Gly Gln Ser Tyr Glu Asn Arg Thr 155	Ile Trp Ala Phe His 160	165	1495
ttg ttt ggt gac aag agc act gaa gct gca acg caa gaa aag ccc att	Leu Phe Gly Asp Lys Ser Thr Glu Ala Thr Gln Glu Lys Pro Ile 170	175	180	1543
att ctt tgg cat gcc aca gtt cac gca aga gaa tgg atc tcc act atg	Ile Leu Trp His Ala Thr Val His Ala Arg Glu Trp Ile Ser Thr Met 185	190	195	1591
g gtaagcagaa cacgcatgag aaaaaggaat actagctaac gctcccag tc atc gag			Val Ile Glu 200	1648
tac cta gcc tac cag ctt att gac ggg tac caa aaa ggc gat gca aat	Tyr Leu Ala Tyr Gln Leu Ile Asp Gly Tyr 205	Gln Lys Gly Asp Ala Asn 210	215	1696
gtg act agt ttt ctg gac cac tac gac ttc tac ctc gtc ccc ttc cac	Val Thr Ser Phe Leu Asp His Tyr Asp Phe Tyr Leu Val Pro Phe His 220	225	230	1744
aac cca gac ggc ttc tcg tac aca caa acc aac gac cga cta tgg cgc	Asn Pro Asp Gly Phe Ser Tyr Thr Gln Thr Asn Asp Arg Leu Trp Arg 235	240	245	1792
aag aac cgg cag ccg cgc ccc caa cta aac acg gcc tgt gtc ggc acc	Lys Asn Arg Gln Pro Arg Pro Gln Leu Asn Thr Ala Cys Val Gly Thr 250	255	260	1840
gac ggc aac cgc aac tgg aag ttt gaa tgg gac gcc acg cct cca gac	Asp Gly Asn Arg Asn Trp Lys Phe Glu Trp Asp Ala Thr Pro Pro Asp 265	270	275	1888
ggt ggt tca acg ccc aat ccg tgc gga gag acg tac cgt ggc gaa gcc	Gly Gly Ser Thr Pro Asn Pro Cys Gly Glu Thr Tyr Arg Gly Glu Ala 285	290	295	1936
gcc ggc gac aca ccc gag aat caa gcc atg gac gga ctc tct gct aag	Ala Gly Asp Thr Pro Glu Asn Gln Ala Met Asp Gly Leu Ser Ala Lys 300	305	310	1984
ctt tcc agc acg ggc gct ggc atc cgg tcc ttc atc gac ttc cac tcg	Leu Ser Ser Thr Gly Ala Gly Ile Arg Ser Phe Ile Asp Phe His Ser 315	320	325	2032
tac agc cag ctt atc ctc act ccc tgg ggt ttc tcg tgc gac ccg ctc	Tyr Ser Gln Leu Ile Leu Thr Pro Trp Gly Phe Ser Cys Asp Pro Leu 330			2080

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340

330 335
 ccc gaa acg ctt ccc cgt atg ctc gag gta gca ggc ggc act gcc aga 2128
 Pro Glu Thr Leu Pro Arg Met Leu Glu Val Ala Gly Gly Thr Ala Arg 360
 345 350 355
 gct atc cag gcg ggc agc gcg cga aac gtc acg tac gag ttt ggg cct 2176
 Ala Ile Gln Ala Gly Ser Ala Arg Asn Val Thr Tyr Glu Phe Gly Pro 375
 365 370 375
 ggc tgt cag att ctg tac ttc tcc acg ggc aac tcg aga gac cac cac 2224
 Gly Cys Gln Ile Leu Tyr Phe Ser Thr Gly Asn Ser Arg Asp His His 390
 380 385 390
 cat gct gtg cat ggc gcg gcg cac tcg tgg act atg gag ctg agc ccc 2272
 His Ala Val His Gly Ala Ala His Ser Trp Thr Met Glu Leu Ser Pro 405
 395 400 405
 cag gac gcg gca gga ggc ggg ttt gtt ctg ccg cct gaa ctc att tgg 2320
 Gln Asp Ala Ala Gly Gly Gly Phe Val Leu Pro Pro Glu Leu Ile Trp 420
 410 415 420
 ccg acg gtc aag gag cag tgg gcg ggc cag ttg tgg ttg ttg aat gat 2368
 Pro Thr Val Lys Glu Gln Trp Ala Gly Gln Leu Trp Leu Leu Asn Asp 440
 425 430 435 440
 gtt tgg gat aac tgagcttttg gtgcaatggc acaggaatat catgcactgt 2420
 Val Trp Asp Asn

tggatggcat atttgccctag attggctacg agatagatgc tatgaaacat tctgtgaact 2480
 ggctcttgaa gcattgcaga tgttcaagtg atgtgtttat gattggagta agatctggag 2540
 cttgacctat aagcagtgcc ttatacccac atcttctctt atccatatcg tcctcatgtc 2600
 ctcatgtcct catgtcctca ttgtcccaac tcacagttac aaaatatcag gagcacaagt 2660
 acaggtttca acattataatc tatttaaagt cgagacagtg gacagttagt aaatgaacag 2720
 gtannnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 2780
 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 2840
 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 2900
 nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 2960
 nncatcatag gcgtcatgtg gcgtgaggag aaacactaaa gttggacaca agggcattgc 3020
 tcactcagaca gagactatga gcttcatccg aacatgcggt tctcgtattg atagatgggc 3080
 agactccatt aggggtagtc agtgcatact ggattggagc aagatcgaaa ctgagtcatc 3140
 atcgcccaaa ggacgatttc gaaaagccca agacctaatac aacgagggtc gtatatggaa 3200
 tcgaaaatct ctcagacgat gagtacttgt gagcatgaaa tgcgaagaat tgataatggc 3260
 acgaggttct ggtgtagtga acgacaagaa gctggtcgca ttgttgacgg cgggttgag 3320
 atttggatct gcaagtgcag tctcgaaaat ctttacggtc aggctctcgt tgggtggtgac 3380

<210> 202

<211> 197

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 202

Met Arg Leu Ser Lys Leu Val Val Ala Ala Gln Leu Ala Ala Ala Ser
 1 5 10 15
 Pro Leu Ala His Asp Ala Ser Ser Val Ser Arg Ser Ala Asn Pro Ser
 20 25 30
 Tyr Asp Gly Tyr Gln Ile Tyr Ser Ile Thr Pro Ser Ser Ala Glu Glu
 35 40 45
 Ala His Asp Ile Asn Lys Arg Phe Ser Asn Tyr His Thr His Pro Ile
 50 55 60
 Arg Asn Thr Leu Ser Val Ala Ile Pro Pro Glu Glu Ile Asp Ser Phe
 65 70 75 80
 Arg Ala Leu Gly Leu Asn Ala Arg Leu Val Asn Ser Asp Leu Gly Lys
 85 90 95
 Tyr Ile Arg Ser Thr Asp Lys Glu Ala Val Tyr Lys Arg Asp Leu His
 100 105 110
 Ala Thr Gly Gln Leu Pro Asp Leu Ser Trp Phe Asp Thr Tyr His Ala

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Tyr Ser Asp His Leu Gln Tyr Trp Asp Asp Leu Val Ala Ala Phe Pro
 115 120 125
 130 135 140
 Gly Asn Ser Glu Lys Phe Ser Ile Gly Gln Ser Tyr Glu Asn Arg Thr
 145 150 155 160
 Ile Trp Ala Phe His Leu Phe Gly Asp Lys Ser Thr Glu Ala Ala Thr
 165 170 175
 Gln Glu Lys Pro Ile Ile Leu Trp His Ala Thr Val His Ala Arg Glu
 180 185 190
 Trp Ile Ser Thr Met
 195

<210> 203

<211> 247

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 203

Val Ile Glu Tyr Leu Ala Tyr Gln Leu Ile Asp Gly Tyr Gln Lys Gly
 1 5 10 15
 Asp Ala Asn Val Thr Ser Phe Leu Asp His Tyr Asp Phe Tyr Leu Val
 20 25 30
 Pro Phe His Asn Pro Asp Gly Phe Ser Tyr Thr Gln Thr Asn Asp Arg
 35 40 45
 Leu Trp Arg Lys Asn Arg Gln Pro Arg Pro Gln Leu Asn Thr Ala Cys
 50 55 60
 Val Gly Thr Asp Gly Asn Arg Asn Trp Lys Phe Glu Trp Asp Ala Thr
 65 70 75 80
 Pro Pro Asp Gly Gly Ser Thr Pro Asn Pro Cys Gly Glu Thr Tyr Arg
 85 90 95
 Gly Glu Ala Ala Gly Asp Thr Pro Glu Asn Gln Ala Met Asp Gly Leu
 100 105 110
 Ser Ala Lys Leu Ser Ser Thr Gly Ala Gly Ile Arg Ser Phe Ile Asp
 115 120 125
 Phe His Ser Tyr Ser Gln Leu Ile Leu Thr Pro Trp Gly Phe Ser Cys
 130 135 140
 Asp Pro Leu Pro Glu Thr Leu Pro Arg Met Leu Glu Val Ala Gly Gly
 145 150 155 160
 Thr Ala Arg Ala Ile Gln Ala Gly Ser Ala Arg Asn Val Thr Tyr Glu
 165 170 175
 Phe Gly Pro Gly Cys Gln Ile Leu Tyr Phe Ser Thr Gly Asn Ser Arg
 180 185 190
 Asp His His His Ala Val His Gly Ala Ala His Ser Trp Thr Met Glu
 195 200 205
 Leu Ser Pro Gln Asp Ala Ala Gly Gly Phe Val Leu Pro Pro Glu
 210 215 220
 Leu Ile Trp Pro Thr Val Lys Glu Gln Trp Ala Gly Gln Leu Trp Leu
 225 230 235 240
 Leu Asn Asp Val Trp Asp Asn
 245

<210> 204

<211> 1332

<212> DNA

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1332)

<400> 204

atg aga ttg tca aag ttg gtg gtg gcc gct caa ttg gca gca gcg tct
 Met Arg Leu Ser Lys Leu Val Val Ala Ala Gln Leu Ala Ala Ala Ser
 1 5 10 15
 cct ttg gca cac gac gct agc tct gtg tct cgc agt gcc aac cca agc
 Pro Leu Ala His Asp Ala Ser Ser Val Ser Arg Ser Ala Asn Pro Ser
 20 25 30

48

96

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tac gat ggc tac caa atc tac tcc att acg cca tct tct gcc gaa gaa Tyr Asp Gly Tyr Gln Ile Tyr Ser Ile Thr Pro Ser Ser Ala Glu Glu 35 40 45	144
gct cat gat atc aac aag cgc ttc tcc aac tac cac act cac ccg att Ala His Asp Ile Asn Lys Arg Phe Ser Asn Tyr His Thr His Pro Ile 50 55 60	192
cgc aac acc ctg tca gtt gct att cca ccc gag gag att gac tct ttt Arg Asn Thr Leu Ser Val Ala Ile Pro Pro Glu Glu Ile Asp Ser Phe 65 70 75 80	240
cgt gca ctg ggt ttg aac gct cgc ctg gtg aac tcg gat ctg ggc aag Arg Ala Leu Gly Leu Asn Ala Arg Leu Val Asn Ser Asp Leu Gly Lys 85 90 95	288
tac att cgc tct acc gac aag gaa gcc gta tac aag cgt gac ttg cat Tyr Ile Arg Ser Thr Asp Lys Glu Ala Val Tyr Lys Arg Asp Leu His 100 105 110	336
gca acg ggt cag ctc ccg gac ctg tcg tgg ttc gac act tac cat gct Ala Thr Gly Gln Leu Pro Asp Leu Ser Trp Phe Asp Thr Tyr His Ala 115 120 125	384
tat tcc gac cac ctt cag tac tgg gac gac ctt gtt gcg gcg ttc cct Tyr Ser Asp His Leu Gln Tyr Trp Asp Asp Leu Val Ala Ala Phe Pro 130 135 140	432
ggt aac tct gag aag ttt tcg att ggc cag agt tat gag aac cgg aca Gly Asn Ser Glu Lys Phe Ser Ile Gly Gln Ser Tyr Glu Asn Arg Thr 145 150 155 160	480
att tgg gcg ttc cat ttg ttt ggt gac aag agc act gaa gct gca acg Ile Trp Ala Phe His Leu Phe Gly Asp Lys Ser Thr Glu Ala Ala Thr 165 170 175	528
caa gaa aag ccc att att ctt tgg cat gcc aca gtt cac gca aga gaa Gln Glu Lys Pro Ile Ile Leu Trp His Ala Thr Val His Ala Arg Glu 180 185 190	576
tgg atc tcc act atg gtc atc gag tac cta gcc tac cag ctt att gac Trp Ile Ser Thr Met Val Ile Glu Tyr Leu Ala Tyr Gln Leu Ile Asp 195 200 205	624
ggg tac caa aaa ggc gat gca aat gtg act agt ttt ctg gac cac tac Gly Tyr Gln Lys Gly Asp Ala Asn Val Thr Ser Phe Leu Asp His Tyr 210 215 220	672
gac ttc tac ctc gtc ccc ttc cac aac cca gac ggc ttc tcg tac aca Asp Phe Tyr Leu Val Pro Phe His Asn Pro Asp Gly Phe Ser Tyr Thr 225 230 235 240	720
caa acc aac gac cga cta tgg cgc aag aac cgg cag ccg cgc ccc caa Gln Thr Asn Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro Arg Pro Gln 245 250 255	768
cta aac acg gcc tgt gtc ggc acc gac ggc aac cgc aac tgg aag ttt Leu Asn Thr Ala Cys Val Gly Thr Asp Gly Asn Arg Asn Trp Lys Phe 260 265 270	816
gaa tgg gac gcc acg cct cca gac ggt ggt tca acg ccc aat ccg tgc Glu Trp Asp Ala Thr Pro Pro Asp Gly Gly Ser Thr Pro Asn Pro Cys 275 280 285	864
gga gag acg tac cgt ggc gaa gcc gcc ggc gac aca ccc gag aat caa Gly Glu Thr Tyr Arg Gly Glu Ala Ala Gly Asp Thr Pro Glu Asn Gln 290 295 300	912

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gcc atg gac gga ctc tct gct aag ctt tcc agc acg ggc gct ggc atc      960
Ala Met Asp Gly Leu Ser Ala Lys Leu Ser Ser Thr Gly Ala Gly Ile
305                               310                               315                               320

cgg tcc ttc atc gac ttc cac tcg tac agc cag ctt atc ctc act ccc      1008
Arg Ser Phe Ile Asp Phe His Ser Tyr Ser Gln Leu Ile Leu Thr Pro
                               325                               330                               335

tgg ggt ttc tcg tgc gac ccg ctc ccc gaa acg ctt ccc cgt atg ctc      1056
Trp Gly Phe Ser Cys Asp Pro Leu Pro Glu Thr Leu Pro Arg Met Leu
                               340                               345                               350

gag gta gca ggc ggc act gcc aga gct atc cag gcg ggc agc gcg cga      1104
Glu Val Ala Gly Gly Thr Ala Arg Ala Ile Gln Ala Gly Ser Ala Arg
                               355                               360                               365

aac gtc acg tac gag ttt ggg cct ggc tgt cag att ctg tac ttc tcc      1152
Asn Val Thr Tyr Glu Phe Gly Pro Gly Cys Gln Ile Leu Tyr Phe Ser
                               370                               375                               380

acg ggc aac tcg aga gac cac cac cat gct gtg cat ggc gcg gcg cac      1200
Thr Gly Asn Ser Arg Asp His His His Ala Val His Gly Ala Ala His
385                               390                               395                               400

tcg tgg act atg gag ctg agc ccc cag gac gcg gca gga ggc ggg ttt      1248
Ser Trp Thr Met Glu Leu Ser Pro Gln Asp Ala Ala Gly Gly Gly Phe
                               405                               410                               415

gtt ctg ccg cct gaa ctc att tgg ccg acg gtc aag gag cag tgg gcg      1296
Val Leu Pro Pro Glu Leu Ile Trp Pro Thr Val Lys Glu Gln Trp Ala
                               420                               425                               430

ggc cag ttg tgg ttg ttg aat gat gtt tgg gat aac      1332
Gly Gln Leu Trp Leu Leu Asn Asp Val Trp Asp Asn
                               435                               440

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<210> 205

<211> 444

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> DOMAIN

<222> (124)...(340)

<223> Zinc carboxypeptidase

<400> 205

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Met Arg Leu Ser Lys Leu Val Val Ala Ala Gln Leu Ala Ala Ala Ser
 1                               5                               10                               15
Pro Leu Ala His Asp Ala Ser Ser Val Ser Arg Ser Ala Asn Pro Ser
                               20                               25                               30
Tyr Asp Gly Tyr Gln Ile Tyr Ser Ile Thr Pro Ser Ser Ala Glu Glu
35                               40                               45
Ala His Asp Ile Asn Lys Arg Phe Ser Asn Tyr His Thr His Pro Ile
50                               55                               60
Arg Asn Thr Leu Ser Val Ala Ile Pro Pro Glu Ile Asp Ser Phe
65                               70                               75                               80
Arg Ala Leu Gly Leu Asn Ala Arg Leu Val Asn Ser Asp Leu Gly Lys
85                               90                               95
Tyr Ile Arg Ser Thr Asp Lys Glu Ala Val Tyr Lys Arg Asp Leu His
100                               105                               110
Ala Thr Gly Gln Leu Pro Asp Leu Ser Trp Phe Asp Thr Tyr His Ala
115                               120                               125
Tyr Ser Asp His Leu Gln Tyr Trp Asp Asp Leu Val Ala Ala Phe Pro
130                               135                               140
Gly Asn Ser Glu Lys Phe Ser Ile Gly Gln Ser Tyr Glu Asn Arg Thr

```


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145      150      155      160
Ile Trp Ala Phe His Leu Phe Gly Asp Lys Ser Thr Glu Ala Ala Thr
165      170      175
Gln Glu Lys Pro Ile Ile Leu Trp His Ala Thr Val His Ala Arg Glu
180      185      190
Trp Ile Ser Thr Met Val Ile Glu Tyr Leu Ala Tyr Gln Leu Ile Asp
195      200      205
Gly Tyr Gln Lys Gly Asp Ala Asn Val Thr Ser Phe Leu Asp His Tyr
210      215      220
Asp Phe Tyr Leu Val Pro Phe His Asn Pro Asp Gly Phe Ser Tyr Thr
225      230      235      240
Gln Thr Asn Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro Arg Pro Gln
245      250      255
Leu Asn Thr Ala Cys Val Gly Thr Asp Gly Asn Arg Asn Trp Lys Phe
260      265      270
Glu Trp Asp Ala Thr Pro Pro Asp Gly Gly Ser Thr Pro Asn Pro Cys
275      280      285
Gly Glu Thr Tyr Arg Gly Glu Ala Ala Gly Asp Thr Pro Glu Asn Gln
290      295      300
Ala Met Asp Gly Leu Ser Ala Lys Leu Ser Ser Thr Gly Ala Gly Ile
305      310      315      320
Arg Ser Phe Ile Asp Phe His Ser Tyr Ser Gln Leu Ile Leu Thr Pro
325      330      335
Trp Gly Phe Ser Cys Asp Pro Leu Pro Glu Thr Leu Pro Arg Met Leu
340      345      350
Glu Val Ala Gly Gly Thr Ala Arg Ala Ile Gln Ala Gly Ser Ala Arg
355      360      365
Asn Val Thr Tyr Glu Phe Gly Pro Gly Cys Gln Ile Leu Tyr Phe Ser
370      375      380
Thr Gly Asn Ser Arg Asp His His His Ala Val His Gly Ala Ala His
385      390      395      400
Ser Trp Thr Met Glu Leu Ser Pro Gln Asp Ala Ala Gly Gly Gly Phe
405      410      415
Val Leu Pro Pro Glu Leu Ile Trp Pro Thr Val Lys Glu Gln Trp Ala
420      425      430
Gly Gln Leu Trp Leu Leu Asn Asp Val Trp Asp Asn
435      440

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<210> 206
 <211> 3999
 <212> DNA
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>
 <221> CDS
 <222> (1265)...(1549)
 <223> Exon

<221> CDS
 <222> (1609)...(1950)
 <223> Exon

<221> CDS
 <222> (2001)...(2999)
 <223> Exon

<221> misc_feature
 <222> (1)...(3999)
 <223> n = A,T,C or G

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<400> 206
cgtgccgagc gtttacttct tttttcctga gccaaaggga cgcagtttgg aggagctgga      60
tgtcattttt gcgagtgcga atcagatggg ggtagtcct gtgaagagag cgagggagat      120
ggagaagctg gtggggaggg agttggatga ggagattgag agattttttg ggggtgatgt      180
ggaggagggt aggcggagga gcagagcttg agaggtggat tggatttttc gatgtgtagg      240
cacgcgtgca ggttgattgt cgtgattttg acgtggcctt gggcggtact ttttttcattg      300
cactctgccg gtgtagggtg tgcccggcca tcttgacacg agtttccggt caacagcaag      360
gttgtagcca gacggcctaa gttgggaaca tcaaattccat gcagcacgag ttgtactgca      420

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aatccaataa	caccctatcg	cgatgatcga	tagatggcga	cctgccgact	gcagctagcg	480
ttacacaccg	gcaatatcga	tgtcgcgggg	ggctgggtgc	ctcattctcc	tcttttgcaa	540
cggtccaaaa	cgccacaacg	ctttcaacta	cgccccaacc	tccagattgg	ggctacaact	600
atgacgttga	taagctttcc	tcgggtcaac	gaacgacttg	gcaagaggcc	ttattccacc	660
attgcgcata	gcgagcttct	tgtttggtga	aggtgtgtga	tttgatgtgc	gtagactact	720
cggaacctcat	tggagaaaac	acacacaaat	cgtcactctc	tttcatcgat	ggaaaaacac	780
gccttagaca	gcagtttcga	tggctgaaaa	attgcggcat	aggttgcatc	tttgactcga	840
tgccctttgt	cctaagccat	aattagtaac	cgggtgataca	aaatccaacc	gcggcaaaca	900
agttgtattt	ctgaaagctc	ttactagtat	tgtcgcctta	acgcggaact	cgcaagatct	960
tcatactcgt	gttatcccg	ccaattgcaa	tgaccagtac	tactttgcag	ttgcctgatt	1020
cggattaaac	ctacctgcac	tggcctaccc	acagatcgca	tttggcctca	catggagcca	1080
gcccgccatg	cagtgtcag	ccatggcagg	cggaagaaaa	tgtacatagc	cgcatcattg	1140
catgttggtt	aacggcttag	cctcgtacgc	attcagtgta	tttaagaagg	ccgagagaag	1200
cggccttctc	ggcaagcccc	ctgcttaagc	cttggtcatt	cttcttcacg	acaagctatt	1260
cacc atg gcg cgc ttc acc cag att	ggt gct gtc ttg gca gca gcg acg					1309
Met Ala Arg Phe Thr Gln Ile	Val Ala Val Leu Ala Ala Ala Thr					
1	5	10	15			
ctc agt cat gct cgc aag cca ttc atc act gag cgt cag gtc ccg gct						1357
Leu Ser His Ala Arg Lys Pro Phe Ile Thr Glu Arg Gln Val Pro Ala						
	20	25	30			
gac ccc act ggc gtc aca acc atc aag tct gct cag ggt gcc gag att						1405
Asp Pro Thr Gly Val Thr Thr Ile Lys Ser Ala Gln Gly Ala Glu Ile						
	35	40	45			
cgc tac aag cag cct gga aag gcg gga gtt tgc gag act act gaa ggt						1453
Arg Tyr Lys Gln Pro Gly Lys Ala Gly Val Cys Glu Thr Thr Glu Gly						
	50	55	60			
ggt gac gat tat gcc ggt tac atc agt ctc aat cct act acc aac atg						1501
Val Asp Asp Tyr Ala Gly Tyr Ile Ser Leu Asn Pro Thr Thr Asn Met						
	65	70	75			
ttc ttt tgg ttc ttc gag gcg cgt gaa aac ccc tcc gaa aag ccg ttg						1549
Phe Phe Trp Phe Phe Glu Ala Arg Glu Asn Pro Ser Glu Lys Pro Leu						
	80	85	90	95		
gcaagtacaa cctatatatttc agctcagaat tcggtagcag attctaactt tgtttccag						1608
aca ctt tgg ttg aat ggt gga cca gga agt gac tcg ctc atc ggt ctc						1656
Thr Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile Gly Leu						
	100	105	110			
ttc caa gaa cac ggc cca tgt aat gtc act gag gat ttg aag aca caa						1704
Phe Gln Glu His Gly Pro Cys Asn Val Thr Glu Asp Leu Lys Thr Gln						
	115	120	125			
ttg aat cct tat tca tgg aac gag cac agc aac atg ctc tac ctc tcg						1752
Leu Asn Pro Tyr Ser Trp Asn Glu His Ser Asn Met Leu Tyr Leu Ser						
	130	135	140			
cag cct gtt ggt gta ggc ttc tcc tac gag acc aca gaa acc gac gcg						1800
Gln Pro Val Gly Val Gly Phe Ser Tyr Glu Thr Thr Glu Thr Asp Ala						
	145	150	155			
gac ggt cga tac tcg ctt gtt gat ccc gat acc aca aac act acc gat						1848
Asp Gly Arg Tyr Ser Leu Val Asp Pro Asp Thr Asn Thr Thr Asp						
	160	165	170			
gct gca gcc atc ggt gcg tgg cac att ctc cag gct ttc ttg gac ctg						1896
Ala Ala Ala Ile Gly Ala Trp His Ile Leu Gln Ala Phe Leu Asp Leu						
	180	185	190			
agc ccc cag ctc gac ccg gat atc act aac ttt aca ttc aat ctt tgg						1944
Ser Pro Gln Leu Asp Pro Asp Ile Thr Asn Phe Thr Phe Asn Leu Trp						
	195	200	205			
act gag aggttagtga ttcagcaaca agactgaaaa cgtattgctc accagtttct						2000

10336256.txt

Thr Glu

agc Ser 210	tac Tyr	gga Gly	gga Gly	cat His	tac Tyr 215	ggc Gly	ccc Pro	ggt Gly	ttc Phe	tac Tyr 220	aac Asn	tac Tyr	ttc Phe	tac Tyr	caa Gln 225	2048
caa Gln	aat Asn	gag Glu	aag Lys	atc Ile 230	aag Lys	aac Asn	ggc Gly	tct Ser	tcc Ser 235	cct Pro	ggt Gly	gtc Val	gag Glu	att Ile 240	cgc Arg	2096
atg Met	gac Asp	act Thr	ctc Leu 245	ggt Gly	ata Ile	atc Ile	aac Asn	gga Gly 250	att Ile	gtc Val	gat Asp	gag Glu	cag Gln 255	atc Ile	cag Gln	2144
gcc Ala	cct Pro	tac Tyr 260	tac Tyr	ccc Pro	gag Glu	ttt Phe	gct Ala 265	gtc Val	aac Asn	aac Asn	acc Thr	tat Tyr 270	ggc Gly	atc Ile	aaa Lys	2192
gca Ala 275	gtt Val	aac Asn	gac Asp	acg Thr	gtt Val	tac Tyr 280	act Thr	ttc Phe	atg Met	aag Lys	aac Asn 285	gcc Ala	tac Tyr	tac Tyr	atg Met	2240
cca Pro 290	gaa Glu	ggc Gly	tgc Cys	cac His	gat Asp 295	caa Gln	atc Ile	gaa Glu	tac Tyr	tgc Cys 300	aag Lys	caa Gln	tcc Ser	gac Asp	cgc Arg 305	2288
acc Thr	acc Thr	caa Gln	gac Asp	ggc Gly 310	tat Tyr	cta Leu	act Thr	tgt Cys	tca Ser 315	tcc Ser	gca Ala	acc Thr	aac Asn	ctc Leu 320	tgc Cys	2336
cga Arg	tcg Ser	ctc Leu	gtc Val 325	gaa Glu	gag Glu	cca Pro	tat Tyr	tac Tyr 330	gca Ala	ttt Phe	ggc Gly	ggg Gly	cgt Arg 335	ggc Gly	gtc Val	2384
tac Tyr	gac Asp	atc Ile 340	cgc Arg	cat His	ccc Pro	tac Tyr	gac Asp 345	gac Asp	cct Pro	acg Thr	ccc Pro	ccc Pro 350	gac Asp	tat Tyr	ttc Phe	2432
gag Glu 355	tcc Ser	ttc Phe	ctg Leu	aac Asn	ctg Leu	gcc Ala 360	tca Ser	acc Thr	caa Gln	gaa Glu	gcc Ala 365	atc Ile	ggc Gly	gta Val	aac Asn	2480
atc Ile 370	aac Asn	tac Tyr	acg Thr	agc Ser	acc Thr 375	aac Asn	gcc Ala	cgc Arg	aac Asn	gtg Val 380	tcc Ser	ctc Leu	ggc Gly	ttc Phe	agt Ser 385	2528
cgc Arg	acc Thr	ggc Gly	gac Asp	ttc Phe 390	gtc Val	ttc Phe	ccc Pro	aac Asn	ttc Phe 395	ctc Leu	gag Glu	gac Asp	ctc Leu	gaa Glu 400	gaa Glu	2576
atc Ile	ctc Leu	gcc Ala	tac Tyr 405	ggc Gly	gtc Val	cgc Arg	gtc Val	gcc Ala 410	ctc Leu	ctc Leu	tac Tyr	ggc Gly	gac Asp 415	gca Ala	gac Asp	2624
tac Tyr	atc Ile	tgc Cys 420	aac Asn	tgg Trp	ttc Phe	ggc Gly	ggc Gly 425	gaa Glu	gcc Ala	gtc Val	tct Ser	ctg Leu 430	gcc Ala	gtc Val	aac Asn	2672
ttc Phe 435	acg Thr	cac His	gcc Ala	gcc Ala	gac Asp	ttc Phe 440	cgc Arg	tcc Ser	gcg Ala	ggc Gly	tac Tyr 445	acg Thr	ccc Pro	ttt Phe	ctc Leu	2720
gtt Val 450	gac Asp	ggc Gly	gtc Val	gag Glu	tac Tyr 455	ggc Gly	gag Glu	gtg Val	cgc Arg	gag Glu 460	tac Tyr	ggc Gly	aac Asn	ttc Phe	tcc Ser 465	2768
ttc	acc	cgc	atc	tac	gag	gcc	ggc	cac	gag	gtc	ccg	tat	tac	cag	cct	2816

10336256.txt

```

Phe Thr Arg Ile Tyr Glu Ala Gly His Glu Val Pro Tyr Tyr Gln Pro
      470      475      480

gaa gct agt ctg gag cat ttt agg cgc gtc ctg cat cat gtc gtt gtt 2864
Glu Ala Ser Leu Glu His Phe Arg Arg Val Leu His His Val Val Val
      485      490      495

gcg gat ggg agc cag gtg gtc acg agt gat tac aag acg aat ggc acc 2912
Ala Asp Gly Ser Gln Val Val Thr Ser Asp Tyr Lys Thr Asn Gly Thr
      500      505      510

gcc aag gcg acg cat aca gag gag ttt gtc ccg ttg ccg ccg acg agt 2960
Ala Lys Ala Thr His Thr Glu Glu Phe Val Pro Leu Pro Pro Thr Ser
      515      520      525

acg ccg agt gct gct agt agg gtg agg agg gga tcg gtg tagattggcc 3009
Thr Pro Ser Ala Ala Ser Arg Val Arg Arg Gly Ser Val
      530      535      540

gtggggggcgg tgagacgggt gatgaagttt agagccttgt gtgaggcatt gatgtatgac 3069
gttaatgact tgaaatgaaa gtaattgaat catgagttca gaggaataac tgcttgtcta 3129
ctgttataag acgtctgaaa tgagtaggtt tgaccctttt accatttgca caatcttttc 3189
tttcgtgtgc acattgcttt ttgtaaactt gttttggctt tcttttaaga gtatcacgcc 3249
ttgttgccga ctgtaccgac gcgtttactt ggcaaatgaa agtcgtttcg aggaaagcta 3309
gggtccgattg attactgttt acttcccttt ccgatcgttc tggatnnnnn nnnnnnnnnn 3369
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3429
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3489
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3549
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnncccccac 3609
caaactcaca cacctctccc atcttatcat acaatggctc aacgcagcgc tactctatta 3669
gcttcaaatg aattagatat tcagcttgcg atctctttaa ttaattctaa gcagattcta 3729
agtaatcggg gtgctgtctg tatctacaac gtgtttaaat gaacgatccg ccgccaacgc 3789
gctggtgtcc ctgctgcgac tgattgccag cctaacttaa agaagctaac ctactagtaa 3849
gaggaggtaa ttgttagcta tatactcaat ctagattagc gtggattcgc gcctacgtac 3909
gcagccgtgc gcgatatagc taataagctg ctagctacgc gtagtagagg acgcgttaga 3969
gttaactagc cgtctacctt tattaagcgt

```

<210> 207

<211> 95

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 207

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Met Ala Arg Phe Thr Gln Ile Val Ala Val Leu Ala Ala Ala Thr Leu
 1      5      10      15
Ser His Ala Arg Lys Pro Phe Ile Thr Glu Arg Gln Val Pro Ala Asp
      20      25      30
Pro Thr Gly Val Thr Thr Ile Lys Ser Ala Gln Gly Ala Glu Ile Arg
      35      40      45
Tyr Lys Gln Pro Gly Lys Ala Gly Val Cys Glu Thr Thr Glu Gly Val
      50      55      60
Asp Asp Tyr Ala Gly Tyr Ile Ser Leu Asn Pro Thr Thr Asn Met Phe
      65      70      75      80
Phe Trp Phe Phe Glu Ala Arg Glu Asn Pro Ser Glu Lys Pro Leu
      85      90      95

```

<210> 208

<211> 114

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 208

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Thr Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile Gly Leu
 1      5      10      15
Phe Gln Glu His Gly Pro Cys Asn Val Thr Glu Asp Leu Lys Thr Gln
      20      25      30
Leu Asn Pro Tyr Ser Trp Asn Glu His Ser Asn Met Leu Tyr Leu Ser
      35      40      45

```

10336256.txt

Gln Pro Val Gly Val Gly Phe Ser Tyr Glu Thr Thr Glu Thr Asp Ala
 50 55 60
 Asp Gly Arg Tyr Ser Leu Val Asp Pro Asp Thr Thr Asn Thr Thr Asp
 65 70 75 80
 Ala Ala Ala Ile Gly Ala Trp His Ile Leu Gln Ala Phe Leu Asp Leu
 85 90 95
 Ser Pro Gln Leu Asp Pro Asp Ile Thr Asn Phe Thr Phe Asn Leu Trp
 100 105 110
 Thr Glu

<210> 209

<211> 333

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 209

Ser Tyr Gly Gly His Tyr Gly Pro Gly Phe Tyr Asn Tyr Phe Tyr Gln
 1 5 10 15
 Gln Asn Glu Lys Ile Lys Asn Gly Ser Ser Pro Gly Val Glu Ile Arg
 20 25 30
 Met Asp Thr Leu Gly Ile Ile Asn Gly Ile Val Asp Glu Gln Ile Gln
 35 40 45
 Ala Pro Tyr Tyr Pro Glu Phe Ala Val Asn Asn Thr Tyr Gly Ile Lys
 50 55 60
 Ala Val Asn Asp Thr Val Tyr Thr Phe Met Lys Asn Ala Tyr Tyr Met
 65 70 75 80
 Pro Glu Gly Cys His Asp Gln Ile Glu Tyr Cys Lys Gln Ser Asp Arg
 85 90 95
 Thr Thr Gln Asp Gly Tyr Leu Thr Cys Ser Ser Ala Thr Asn Leu Cys
 100 105 110
 Arg Ser Leu Val Glu Glu Pro Tyr Tyr Ala Phe Gly Gly Arg Gly Val
 115 120 125
 Tyr Asp Ile Arg His Pro Tyr Asp Asp Pro Thr Pro Pro Asp Tyr Phe
 130 135 140
 Glu Ser Phe Leu Asn Leu Ala Ser Thr Gln Glu Ala Ile Gly Val Asn
 145 150 155 160
 Ile Asn Tyr Thr Ser Thr Asn Ala Arg Asn Val Ser Leu Gly Phe Ser
 165 170 175
 Arg Thr Gly Asp Phe Val Phe Pro Asn Phe Leu Glu Asp Leu Glu Glu
 180 185 190
 Ile Leu Ala Tyr Gly Val Arg Val Ala Leu Leu Tyr Gly Asp Ala Asp
 195 200 205
 Tyr Ile Cys Asn Trp Phe Gly Gly Glu Ala Val Ser Leu Ala Val Asn
 210 215 220
 Phe Thr His Ala Ala Asp Phe Arg Ser Ala Gly Tyr Thr Pro Phe Leu
 225 230 235 240
 Val Asp Gly Val Glu Tyr Gly Glu Val Arg Glu Tyr Gly Asn Phe Ser
 245 250 255
 Phe Thr Arg Ile Tyr Glu Ala Gly His Glu Val Pro Tyr Tyr Gln Pro
 260 265 270
 Glu Ala Ser Leu Glu His Phe Arg Arg Val Leu His His Val Val Val
 275 280 285
 Ala Asp Gly Ser Gln Val Val Thr Ser Asp Tyr Lys Thr Asn Gly Thr
 290 295 300
 Ala Lys Ala Thr His Thr Glu Glu Phe Val Pro Leu Pro Pro Thr Ser
 305 310 315 320
 Thr Pro Ser Ala Ala Ser Arg Val Arg Arg Gly Ser Val
 325 330

<210> 210

<211> 1626

<212> DNA

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1626)

10336256.txt

<400> 210

atg gcg cgc ttc acc cag att gtt gct gtc ttg gca gca gcg acg ctc	48
Met Ala Arg Phe Thr Gln Ile Val Ala Val Leu Ala Ala Ala Thr Leu	
1 5 10 15	
agt cat gct cgc aag cca ttc atc act gag cgt cag gtc ccg gct gac	96
Ser His Ala Arg Lys Pro Phe Ile Thr Glu Arg Gln Val Pro Ala Asp	
20 25 30	
ccc act ggc gtc aca acc atc aag tct gct cag ggt gcc gag att cgc	144
Pro Thr Gly Val Thr Thr Ile Lys Ser Ala Gln Gly Ala Glu Ile Arg	
35 40 45	
tac aag cag cct gga aag gcg gga gtt tgc gag act act gaa ggt gtt	192
Tyr Lys Gln Pro Gly Lys Ala Gly Val Cys Glu Thr Thr Glu Gly Val	
50 55 60	
gac gat tat gcc ggt tac atc agt ctc aat cct act acc aac atg ttc	240
Asp Asp Tyr Ala Gly Tyr Ile Ser Leu Asn Pro Thr Thr Asn Met Phe	
65 70 75 80	
ttt tgg ttc ttc gag gcg cgt gaa aac ccc tcc gaa aag ccg ttg aca	288
Phe Trp Phe Phe Glu Ala Arg Glu Asn Pro Ser Glu Lys Pro Leu Thr	
85 90 95	
ctt tgg ttg aat ggt gga cca gga agt gac tgc ctc atc ggt ctc ttc	336
Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile Gly Leu Phe	
100 105 110	
caa gaa cac ggc cca tgt aat gtc act gag gat ttg aag aca caa ttg	384
Gln Glu His Gly Pro Cys Asn Val Thr Glu Asp Leu Lys Thr Gln Leu	
115 120 125	
aat cct tat tca tgg aac gag cac agc aac atg ctc tac ctc tgc cag	432
Asn Pro Tyr Ser Trp Asn Glu His Ser Asn Met Leu Tyr Leu Ser Gln	
130 135 140	
cct gtt ggt gta ggc ttc tcc tac gag acc aca gaa acc gac gcg gac	480
Pro Val Gly Val Gly Phe Ser Tyr Glu Thr Thr Glu Thr Asp Ala Asp	
145 150 155 160	
ggt cga tac tgc ctt gtt gat ccc gat acc aca aac act acc gat gct	528
Gly Arg Tyr Ser Leu Val Asp Pro Asp Thr Thr Asn Thr Thr Asp Ala	
165 170 175	
gca gcc atc ggt gcg tgg cac att ctc cag gct ttc ttg gac ctg agc	576
Ala Ala Ile Gly Ala Trp His Ile Leu Gln Ala Phe Leu Asp Leu Ser	
180 185 190	
ccc cag ctc gac ccg gat atc act aac ttt aca ttc aat ctt tgg act	624
Pro Gln Leu Asp Pro Asp Ile Thr Asn Phe Thr Phe Asn Leu Trp Thr	
195 200 205	
gag agc tac gga gga cat tac ggc ccc ggt ttc tac aac tac ttc tac	672
Glu Ser Tyr Gly Gly His Tyr Gly Pro Gly Phe Tyr Asn Tyr Phe Tyr	
210 215 220	
caa caa aat gag aag atc aag aac ggc tct tcc cct ggt gtc gag att	720
Gln Gln Asn Glu Lys Ile Lys Asn Gly Ser Ser Pro Gly Val Glu Ile	
225 230 235 240	
cgc atg gac act ctc ggt ata atc aac gga att gtc gat gag cag atc	768
Arg Met Asp Thr Leu Gly Ile Ile Asn Gly Ile Val Asp Glu Gln Ile	
245 250 255	
cag gcc cct tac tac ccc gag ttt gct gtc aac aac acc tat ggc atc	816
Gln Ala Pro Tyr Tyr Pro Glu Phe Ala Val Asn Asn Thr Tyr Gly Ile	

10336256.txt																
260						265						270				
aaa Lys	gca Ala	gtt Val 275	aac Asn	gac Asp	acg Thr	gtt Val	tac Tyr 280	act Thr	ttc Phe	atg Met	aag Lys	aac Asn 285	gcc Ala	tac Tyr	tac Tyr	864
atg Met	cca Pro 290	gaa Glu	ggc Gly	tgc Cys	cac His	gat Asp 295	caa Gln	atc Ile	gaa Glu	tac Tyr	tgc Cys 300	aag Lys	caa Gln	tcc Ser	gac Asp	912
cgc Arg 305	acc Thr	acc Thr	caa Gln	gac Asp	ggc Gly 310	tat Tyr	cta Leu	act Thr	tgt Cys	tca Ser 315	tcc Ser	gca Ala	acc Thr	aac Asn	ctc Leu 320	960
tgc Cys	cga Arg	tcg Ser	ctc Leu	gtc Val 325	gaa Glu	gag Glu	cca Pro	tat Tyr	tac Tyr 330	gca Ala	ttt Phe	ggc Gly	ggg Gly	cgt Arg 335	ggc Gly	1008
gtc Val	tac Tyr	gac Asp	atc Ile 340	cgc Arg	cat His	ccc Pro	tac Tyr	gac Asp 345	gac Asp	cct Pro	acg Thr	ccc Pro	ccc Pro 350	gac Asp	tat Tyr	1056
ttc Phe	gag Glu	tcc Ser 355	ttc Phe	ctg Leu	aac Asn	ctg Leu	gcc Ala 360	tca Ser	acc Thr	caa Gln	gaa Glu	gcc Ala 365	atc Ile	ggc Gly	gta Val	1104
aac Asn	atc Ile 370	aac Asn	tac Tyr	acg Thr	agc Ser	acc Thr 375	aac Asn	gcc Ala	cgc Arg	aac Asn	gtg Val 380	tcc Ser	ctc Leu	ggc Gly	ttc Phe	1152
agt Ser 385	cgc Arg	acc Thr	ggc Gly	gac Asp	ttc Phe 390	gtc Val	ttc Phe	ccc Pro	aac Asn	ttc Phe 395	ctc Leu	gag Glu	gac Asp	ctc Leu	gaa Glu 400	1200
gaa Glu	atc Ile	ctc Leu	gcc Ala	tac Tyr 405	ggc Gly	gtc Val	cgc Arg	gtc Val	gcc Ala 410	ctc Leu	ctc Leu	tac Tyr	ggc Gly	gac Asp 415	gca Ala	1248
gac Asp	tac Tyr	atc Ile	tgc Cys 420	aac Asn	tgg Trp	ttc Phe	ggc Gly	ggc Gly 425	gaa Glu	gcc Ala	gtc Val	tct Ser	ctg Leu 430	gcc Ala	gtc Val	1296
aac Asn	ttc Phe	acg Thr 435	cac His	gcc Ala	gcc Ala	gac Asp	ttc Phe 440	cgc Arg	tcc Ser	gcg Ala	ggc Gly	tac Tyr 445	acg Thr	ccc Pro	ttt Phe	1344
ctc Leu	gtt Val 450	gac Asp	ggc Gly	gtc Val	gag Glu	tac Tyr 455	ggc Gly	gag Glu	gtg Val	cgc Arg	gag Glu 460	tac Tyr	ggc Gly	aat Asn	ttc Phe	1392
tcc Ser 465	ttc Phe	acc Thr	cgc Arg	atc Ile	tac Tyr 470	gag Glu	gcc Ala	ggc Gly	cac His	gag Glu 475	gtc Val	ccg Pro	tat Tyr	tac Tyr	cag Gln 480	1440
cct Pro	gaa Glu	gct Ala	agt Ser	ctg Leu 485	gag Glu	cat His	ttt Phe	agg Arg	cgc Arg 490	gtc Val	ctg Leu	cat His	cat His	gtc Val 495	gtt Val	1488
gtt Val	gcg Ala	gat Asp	ggg Gly 500	agc Ser	cag Gln	gtg Val	gtc Val	acg Thr 505	agt Ser	gat Asp	tac Tyr	aag Lys	acg Thr 510	aat Asn	ggc Gly	1536
acc Thr	gcc Ala	aag Lys 515	gcg Ala	acg Thr	cat His	aca Thr	gag Glu 520	gag Glu	ttt Phe	gtc Val	ccg Pro	ttg Leu 525	ccg Pro	ccg Pro	acg Thr	1584
agt Ser	acg Thr	ccg Pro	agt Ser	gct Ala	gct Ala	agt Ser	agg Arg	gtg Val	agg Arg	agg Arg	gga Gly	tcg Ser	gtg Val			1626

530

535

10336256.txt
540

<210> 211
 <211> 542
 <212> PRT
 <213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>
 <221> SIGNAL
 <222> (1)...(19)

<221> DOMAIN
 <222> (52)...(494)
 <223> Serine carboxypeptidase

<400> 211
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 1 5 10 15
 Ser His Ala Arg Lys Pro Phe Ile Thr Glu Arg Gln Val Pro Ala Asp
 20 25 30
 Pro Thr Gly Val Thr Thr Ile Lys Ser Ala Gln Gly Ala Glu Ile Arg
 35 40 45
 Tyr Lys Gln Pro Gly Lys Ala Gly Val Cys Glu Thr Thr Glu Gly Val
 50 55 60
 Asp Asp Tyr Ala Gly Tyr Ile Ser Leu Asn Pro Thr Thr Asn Met Phe
 65 70 75 80
 Phe Trp Phe Phe Glu Ala Arg Glu Asn Pro Ser Glu Lys Pro Leu Thr
 85 90 95
 Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile Gly Leu Phe
 100 105 110
 Gln Glu His Gly Pro Cys Asn Val Thr Glu Asp Leu Lys Thr Gln Leu
 115 120 125
 Asn Pro Tyr Ser Trp Asn Glu His Ser Asn Met Leu Tyr Leu Ser Gln
 130 135 140
 Pro Val Gly Val Gly Phe Ser Tyr Glu Thr Thr Glu Thr Asp Ala Asp
 145 150 155 160
 Gly Arg Tyr Ser Leu Val Asp Pro Asp Thr Thr Asn Thr Thr Asp Ala
 165 170 175
 Ala Ala Ile Gly Ala Trp His Ile Leu Gln Ala Phe Leu Asp Leu Ser
 180 185 190
 Pro Gln Leu Asp Pro Asp Ile Thr Asn Phe Thr Phe Asn Leu Trp Thr
 195 200 205
 Glu Ser Tyr Gly Gly His Tyr Gly Pro Gly Phe Tyr Asn Tyr Phe Tyr
 210 215 220
 Gln Gln Asn Glu Lys Ile Lys Asn Gly Ser Ser Pro Gly Val Glu Ile
 225 230 235 240
 Arg Met Asp Thr Leu Gly Ile Ile Asn Gly Ile Val Asp Glu Gln Ile
 245 250 255
 Gln Ala Pro Tyr Tyr Pro Glu Phe Ala Val Asn Asn Thr Tyr Gly Ile
 260 265 270
 Lys Ala Val Asn Asp Thr Val Tyr Thr Phe Met Lys Asn Ala Tyr Tyr
 275 280 285
 Met Pro Glu Gly Cys His Asp Gln Ile Glu Tyr Cys Lys Gln Ser Asp
 290 295 300
 Arg Thr Thr Gln Asp Gly Tyr Leu Thr Cys Ser Ser Ala Thr Asn Leu
 305 310 315 320
 Cys Arg Ser Leu Val Glu Glu Pro Tyr Tyr Ala Phe Gly Gly Arg Gly
 325 330 335
 Val Tyr Asp Ile Arg His Pro Tyr Asp Asp Pro Thr Pro Pro Asp Tyr
 340 345 350
 Phe Glu Ser Phe Leu Asn Leu Ala Ser Thr Gln Glu Ala Ile Gly Val
 355 360 365
 Asn Ile Asn Tyr Thr Ser Thr Asn Ala Arg Asn Val Ser Leu Gly Phe
 370 375 380
 Ser Arg Thr Gly Asp Phe Val Phe Pro Asn Phe Leu Glu Asp Leu Glu
 385 390 395 400
 Glu Ile Leu Ala Tyr Gly Val Arg Val Ala Leu Leu Tyr Gly Asp Ala

10336256.txt

```

      405      410      415
Asp Tyr Ile Cys Asn Trp Phe Gly Gly Glu Ala Val Ser Leu Ala Val
      420      425      430
Asn Phe Thr His Ala Ala Asp Phe Arg Ser Ala Gly Tyr Thr Pro Phe
      435      440      445
Leu Val Asp Gly Val Glu Tyr Gly Glu Val Arg Glu Tyr Gly Asn Phe
      450      455      460
Ser Phe Thr Arg Ile Tyr Glu Ala Gly His Glu Val Pro Tyr Tyr Gln
      465      470      475      480
Pro Glu Ala Ser Leu Glu His Phe Arg Arg Val Leu His His Val Val
      485      490      495
Val Ala Asp Gly Ser Gln Val Val Thr Ser Asp Tyr Lys Thr Asn Gly
      500      505      510
Thr Ala Lys Ala Thr His Thr Glu Glu Phe Val Pro Leu Pro Pro Thr
      515      520      525
Ser Thr Pro Ser Ala Ala Ser Arg Val Arg Arg Gly Ser Val
      530      535      540

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<210> 212
 <211> 4330
 <212> DNA
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>
 <221> CDS
 <222> (861)...(1172)
 <223> Exon

<221> CDS
 <222> (1222)...(1461)
 <223> Exon

<221> CDS
 <222> (1520)...(1714)
 <223> Exon

<221> CDS
 <222> (1768)...(1931)
 <223> Exon

<221> CDS
 <222> (2000)...(2330)
 <223> Exon

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<400> 212
catgtgggct gactgcctaa tcgttattcc gcgtcggagt ggcagcacag aggggtgcaag      60
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atggcctaga attggttgtg caaacgtgct cagggaactg ggtgtgcctt cttaggagga      180
gtaaactgca gacatgtcgg tcgtcggcac ctgtcgcttt caaccaggct agttataatg      240
tgcatgcctg tctaccactt ggcggccgcc ttccaatgat ctcttcccgc tttcagctca      300
tcgcttcgaa ccagctatgc ccttgctaca ctgcatcggg tcgactagtt gcccatcacg      360
acaagatcac gtcttccagc tacgcacacc ttgatttgcc ctatcgcata gccaagacca      420
gccatcatgc tctccgagaa ttccgggccc tacacctgcc taaccgggta agcacatacg      480
actccggacc aatcatcttg ttccgcgcca cgtctctcct ccagcgcgcc aagtgattcc      540
ataaattaat cctccatcca tggcccaggc gtttactccg acctccttcg aatgaccatc      600
tcccgcgctt gtaaggccta tcttggtctt cttattcgag tgcacatctc ccgttcgtgc      660
agacgactac cacgaaactg gggtaacctg ctattccata caatttcgat taagagacag      720
ggacatgtcg gccatgctac ttgacaggaa ggtagatcgt aactagggtat gactatggag      780
aagcataaaa agcagcgctc cccacggcct gtattacggt gcaccttgct tctacagagt      840
cagtgtctcc atctctcatc atg aag act act atc ttt acc tcc gcc ctt ctc      893

```

```

      Met Lys Thr Thr Ile Phe Thr Ser Ala Leu Leu
      1           5           10

```

```

ctt ggc tcc act gcc ttg ggc agc gct gtc cca acc gct ggc aag aag      941
Leu Gly Ser Thr Ala Leu Gly Ser Ala Val Pro Thr Ala Gly Lys Lys
      15           20           25

```

```

gtc gat tac aat ggc ttc aag gtc ctg cgc gtt tct agc acc gac gct      989

```

10336256.txt

Val	Asp	Tyr	Asn	Gly	Phe	Lys	Val	Leu	Arg	Val	Ser	Ser	Thr	Asp	Ala		
		30					35					40					
gtc	aag	agt	caa	atc	gag	aac	ttg	gct	gcc	cac	atc	ctc	aac	cct	ggc		1037
Val	Lys	Ser	Gln	Ile	Glu	Asn	Leu	Ala	Ala	His	Ile	Leu	Asn	Pro	Gly		
	45					50					55						
aag	tct	gcc	gag	atg	gat	gta	gtt	gtt	gca	ccc	gaa	aac	gtt	gcg	gca		1085
Lys	Ser	Ala	Glu	Met	Asp	Val	Val	Val	Ala	Pro	Glu	Asn	Val	Ala	Ala		
	60				65					70					75		
ttg	act	gcg	ttg	gct	tcc	gag	agc	aag	gtc	atc	aat	gag	gat	gtt	ggt		1133
Leu	Thr	Ala	Leu	Ala	Ser	Glu	Ser	Lys	Val	Ile	Asn	Glu	Asp	Val	Gly		
				80					85					90			
gct	gcc	ctc	aag	gaa	gaa	ggc	gag	atg	gga	atc	tac	gct	ggtttgtaat				1182
Ala	Ala	Leu	Lys	Glu	Glu	Gly	Glu	Met	Gly	Ile	Tyr	Ala					
			95					100									
tggtctcaata	tcttcgaggt	tacacactca	ccgaatata	ggt	ccc	agc	gag	tcg									1236
				Val	Pro	Ser	Glu	Ser									
				105													
tggttc	aca	gca	tac	cac	cca	tat	gcc	gat	cat	ctt	caa	ttc	ctc	cgc			1284
Trp	Phe	Thr	Ala	Tyr	His	Pro	Tyr	Ala	Asp	His	Leu	Gln	Phe	Leu	Arg		
				115					120					125			
gat	ctg	caa	gcc	ggc	tac	act	agc	aat	tcc	gag	att	gtc	acc	ctt	ggt		1332
Asp	Leu	Gln	Ala	Gly	Tyr	Thr	Ser	Asn	Ser	Glu	Ile	Val	Thr	Leu	Gly		
				130					135					140			
aac	tca	gtc	caa	gga	cgt	acc	ttg	act	ggt	atc	cat	atc	tgg	ggc	agc		1380
Asn	Ser	Val	Gln	Gly	Arg	Thr	Leu	Thr	Gly	Ile	His	Ile	Trp	Gly	Ser		
			145					150					155				
ggc	ggc	aag	gga	tcc	aag	cct	gcc	gtt	att	atc	cac	gga	aac	gtt	cac		1428
Gly	Gly	Lys	Gly	Ser	Lys	Pro	Ala	Val	Ile	Ile	His	Gly	Asn	Val	His		
		160					165					170					
gcc	cga	gag	tgg	atc	act	tcc	atg	acc	act	gag	taagccaccc	tgctatgaga					1481
Ala	Arg	Glu	Trp	Ile	Thr	Ser	Met	Thr	Thr	Glu							
	175					180											
ttattattga	aaaaaaacaa	gctaattctcc	acctcagg	tac	ttc	gcg	tgg	caa	ctt								1537
				Tyr	Phe	Ala	Trp	Gln	Leu								
				185				190									
cta	acc	aag	tac	gcc	tcc	gac	tca	agc	gtc	aag	gct	ctc	gtc	gac	aag		1585
Leu	Thr	Lys	Tyr	Ala	Ser	Asp	Ser	Ser	Val	Lys	Ala	Leu	Val	Asp	Lys		
				195					200					205			
ttc	gac	ttt	tac	atc	acc	ccc	atc	gtc	aac	ccc	gac	gga	ttc	gtc	tac		1633
Phe	Asp	Phe	Tyr	Ile	Thr	Pro	Ile	Val	Asn	Pro	Asp	Gly	Phe	Val	Tyr		
			210					215					220				
tcg	cag	acc	acg	gac	cgt	ctc	tgg	cgc	aag	aac	cgt	cag	act	gtc	agc		1681
Ser	Gln	Thr	Thr	Asp	Arg	Leu	Trp	Arg	Lys	Asn	Arg	Gln	Thr	Val	Ser		
		225					230					235					
acc	agc	tcg	tgt	gtt	ggc	cgc	gat	atc	aac	cgt	aagggacccat	agaaattatt					1734
Thr	Ser	Ser	Cys	Val	Gly	Arg	Asp	Ile	Asn	Arg							
	240					245											
gtatgattaa	catgctaaca	ttttatcaaa	ggc	aac	tgg	cca	tac	aag	tgg	gag							1788
				Asn	Trp	Pro	Tyr	Lys	Trp	Glu							
				250				255									
gta	act	ggc	gga	gcc	tcc	acc	aac	cct	tgc	tcg	gag	acc	tac	aag	ggt		1836

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Val	Thr	Gly	Gly	Ala	Ser	Thr	Asn	Pro	Cys	Ser	Glu	Thr	Tyr	Lys	Gly		
			260					265					270				
cag	gcc	gct	gga	gac	gcc	ccc	gag	ctc	agg	gcc	atc	aaa	gcc	caa	gtc	1884	
Gln	Ala	Ala	Gly	Asp	Ala	Pro	Glu	Leu	Arg	Ala	Ile	Lys	Ala	Gln	Val		
		275					280					285					
gat	gct	ctg	aag	gga	acg	cgc	gga	atc	agc	ctc	tac	ctc	gac	gtg	ca	1931	
Asp	Ala	Leu	Lys	Gly	Thr	Arg	Gly	Ile	Ser	Leu	Tyr	Leu	Asp	Val	His		
		290				295					300						
gtatgtcccc	cttgcattccc	cttctcccct	ttgccaaatc	aagccaaagc	taaccaccct											1991	
acccttag	c	tcc	tac	ggc	caa	tac	atc	ctc	tgg	ccc	tac	ggc	tac	gac		2039	
	Ser	Tyr	Gly	Gln	Tyr	Ile	Leu	Trp	Pro	Tyr	Gly	Tyr	Asp				
		305				310					315						
tgc	agt	ctc	cgc	ccc	gaa	aac	gac	gcc	cag	ctc	cgc	agt	ctc	gca	tcc	2087	
Cys	Ser	Leu	Arg	Pro	Glu	Asn	Asp	Ala	Gln	Leu	Arg	Ser	Leu	Ala	Ser		
		320					325					330					
cgc	gct	caa	tca	gcc	atc	cgt	gct	gtc	tca	gga	act	gca	tac	acc	att	2135	
Arg	Ala	Gln	Ser	Ala	Ile	Arg	Ala	Val	Ser	Gly	Thr	Ala	Tyr	Thr	Ile		
		335				340					345						
ggc	ccc	agc	tgc	tct	act	ctc	tac	gcc	acc	act	ggc	tct	tcc	act	gat	2183	
Gly	Pro	Ser	Cys	Ser	Thr	Leu	Tyr	Ala	Thr	Thr	Gly	Ser	Ser	Thr	Asp		
		350			355					360					365		
tac	acc	gat	gtc	gag	ggt	aat	gct	acc	tac	tgc	tac	act	tat	gag	ctg	2231	
Tyr	Thr	Asp	Val	Glu	Gly	Asn	Ala	Thr	Tyr	Ser	Tyr	Thr	Tyr	Glu	Leu		
			370						375					380			
agg	gat	acc	ggt	aca	tac	ggc	ttc	tgc	ctc	cct	gcc	aac	cag	att	cgt	2279	
Arg	Asp	Thr	Gly	Thr	Tyr	Gly	Phe	Ser	Leu	Pro	Ala	Asn	Gln	Ile	Arg		
			385					390					395				
ccc	act	gtt	ttg	gag	act	tgg	gct	ggt	gtt	act	agc	atg	ctc	cgc	gat	2327	
Pro	Thr	Val	Leu	Glu	Thr	Trp	Ala	Gly	Val	Thr	Ser	Met	Leu	Arg	Asp		
		400					405					410					
gct	tagaatgatt	tatgatggat	gagaaagggg	gaaacttttg	taaatacttt											2380	
Ala																	
ttgacttggt	caacttgaac	ataaatcatg	atgaaagtca	tggtattatta	attttttgtt	2440											
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acattctcca	tcattgtaaa	agccaaaaca	aataaatttg	ctggatgaat	cagtcgtact	3160											
atctaaaacc	atgttctctg	tcagaagcga	cccaaatcaa	cccacacaac	aatacaacag	3220											
ccatgttgaa	acggaattca	aggtagacaa	ccccatcatc	ctttgccatg	gagaaccctt	3280											
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gtcctggcgc	aaaaacggg	ataataaccg	ctccatcatc	agtcttcac	ctgctctgcc	3460											
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aaggaaacgc	tgccggagac	gtagagttgg	gtagagaggg	gagcagcaag	aagaatgcgg	3580											
tattggagag	tcgggtggag	attgtttgtg	agggagaggg	gagagagggc	agggagccga	3640											
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aggacttttc	gggaaggaac	gagtgaagaa	tagggtcggc	gagggtaggt	ggaaggtgga	3820											

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aggtggtatg gatgtgatgg aagaggatgt aatacatctt taattagcga gatgaattgt 3880
aataagaagc aggcgtgtgc gaatattgca tctatgcccc tgaaaagtgc tcagtattga 3940
aatacacgcc cccgctcctt gcacctgtca tgatcttttag gttctcggct gcaacggcat 4000
ttctcacatc gttctgcatc gtcttcggcc cgcagatata cacgttcagc gtctcatctg 4060
cttccgctgc tttctctgcc tcttcctgca cgatgagcgg tagttgtggt cggcccgtat 4120
gttctttgcc tgatacaatt gtttcgcctt ctttctcggg actaaagacg atgtcattcg 4180
acgcttcaga tggcactgag tgggttgatg gctgtactat ttttgacagg atgtcagctt 4240
gatttgccac ttcaccagtg aagtggacct cgatttggac ggatgacaag acttcagttg 4300
gatattgtga aaacatgact tgcagtgttt 4330

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<210> 213

<211> 104

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 213

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Met Lys Thr Thr Ile Phe Thr Ser Ala Leu Leu Leu Gly Ser Thr Ala
1      5      10      15
Leu Gly Ser Ala Val Pro Thr Ala Gly Lys Lys Val Asp Tyr Asn Gly
20      25      30
Phe Lys Val Leu Arg Val Ser Ser Thr Asp Ala Val Lys Ser Gln Ile
35      40      45
Glu Asn Leu Ala Ala His Ile Leu Asn Pro Gly Lys Ser Ala Glu Met
50      55      60
Asp Val Val Val Ala Pro Glu Asn Val Ala Ala Leu Thr Ala Leu Ala
65      70      75      80
Ser Glu Ser Lys Val Ile Asn Glu Asp Val Gly Ala Ala Leu Lys Glu
85      90      95
Glu Gly Glu Met Gly Ile Tyr Ala
100

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<210> 214

<211> 80

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 214

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Val Pro Ser Glu Ser Trp Phe Thr Ala Tyr His Pro Tyr Ala Asp His
1      5      10      15
Leu Gln Phe Leu Arg Asp Leu Gln Ala Gly Tyr Thr Ser Asn Ser Glu
20      25      30
Ile Val Thr Leu Gly Asn Ser Val Gln Gly Arg Thr Leu Thr Gly Ile
35      40      45
His Ile Trp Gly Ser Gly Gly Lys Gly Ser Lys Pro Ala Val Ile Ile
50      55      60
His Gly Asn Val His Ala Arg Glu Trp Ile Thr Ser Met Thr Thr Glu
65      70      75      80

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<210> 215

<211> 65

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 215

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Tyr Phe Ala Trp Gln Leu Leu Thr Lys Tyr Ala Ser Asp Ser Ser Val
1      5      10      15
Lys Ala Leu Val Asp Lys Phe Asp Phe Tyr Ile Thr Pro Ile Val Asn
20      25      30
Pro Asp Gly Phe Val Tyr Ser Gln Thr Thr Asp Arg Leu Trp Arg Lys
35      40      45
Asn Arg Gln Thr Val Ser Thr Ser Ser Cys Val Gly Arg Asp Ile Asn
50      55      60
Arg
65

```

<210> 216

<211> 55

<212> PRT

10336256.txt

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 216

Asn Trp Pro Tyr Lys Trp Glu Val Thr Gly Gly Ala Ser Thr Asn Pro
 1 5 10 15
 Cys Ser Glu Thr Tyr Lys Gly Gln Ala Ala Gly Asp Ala Pro Glu Leu
 20 25 30
 Arg Ala Ile Lys Ala Gln Val Asp Ala Leu Lys Gly Thr Arg Gly Ile
 35 40 45
 Ser Leu Tyr Leu Asp Val His
 50 55

<210> 217

<211> 110

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 217

Ser Tyr Gly Gln Tyr Ile Leu Trp Pro Tyr Gly Tyr Asp Cys Ser Leu
 1 5 10 15
 Arg Pro Glu Asn Asp Ala Gln Leu Arg Ser Leu Ala Ser Arg Ala Gln
 20 25 30
 Ser Ala Ile Arg Ala Val Ser Gly Thr Ala Tyr Thr Ile Gly Pro Ser
 35 40 45
 Cys Ser Thr Leu Tyr Ala Thr Thr Gly Ser Ser Thr Asp Tyr Thr Asp
 50 55 60
 Val Glu Gly Asn Ala Thr Tyr Ser Tyr Thr Tyr Glu Leu Arg Asp Thr
 65 70 75 80
 Gly Thr Tyr Gly Phe Ser Leu Pro Ala Asn Gln Ile Arg Pro Thr Val
 85 90 95
 Leu Glu Thr Trp Ala Gly Val Thr Ser Met Leu Arg Asp Ala
 100 105 110

<210> 218

<211> 1242

<212> DNA

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1242)

<400> 218

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Met Lys Thr Thr Ile Phe Thr Ser Ala Leu Leu Gly Ser Thr Ala	
1 5 10 15	
ttg ggc agc gct gtc cca acc gct ggc aag aag gtc gat tac aat ggc	96
Leu Gly Ser Ala Val Pro Thr Ala Gly Lys Lys Val Asp Tyr Asn Gly	
20 25 30	
ttc aag gtc ctg cgc gtt tct agc acc gac gct gtc aag agt caa atc	144
Phe Lys Val Leu Arg Val Ser Ser Thr Asp Ala Val Lys Ser Gln Ile	
35 40 45	
gag aac ttg gct gcc cac atc ctc aac cct ggc aag tct gcc gag atg	192
Glu Asn Leu Ala Ala His Ile Leu Asn Pro Gly Lys Ser Ala Glu Met	
50 55 60	
gat gta gtt gtt gca ccc gaa aac gtt gcg gca ttg act gcg ttg gct	240
Asp Val Val Val Ala Pro Glu Asn Val Ala Ala Leu Thr Ala Leu Ala	
65 70 75 80	
tcc gag agc aag gtc atc aat gag gat gtt ggt gct gcc ctc aag gaa	288
Ser Glu Ser Lys Val Ile Asn Glu Asp Val Gly Ala Ala Leu Lys Glu	
85 90 95	
gaa ggc gag atg gga atc tac gct gtt ccc agc gag tcg tgg ttc aca	336

10336256.txt																
Glu	Gly	Glu	Met	Gly	Ile	Tyr	Ala	Val	Pro	Ser	Glu	Ser	Trp	Phe	Thr	
			100					105					110			
gca	tac	cac	cca	tat	gcc	gat	cat	ctt	caa	ttc	ctc	cgc	gat	ctg	caa	384
Ala	Tyr	His	Pro	Tyr	Ala	Asp	His	Leu	Gln	Phe	Leu	Arg	Asp	Leu	Gln	
		115					120					125				
gcc	ggc	tac	act	agc	aat	tcc	gag	att	gtc	acc	ctt	ggt	aac	tca	gtc	432
Ala	Gly	Tyr	Thr	Ser	Asn	Ser	Glu	Ile	Val	Thr	Leu	Gly	Asn	Ser	Val	
	130					135					140					
caa	gga	cgt	acc	ttg	act	ggg	atc	cat	atc	tgg	ggc	agc	ggc	ggc	aag	480
Gln	Gly	Arg	Thr	Leu	Thr	Gly	Ile	His	Ile	Trp	Gly	Ser	Gly	Gly	Lys	
145					150					155					160	
gga	tcc	aag	cct	gcc	gtt	att	atc	cac	gga	aac	gtt	cac	gcc	cga	gag	528
Gly	Ser	Lys	Pro	Ala	Val	Ile	Ile	His	Gly	Asn	Val	His	Ala	Arg	Glu	
				165					170					175		
tgg	atc	act	tcc	atg	acc	act	gag	tac	ttc	gcg	tgg	caa	ctt	cta	acc	576
Trp	Ile	Thr	Ser	Met	Thr	Thr	Glu	Tyr	Phe	Ala	Trp	Gln	Leu	Leu	Thr	
			180				185						190			
aag	tac	gcc	tcc	gac	tca	agc	gtc	aag	gct	ctc	gtc	gac	aag	ttc	gac	624
Lys	Tyr	Ala	Ser	Asp	Ser	Ser	Val	Lys	Ala	Leu	Val	Asp	Lys	Phe	Asp	
		195					200					205				
ttt	tac	atc	acc	ccc	atc	gtc	aac	ccc	gac	gga	ttc	gtc	tac	tcg	cag	672
Phe	Tyr	Ile	Thr	Pro	Ile	Val	Asn	Pro	Asp	Gly	Phe	Val	Tyr	Ser	Gln	
	210					215					220					
acc	acg	gac	cgt	ctc	tgg	cgc	aag	aac	cgt	cag	act	gtc	agc	acc	agc	720
Thr	Thr	Asp	Arg	Leu	Trp	Arg	Lys	Asn	Arg	Gln	Thr	Val	Ser	Thr	Ser	
225					230					235					240	
tcg	tgt	gtt	ggc	cgc	gat	atc	aac	cgt	aac	tgg	cca	tac	aag	tgg	gag	768
Ser	Cys	Val	Gly	Arg	Asp	Ile	Asn	Arg	Asn	Trp	Pro	Tyr	Lys	Trp	Glu	
				245					250					255		
gta	act	ggc	gga	gcc	tcc	acc	aac	cct	tgc	tcg	gag	acc	tac	aag	ggt	816
Val	Thr	Gly	Gly	Ala	Ser	Thr	Asn	Pro	Cys	Ser	Glu	Thr	Tyr	Lys	Gly	
			260					265					270			
cag	gcc	gct	gga	gac	gcc	ccc	gag	ctc	agg	gcc	atc	aaa	gcc	caa	gtc	864
Gln	Ala	Ala	Gly	Asp	Ala	Pro	Glu	Leu	Arg	Ala	Ile	Lys	Ala	Gln	Val	
		275					280					285				
gat	gct	ctg	aag	gga	acg	cgc	gga	atc	agc	ctc	tac	ctc	gac	gtg	cac	912
Asp	Ala	Leu	Lys	Gly	Thr	Arg	Gly	Ile	Ser	Leu	Tyr	Leu	Asp	Val	His	
	290					295					300					
tcc	tac	ggc	caa	tac	atc	ctc	tgg	ccc	tac	ggc	tac	gac	tgc	agt	ctc	960
Ser	Tyr	Gly	Gln	Tyr	Ile	Leu	Trp	Pro	Tyr	Gly	Tyr	Asp	Cys	Ser	Leu	
					310					315					320	
cgc	ccc	gaa	aac	gac	gcc	cag	ctc	cgc	agt	ctc	gca	tcc	cgc	gct	caa	1008
Arg	Pro	Glu	Asn	Asp	Ala	Gln	Leu	Arg	Ser	Leu	Ala	Ser	Arg	Ala	Gln	
				325					330					335		
tca	gcc	atc	cgt	gct	gtc	tca	gga	act	gca	tac	acc	att	ggc	ccc	agc	1056
Ser	Ala	Ile	Arg	Ala	Val	Ser	Gly	Thr	Ala	Tyr	Thr	Ile	Gly	Pro	Ser	
			340				345						350			
tgc	tct	act	ctc	tac	gcc	acc	act	ggc	tct	tcc	act	gat	tac	acc	gat	1104
Cys	Ser	Thr	Leu	Tyr	Ala	Thr	Thr	Gly	Ser	Ser	Thr	Asp	Tyr	Thr	Asp	
		355					360					365				
gtc	gag	ggg	aat	gct	acc	tac	tcg	tac	act	tat	gag	ctg	agg	gat	acc	1152

10336256.txt

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Val Glu Gly Asn Ala Thr Tyr Ser Tyr Thr Tyr Glu Leu Arg Asp Thr
  370                               375                               380

ggt aca tac ggc ttc tcg ctc cct gcc aac cag att cgt ccc act gtt      1200
Gly Thr Tyr Gly Phe Ser Leu Pro Ala Asn Gln Ile Arg Pro Thr Val
385                               390                               395                               400

ttg gag act tgg gct ggt gtt act agc atg ctc cgc gat gct      1242
Leu Glu Thr Trp Ala Gly Val Thr Ser Met Leu Arg Asp Ala
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<210> 219

<211> 414

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> DOMAIN

<222> (112)...(317)

<223> Zinc carboxypeptidase

<400> 219

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  20      25      30
Phe Lys Val Leu Arg Val Ser Ser Thr Asp Ala Val Lys Ser Gln Ile
  35      40      45
Glu Asn Leu Ala Ala His Ile Leu Asn Pro Gly Lys Ser Ala Glu Met
  50      55      60
Asp Val Val Val Ala Pro Glu Asn Val Ala Ala Leu Thr Ala Leu Ala
  65      70      75      80
Ser Glu Ser Lys Val Ile Asn Glu Asp Val Gly Ala Ala Leu Lys Glu
  85      90      95
Glu Gly Glu Met Gly Ile Tyr Ala Val Pro Ser Glu Ser Trp Phe Thr
  100      105      110
Ala Tyr His Pro Tyr Ala Asp His Leu Gln Phe Leu Arg Asp Leu Gln
  115      120      125
Ala Gly Tyr Thr Ser Asn Ser Glu Ile Val Thr Leu Gly Asn Ser Val
  130      135      140
Gln Gly Arg Thr Leu Thr Gly Ile His Ile Trp Gly Ser Gly Gly Lys
  145      150      155      160
Gly ser Lys Pro Ala Val Ile Ile His Gly Asn Val His Ala Arg Glu
  165      170      175
Trp Ile Thr Ser Met Thr Thr Glu Tyr Phe Ala Trp Gln Leu Leu Thr
  180      185      190
Lys Tyr Ala Ser Asp Ser Ser Val Lys Ala Leu Val Asp Lys Phe Asp
  195      200      205
Phe Tyr Ile Thr Pro Ile Val Asn Pro Asp Gly Phe Val Tyr Ser Gln
  210      215      220
Thr Thr Asp Arg Leu Trp Arg Lys Asn Arg Gln Thr Val Ser Thr Ser
  225      230      235      240
Ser cys Val Gly Arg Asp Ile Asn Arg Asn Trp Pro Tyr Lys Trp Glu
  245      250      255
Val Thr Gly Gly Ala Ser Thr Asn Pro Cys Ser Glu Thr Tyr Lys Gly
  260      265      270
Gln Ala Ala Gly Asp Ala Pro Glu Leu Arg Ala Ile Lys Ala Gln Val
  275      280      285
Asp Ala Leu Lys Gly Thr Arg Gly Ile Ser Leu Tyr Leu Asp Val His
  290      295      300
Ser Tyr Gly Gln Tyr Ile Leu Trp Pro Tyr Gly Tyr Asp Cys Ser Leu
  305      310      315      320
Arg Pro Glu Asn Asp Ala Gln Leu Arg Ser Leu Ala Ser Arg Ala Gln
  325      330      335
ser Ala Ile Arg Ala Val Ser Gly Thr Ala Tyr Thr Ile Gly Pro Ser
  340      345      350
Cys ser Thr Leu Tyr Ala Thr Thr Gly Ser Ser Thr Asp Tyr Thr Asp

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355 360 365
 Val Glu Gly Asn Ala Thr Tyr Ser Tyr Thr Tyr Glu Leu Arg Asp Thr
 370 375 380
 Gly Thr Tyr Gly Phe Ser Leu Pro Ala Asn Gln Ile Arg Pro Thr Val
 385 390 395 400
 Leu Glu Thr Trp Ala Gly Val Thr Ser Met Leu Arg Asp Ala
 405 410

<210> 220
 <211> 3554
 <212> DNA
 <213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>
 <221> CDS
 <222> (1001)...(2554)
 <223> Exon

<221> misc_feature
 <222> (1)...(3554)
 <223> n = A,T,C or G

<400> 220
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 acacatccta gtcaacacta tggagcgtgg cgcattcgtt gtcaagttgc aggcggggtt 120
 cgacaaataa gcaaagaagg aataatgata atgatggcct aggccttctt gtatctagtc 180
 gagacgttgt agttctgtaa atatctatcg gtcctagtcg tattcggccg gtgcgagtgt 240
 ggcttgactt atcaattcgt aatttggcca aacatactcg gctttattcc ttgcccgctc 300
 tttttttgat catatacccg ttgccaagtc cagcgcataa tagccgtagc agtagcgtag 360
 tgaaggctac cgaggctcgg tttggctctgg cacaacaagc cactttagtc acacattgcg 420
 tattcttttg atcaaaatgg gaacaacctg ctgctaagcc gagagcttct cgaagtgttc 480
 cagtggcggg atcgtcgttt tgcctcctcc attatcatcc gccctgattc tggcgctatc 540
 atgccaaggc gattcgatgg gggatggatg tctcttgccg gggagtagat tcttgccgcg 600
 catctagctt cccaatcaag tgtcgtctgg ccgtgagcta ggtatgtccg agagatgatg 660
 cggctattct ccttcctcat acaacacagc atcacgcagc caagtcgact ttcattcaatt 720
 tcgtcgctt cgccccagc ccttcaccgg gctaccgctc accaataacc cacagcatgc 780
 cttgaatacc catttcccg ttcccgaaaa ttgggtcaact agcgatcgcg atagcagctg 840
 cctgaactgg ctaggccagg gagcacgcga ctatgctaac ccaactctcg tagtcgttta 900
 tgaggatgtc agccagagta tatagagcca tgcaattccg gctgcatctg gcacggcagc 960
 cctctcagtc tttgctcatc cctcgttctc aatattcaag atg agg ttc gtt cca 1015
 Met Arg Phe Val Pro
 1 5

ttc gtt gcg ctc gct gcg cct gtc ctt gcc cag gtc ggt ccc aag cca 1063
 Phe Val Ala Leu Ala Ala Pro Val Leu Ala Gln Val Gly Pro Lys Pro
 10 15 20

aac cca aac aca aag ccc ggc aag cct cca aag cct gac gac aag cct 1111
 Asn Pro Asn Thr Lys Pro Gly Lys Pro Pro Lys Pro Asp Asp Lys Pro
 25 30 35

aag aag ctc gtc act ccc aag gat ctg atc aag gac atc aaa ctt gag 1159
 Lys Lys Leu Val Thr Pro Lys Asp Leu Ile Lys Asp Ile Lys Leu Glu
 40 45 50

gat ctg ctc aag ggc tcc caa aag ctc caa gac att gcc gac gaa gct 1207
 Asp Leu Leu Lys Gly Ser Gln Lys Leu Gln Asp Ile Ala Asp Glu Ala
 55 60 65

ggc ggt aac cgt gct ttt ggt ggc aca ggg cac aac gcg acc acc gaa 1255
 Gly Gly Asn Arg Ala Phe Gly Gly Thr Gly His Asn Ala Thr Thr Glu
 70 75 80 85

tgg ttg tac cag act ttg ttg gcc act ggt tac tat gac gtg tac aag 1303
 Trp Leu Tyr Gln Thr Leu Leu Ala Thr Gly Tyr Tyr Asp Val Tyr Lys
 90 95 100

cag cca ttc gtt gag ctt ttc acc gct gct acg acc aag ttc act gct 1351
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Gln	Pro	Phe	Val	Glu	Leu	Phe	Thr	Ala	Ala	Thr	Thr	Lys	Phe	Thr	Ala	
			105					110					115			
ggt	ggt	gaa	gag	att	ccc	gtc	tct	tac	atg	acc	ttt	ggc	ccc	tct	ggc	1399
Gly	Gly	Glu	Glu	Ile	Pro	Val	Ser	Tyr	Met	Thr	Phe	Gly	Pro	Ser	Gly	
		120					125					130				
gat	gcc	act	gcc	aac	att	gtc	aag	gtt	aac	aac	ctg	gga	tgc	gcc	gcc	1447
Asp	Ala	Thr	Ala	Asn	Ile	Val	Lys	Val	Asn	Asn	Leu	Gly	Cys	Ala	Ala	
	135					140					145					
gaa	gac	tac	ccc	gct	agt	gtt	tct	ggc	caa	cac	gca	ctc	gtc	tcc	cga	1495
Glu	Asp	Tyr	Pro	Ala	Ser	Val	Ser	Gly	Gln	His	Ala	Leu	Val	Ser	Arg	
150					155				160						165	
ggc	aca	tgt	act	ttt	gcc	caa	aag	tct	acc	ctg	gcc	aag	gct	gct	ggt	1543
Gly	Thr	Cys	Thr	Phe	Ala	Gln	Lys	Ser	Thr	Leu	Ala	Lys	Ala	Ala	Gly	
			170					175						180		
gct	gta	ggc	gcg	ctc	atc	tac	aac	aat	gag	cca	gag	cag	ccc	ctc	tca	1591
Ala	Val	Gly	Ala	Leu	Ile	Tyr	Asn	Asn	Glu	Pro	Glu	Gln	Pro	Leu	Ser	
			185					190					195			
ggt	act	ctt	gga	ggt	gca	ggt	gac	tac	gct	cct	act	gtc	ggt	atg	acc	1639
Gly	Thr	Leu	Gly	Gly	Ala	Gly	Asp	Tyr	Ala	Pro	Thr	Val	Gly	Met	Thr	
		200					205					210				
aag	gag	gct	gga	gag	tct	ctc	att	gct	aag	ctt	gga	aac	ggc	act	aca	1687
Lys	Glu	Ala	Gly	Glu	Ser	Leu	Ile	Ala	Lys	Leu	Gly	Asn	Gly	Thr	Thr	
	215					220					225					
ctt	gag	gga	acc	ctc	ttc	atc	gat	gcc	atc	cag	gaa	aac	cgc	acc	aac	1735
Leu	Glu	Gly	Thr	Leu	Phe	Ile	Asp	Ala	Ile	Gln	Glu	Asn	Arg	Thr	Asn	
230					235					240					245	
tac	aac	gtc	att	gct	gag	aca	aag	gag	ggc	gac	cac	aac	aac	gtt	ctc	1783
Tyr	Asn	Val	Ile	Ala	Glu	Thr	Lys	Glu	Gly	Asp	His	Asn	Asn	Val	Leu	
				250					255					260		
atg	att	ggt	ggc	cac	acc	gac	tcc	gtc	ttc	cag	ggt	cct	ggt	atc	aac	1831
Met	Ile	Gly	Gly	His	Thr	Asp	Ser	Val	Phe	Gln	Gly	Pro	Gly	Ile	Asn	
			265					270					275			
gat	gac	gga	tct	ggt	act	att	ggt	act	ctg	gtt	act	ggt	ctt	gct	ctc	1879
Asp	Asp	Gly	Ser	Gly	Thr	Ile	Gly	Thr	Leu	Val	Thr	Gly	Leu	Ala	Leu	
		280					285					290				
acc	aag	tac	aag	atc	aag	aac	gcc	gtt	cgt	ctt	ggt	ttc	tgg	ggc	gcc	1927
Thr	Lys	Tyr	Lys	Ile	Lys	Asn	Ala	Val	Arg	Leu	Gly	Phe	Trp	Gly	Ala	
	295					300					305					
gag	gag	ttt	ggc	aag	ctt	gga	tcc	ttc	tac	tac	atg	aag	acc	atc	aac	1975
Glu	Glu	Phe	Gly	Lys	Leu	Gly	Ser	Phe	Tyr	Tyr	Met	Lys	Thr	Ile	Asn	
310					315					320					325	
ggt	act	ttc	ggc	ggc	agc	acc	gca	gag	gct	aac	aag	atc	cgt	gcc	tac	2023
Gly	Thr	Phe	Gly	Gly	Ser	Thr	Ala	Glu	Ala	Asn	Lys	Ile	Arg	Ala	Tyr	
				330					335					340		
ctc	aac	ttc	gac	atg	att	gcc	tcg	ccc	aac	tat	gtc	ctc	ggt	atc	tac	2071
Leu	Asn	Phe	Asp	Met	Ile	Ala	Ser	Pro	Asn	Tyr	Val	Leu	Gly	Ile	Tyr	
			345					350					355			
gat	ggt	gat	ggc	agt	gca	ttc	aac	ttt	tct	ggc	gca	gcc	ggt	tcc	gac	2119
Asp	Gly	Asp	Gly	Ser	Ala	Phe	Asn	Phe	Ser	Gly	Ala	Ala	Gly	Ser	Asp	
		360					365					370				
aag	atc	gag	aag	gac	ttt	gaa	gag	ttt	tac	gag	gag	cgt	ggc	ctt	cct	2167

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Lys Ile Glu Lys Asp Phe Glu Glu Phe Tyr Glu Glu Arg Gly Leu Pro
 375 380 385

cac gtc ccc tcc ctc ttt acc ctc cgc tcc gac tac gct gcc ttc ctc 2215
 His Val Pro Ser Leu Phe Thr Leu Arg Ser Asp Tyr Ala Ala Phe Leu
 390 395 400 405

gag aac ggt atc ccc tct ggc ggt ctc ttc acc ggt gcc gaa gtc ctc 2263
 Glu Asn Gly Ile Pro Ser Gly Gly Leu Phe Thr Gly Ala Glu Val Leu
 410 415 420

aag acc gag gag gag gcc cag ctc ttc ggc ggt gaa gcc ggc aag ccc 2311
 Lys Thr Glu Glu Glu Ala Gln Leu Phe Gly Gly Glu Ala Gly Lys Pro
 425 430 435

ctc gac gga tgc tac cac cag gcc tgc gac gac atc aac aac ctt gcc 2359
 Leu Asp Gly Cys Tyr His Gln Ala Cys Asp Asp Ile Asn Asn Leu Ala
 440 445 450

cac gac gcc tac ctc ctc aac acc cag agc att gcc aac tcc gtt gcc 2407
 His Asp Ala Tyr Leu Leu Asn Thr Gln Ser Ile Ala Asn Ser Val Ala
 455 460 465

aag tac gcc gtc tct ttc gag ggt atc ccc aag gcc aac gct act ctc 2455
 Lys Tyr Ala Val Ser Phe Glu Gly Ile Pro Lys Ala Asn Ala Thr Leu
 470 475 480 485

cgc aaa cgc ggt gct gag tgc gca agg ttc atg agc agg ttc gac cac 2503
 Arg Lys Arg Gly Ala Glu Ser Ala Arg Phe Met Ser Arg Phe Asp His
 490 495 500

ggt ggc cat gag cac ctt ggt cag cct tgc ggt gct gga aag cac gct 2551
 Gly Gly His Glu His Leu Gly Gln Pro Cys Gly Ala Gly Lys His Ala
 505 510 515

att taaatttcaa tgtctataat gatttgctgg ggtgaaagga aatgatgaga 2604
 Ile

tgataccatg agagaaatct tttgtaaaag tagatgaaga ataataccca tttttttgtg 2664
 ttcatTTTTga ctagtcttat gctgtgcctg gcgattgaat gctgtgaaat ttcttttggg 2724
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<210> 221

<211> 518

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 221

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 Val Gly Pro Lys Pro Asn Pro Asn Thr Lys Pro Gly Lys Pro Pro Lys
 20 25 30
 Pro Asp Asp Lys Pro Lys Lys Leu Val Thr Pro Lys Asp Leu Ile Lys
 35 40 45

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Asp Ile Lys Leu Glu Asp Leu Leu Lys Gly Ser Gln Lys Leu Gln Asp
 50 55 60
 Ile Ala Asp Glu Ala Gly Gly Asn Arg Ala Phe Gly Gly Thr Gly His
 65 70 75 80
 Asn Ala Thr Thr Glu Trp Leu Tyr Gln Thr Leu Leu Ala Thr Gly Tyr
 85 90 95
 Tyr Asp Val Tyr Lys Gln Pro Phe Val Glu Leu Phe Thr Ala Ala Thr
 100 105 110
 Thr Lys Phe Thr Ala Gly Gly Glu Glu Ile Pro Val Ser Tyr Met Thr
 115 120 125
 Phe Gly Pro Ser Gly Asp Ala Thr Ala Asn Ile Val Lys Val Asn Asn
 130 135 140
 Leu Gly Cys Ala Ala Glu Asp Tyr Pro Ala Ser Val Ser Gly Gln His
 145 150 155 160
 Ala Leu Val Ser Arg Gly Thr Cys Thr Phe Ala Gln Lys Ser Thr Leu
 165 170 175
 Ala Lys Ala Ala Gly Ala Val Gly Ala Leu Ile Tyr Asn Asn Glu Pro
 180 185 190
 Glu Gln Pro Leu Ser Gly Thr Leu Gly Gly Ala Gly Asp Tyr Ala Pro
 195 200 205
 Thr Val Gly Met Thr Lys Glu Ala Gly Glu Ser Leu Ile Ala Lys Leu
 210 215 220
 Gly Asn Gly Thr Thr Leu Glu Gly Thr Leu Phe Ile Asp Ala Ile Gln
 225 230 235 240
 Glu Asn Arg Thr Asn Tyr Asn Val Ile Ala Glu Thr Lys Glu Gly Asp
 245 250 255
 His Asn Asn Val Leu Met Ile Gly Gly His Thr Asp Ser Val Phe Gln
 260 265 270
 Gly Pro Gly Ile Asn Asp Asp Gly Ser Gly Thr Ile Gly Thr Leu Val
 275 280 285
 Thr Gly Leu Ala Leu Thr Lys Tyr Lys Ile Lys Asn Ala Val Arg Leu
 290 295 300
 Gly Phe Trp Gly Ala Glu Glu Phe Gly Lys Leu Gly Ser Phe Tyr Tyr
 305 310 315 320
 Met Lys Thr Ile Asn Gly Thr Phe Gly Gly Ser Thr Ala Glu Ala Asn
 325 330 335
 Lys Ile Arg Ala Tyr Leu Asn Phe Asp Met Ile Ala Ser Pro Asn Tyr
 340 345 350
 Val Leu Gly Ile Tyr Asp Gly Asp Gly Ser Ala Phe Asn Phe Ser Gly
 355 360 365
 Ala Ala Gly Ser Asp Lys Ile Glu Lys Asp Phe Glu Glu Phe Tyr Glu
 370 375 380
 Glu Arg Gly Leu Pro His Val Pro Ser Leu Phe Thr Leu Arg Ser Asp
 385 390 395 400
 Tyr Ala Ala Phe Leu Glu Asn Gly Ile Pro Ser Gly Gly Leu Phe Thr
 405 410 415
 Gly Ala Glu Val Leu Lys Thr Glu Glu Glu Ala Gln Leu Phe Gly Gly
 420 425 430
 Glu Ala Gly Lys Pro Leu Asp Gly Cys Tyr His Gln Ala Cys Asp Asp
 435 440 445
 Ile Asn Asn Leu Ala His Asp Ala Tyr Leu Leu Asn Thr Gln Ser Ile
 450 455 460
 Ala Asn Ser Val Ala Lys Tyr Ala Val Ser Phe Glu Gly Ile Pro Lys
 465 470 475 480
 Ala Asn Ala Thr Leu Arg Lys Arg Gly Ala Glu Ser Ala Arg Phe Met
 485 490 495
 Ser Arg Phe Asp His Gly Gly His Glu His Leu Gly Gln Pro Cys Gly
 500 505 510
 Ala Gly Lys His Ala Ile
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<210> 222

<211> 1554

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

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<400> 222

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gtc ggt ccc aag cca aac cca aac aca aag ccc ggc aag cct cca aag	96
Val Gly Pro Lys Pro Asn Pro Asn Thr Lys Pro Gly Lys Pro Pro Lys	
20 25 30	
cct gac gac aag cct aag aag ctc gtc act ccc aag gat ctg atc aag	144
Pro Asp Asp Lys Pro Lys Lys Leu Val Thr Pro Lys Asp Leu Ile Lys	
35 40 45	
gac atc aaa ctt gag gat ctg ctc aag ggc tcc caa aag ctc caa gac	192
Asp Ile Lys Leu Glu Asp Leu Leu Lys Gly Ser Gln Lys Leu Gln Asp	
50 55 60	
att gcc gac gaa gct ggc ggt aac cgt gct ttt ggt ggc aca ggg cac	240
Ile Ala Asp Glu Ala Gly Gly Asn Arg Ala Phe Gly Gly Thr Gly His	
65 70 75 80	
aac gcg acc acc gaa tgg ttg tac cag act ttg ttg gcc act ggt tac	288
Asn Ala Thr Thr Glu Trp Leu Tyr Gln Thr Leu Leu Ala Thr Gly Tyr	
85 90 95	
tat gac gtg tac aag cag cca ttc gtt gag ctt ttc acc gct gct acg	336
Tyr Asp Val Tyr Lys Gln Pro Phe Val Glu Leu Phe Thr Ala Ala Thr	
100 105 110	
acc aag ttc act gct ggt ggt gaa gag att ccc gtc tct tac atg acc	384
Thr Lys Phe Thr Ala Gly Gly Glu Glu Ile Pro Val Ser Tyr Met Thr	
115 120 125	
ttt ggc ccc tct ggc gat gcc act gcc aac att gtc aag gtt aac aac	432
Phe Gly Pro Ser Gly Asp Ala Thr Ala Asn Ile Val Lys Val Asn Asn	
130 135 140	
ctg gga tgc gcc gcc gaa gac tac ccc gct agt gtt tct ggc caa cac	480
Leu Gly Cys Ala Ala Glu Asp Tyr Pro Ala Ser Val Ser Gly Gln His	
145 150 155 160	
gca ctc gtc tcc cga ggc aca tgt act ttt gcc caa aag tct acc ctg	528
Ala Leu Val Ser Arg Gly Thr Cys Thr Phe Ala Gln Lys Ser Thr Leu	
165 170 175	
gcc aag gct gct ggt gct gta ggc gcg ctc atc tac aac aat gag cca	576
Ala Lys Ala Ala Gly Ala Val Gly Ala Leu Ile Tyr Asn Asn Glu Pro	
180 185 190	
gag cag ccc ctc tca ggt act ctt gga ggt gca ggt gac tac gct cct	624
Glu Gln Pro Leu Ser Gly Thr Leu Gly Gly Ala Gly Asp Tyr Ala Pro	
195 200 205	
act gtc ggt atg acc aag gag gct gga gag tct ctc att gct aag ctt	672
Thr Val Gly Met Thr Lys Glu Ala Gly Glu Ser Leu Ile Ala Lys Leu	
210 215 220	
gga aac ggc act aca ctt gag gga acc ctc ttc atc gat gcc atc cag	720
Gly Asn Gly Thr Thr Leu Glu Gly Thr Leu Phe Ile Asp Ala Ile Gln	
225 230 235 240	
gaa aac cgc acc aac tac aac gtc att gct gag aca aag gag ggc gac	768
Glu Asn Arg Thr Asn Tyr Asn Val Ile Ala Glu Thr Lys Glu Gly Asp	
245 250 255	
cac aac aac gtt ctc atg att ggt ggc	816

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His	Asn	Asn	Val	Leu	Met	Ile	Gly	Gly	His	Thr	Asp	Ser	Val	Phe	Gln	
			260					265					270			
ggt	cct	ggt	atc	aac	gat	gac	gga	tct	ggt	act	att	ggt	act	ctg	ggt	864
Gly	Pro	Gly	Ile	Asn	Asp	Asp	Gly	Ser	Gly	Thr	Ile	Gly	Thr	Leu	Val	
		275					280					285				
act	ggt	ctt	gct	ctc	acc	aag	tac	aag	atc	aag	aac	gcc	ggt	cgt	ctt	912
Thr	Gly	Leu	Ala	Leu	Thr	Lys	Tyr	Lys	Ile	Lys	Asn	Ala	Val	Arg	Leu	
	290					295					300					
ggt	ttc	tgg	ggc	gcc	gag	gag	ttt	ggc	aag	ctt	gga	tcc	ttc	tac	tac	960
Gly	Phe	Trp	Gly	Ala	Glu	Glu	Phe	Gly	Lys	Leu	Gly	Ser	Phe	Tyr	Tyr	
305					310					315					320	
atg	aag	acc	atc	aac	ggt	act	ttc	ggc	ggc	agc	acc	gca	gag	gct	aac	1008
Met	Lys	Thr	Ile	Asn	Gly	Thr	Phe	Gly	Gly	Ser	Thr	Ala	Glu	Ala	Asn	
				325					330					335		
aag	atc	cgt	gcc	tac	ctc	aac	ttc	gac	atg	att	gcc	tcg	ccc	aac	tat	1056
Lys	Ile	Arg	Ala	Tyr	Leu	Asn	Phe	Asp	Met	Ile	Ala	Ser	Pro	Asn	Tyr	
			340					345					350			
gtc	ctc	ggt	atc	tac	gat	ggt	gat	ggc	agt	gca	ttc	aac	ttt	tct	ggc	1104
Val	Leu	Gly	Ile	Tyr	Asp	Gly	Asp	Gly	Ser	Ala	Phe	Asn	Phe	Ser	Gly	
		355					360					365				
gca	gcc	ggt	tcc	gac	aag	atc	gag	aag	gac	ttt	gaa	gag	ttt	tac	gag	1152
Ala	Ala	Gly	Ser	Asp	Lys	Ile	Glu	Lys	Asp	Phe	Glu	Glu	Phe	Tyr	Glu	
	370					375					380					
gag	cgt	ggc	ctt	cct	cac	gtc	ccc	tcc	ctc	ttt	acc	ctc	cgc	tcc	gac	1200
Glu	Arg	Gly	Leu	Pro	His	Val	Pro	Ser	Leu	Phe	Thr	Leu	Arg	Ser	Asp	
385					390					395					400	
tac	gct	gcc	ttc	ctc	gag	aac	ggt	atc	ccc	tct	ggc	ggt	ctc	ttc	acc	1248
Tyr	Ala	Ala	Phe	Leu	Glu	Asn	Gly	Ile	Pro	Ser	Gly	Gly	Leu	Phe	Thr	
				405					410					415		
ggt	gcc	gaa	gtc	ctc	aag	acc	gag	gag	gag	gcc	cag	ctc	ttc	ggc	ggt	1296
Gly	Ala	Glu	Val	Leu	Lys	Thr	Glu	Glu	Glu	Ala	Gln	Leu	Phe	Gly	Gly	
			420					425					430			
gaa	gcc	ggc	aag	ccc	ctc	gac	gga	tgc	tac	cac	cag	gcc	tgc	gac	gac	1344
Glu	Ala	Gly	Lys	Pro	Leu	Asp	Gly	Cys	Tyr	His	Gln	Ala	Cys	Asp	Asp	
		435					440					445				
atc	aac	aac	ctt	gcc	cac	gac	gcc	tac	ctc	ctc	aac	acc	cag	agc	att	1392
Ile	Asn	Asn	Leu	Ala	His	Asp	Ala	Tyr	Leu	Leu	Asn	Thr	Gln	Ser	Ile	
	450					455					460					
gcc	aac	tcc	gtt	gcc	aag	tac	gcc	gtc	tct	ttc	gag	ggt	atc	ccc	aag	1440
Ala	Asn	Ser	Val	Ala	Lys	Tyr	Ala	Val	Ser	Phe	Glu	Gly	Ile	Pro	Lys	
				470					475						480	
gcc	aac	gct	act	ctc	cgc	aaa	cgc	ggt	gct	gag	tcg	gca	agg	ttc	atg	1488
Ala	Asn	Ala	Thr	Leu	Arg	Lys	Arg	Gly	Ala	Glu	Ser	Ala	Arg	Phe	Met	
				485					490					495		
agc	agg	ttc	gac	cac	ggt	ggc	cat	gag	cac	ctt	ggt	cag	cct	tgc	ggt	1536
Ser	Arg	Phe	Asp	His	Gly	Gly	His	Glu	His	Leu	Gly	Gln	Pro	Cys	Gly	
			500					505					510			
gct	gga	aag	cac	gct	att											1554
Ala	Gly	Lys	His	Ala	Ile											
		515														

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<210> 223
 <211> 518
 <212> PRT
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>
 <221> SIGNAL
 <222> (1)...(15)

<221> DOMAIN
 <222> (234)...(471)
 <223> Peptidase family M28

<221> DOMAIN
 <222> (115)...(224)
 <223> PA (protease associate) domain

<400> 223
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 Pro Asp Asp Lys Pro Lys Lys Leu Val Thr Pro Lys Asp Leu Ile Lys
 35 40 45
 Asp Ile Lys Leu Glu Asp Leu Lys Gly Ser Gln Lys Leu Gln Asp
 50 55 60
 Ile Ala Asp Glu Ala Gly Gly Asn Arg Ala Phe Gly Gly Thr Gly His
 65 70 75 80
 Asn Ala Thr Thr Glu Trp Leu Tyr Gln Thr Leu Leu Ala Thr Gly Tyr
 85 90 95
 Tyr Asp Val Tyr Lys Gln Pro Phe Val Glu Leu Phe Thr Ala Ala Thr
 100 105 110
 Thr Lys Phe Thr Ala Gly Gly Glu Glu Ile Pro Val Ser Tyr Met Thr
 115 120 125
 Phe Gly Pro Ser Gly Asp Ala Thr Ala Asn Ile Val Lys Val Asn Asn
 130 135 140
 Leu Gly Cys Ala Ala Glu Asp Tyr Pro Ala Ser Val Ser Gly Gln His
 145 150 155 160
 Ala Leu Val Ser Arg Gly Thr Cys Thr Phe Ala Gln Lys Ser Thr Leu
 165 170 175
 Ala Lys Ala Ala Gly Ala Val Gly Ala Leu Ile Tyr Asn Asn Glu Pro
 180 185 190
 Glu Gln Pro Leu Ser Gly Thr Leu Gly Gly Ala Gly Asp Tyr Ala Pro
 195 200 205
 Thr Val Gly Met Thr Lys Glu Ala Gly Glu Ser Leu Ile Ala Lys Leu
 210 215 220
 Gly Asn Gly Thr Thr Leu Glu Gly Thr Leu Phe Ile Asp Ala Ile Gln
 225 230 235 240
 Glu Asn Arg Thr Asn Tyr Asn Val Ile Ala Glu Thr Lys Glu Gly Asp
 245 250 255
 His Asn Asn Val Leu Met Ile Gly Gly His Thr Asp Ser Val Phe Gln
 260 265 270
 Gly Pro Gly Ile Asn Asp Asp Gly Ser Gly Thr Ile Gly Thr Leu Val
 275 280 285
 Thr Gly Leu Ala Leu Thr Lys Tyr Lys Ile Lys Asn Ala Val Arg Leu
 290 295 300
 Gly Phe Trp Gly Ala Glu Phe Gly Lys Leu Gly Ser Phe Tyr Tyr
 305 310 315 320
 Met Lys Thr Ile Asn Gly Thr Phe Gly Gly Ser Thr Ala Glu Ala Asn
 325 330 335
 Lys Ile Arg Ala Tyr Leu Asn Phe Asp Met Ile Ala Ser Pro Asn Tyr
 340 345 350
 Val Leu Gly Ile Tyr Asp Gly Asp Gly Ser Ala Phe Asn Phe Ser Gly
 355 360 365
 Ala Ala Gly Ser Asp Lys Ile Glu Lys Asp Phe Glu Glu Phe Tyr Glu
 370 375 380
 Glu Arg Gly Leu Pro His Val Pro Ser Leu Phe Thr Leu Arg Ser Asp
 385 390 395 400

10336256.txt

Tyr Ala Ala Phe Leu Glu Asn Gly Ile Pro Ser Gly Gly Leu Phe Thr
 Gly Ala Glu Val⁴⁰⁵ Leu Lys Thr Glu⁴¹⁰ Glu Ala Gln Leu⁴¹⁵ Phe Gly Gly
 Glu Ala Gly Lys⁴²⁰ Pro Leu Asp Gly⁴²⁵ Cys Tyr His Gln Ala⁴³⁰ Cys Asp Asp
 Ile Asn Asn Leu Ala His Asp⁴³⁵ Ala Tyr Leu Leu Asn⁴⁴⁰ Thr Gln Ser Ile
 Ala Asn Ser Val⁴⁴⁵ Ala Lys Tyr Ala Val Ser Phe⁴⁵⁰ Glu Gly Ile Pro Lys
 Ala Asn Ala Thr⁴⁵⁵ Leu Arg Lys Arg Gly⁴⁶⁰ Ala Glu Ser Ala Arg Phe Met
 Ser Arg Phe Asp⁴⁶⁵ His Gly Gly His Glu⁴⁷⁰ His Leu Gly Gln Pro Cys Gly
 Ala Gly Lys⁴⁷⁵ His Ala Ile
 515

<210> 224

<211> 3377

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1001)...(1321)

<223> Exon

<221> CDS

<222> (1379)...(1536)

<223> Exon

<221> CDS

<222> (1589)...(1694)

<223> Exon

<221> CDS

<222> (1745)...(2377)

<223> Exon

<400> 224

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aacaatgcaa	ctacaaaagc	atgccacaag	gtataagcag	tgtaggtttc	ggatatctgg	180
aatcgtttgc	ataagagatg	agaaaaagag	acaagggcga	agtttcacgg	aactctttgg	240
ccgtaaagcg	atcaaaattg	catatgggta	gttttggcct	ataaagtga	ttttctcaca	300
gcatgcctag	ctctatcaat	tgctacctaa	aacctgagcg	ctggccaaaa	aacgacaaaa	360
tcatttctct	gattggctcg	ttctaaggca	gtaatactaa	ctgttctcca	gactttgtct	420
agatatgggt	tagggtagag	cgcaggcccc	catgctcctt	ggcccttcaa	cataaccgac	480
tccagggagg	tttacatcga	ctgatattcg	ttctcagagc	gctgaaacgt	catagatcct	540
ctttagagact	gcctttttta	attacaaaac	tactggcata	gatcttccga	gacttgattc	600
agccgcgaaa	gctccaacac	aggcccacaa	aacgcgatgc	tgggtcccga	gacccgtcgc	660
ttcccatact	actacggtta	aggcgctcaa	attggcaagc	gttggccgag	agaacaggga	720
tttccgcctt	cccacattcc	tattatttcc	taaatacccc	ttacgcaatt	ccttggccac	780
ccatgactcg	gaggatttta	ttaagctata	cgaatattgt	tgcagatcct	atgcccacac	840
aggcagaagt	taagaaacaa	caagacctgc	ttggatgtgg	gacttttttt	caattacaat	900
ggcttatgcg	acaacggcca	tgatgcaatt	caaaaagtgt	gtctagtcca	gcagtgttgg	960
gcaagccgcc	tctgtttccac	acgccttgcc	ttcgttcaca	atg cgc ttc ttc act		1015
				Met Arg Phe Phe Thr		
				1 5		

cgt ttc acc gcg cta gtc aca gcc gca gct ccg ttc att gct ctt gct	1063
Arg Phe Thr Ala Leu Val Thr Ala Ala Ala Pro Phe Ile Ala Leu Ala	
10 15 20	

gct ccc gtc gca gca cct cca gag aat gac ata att cct gga aaa tac	1111
Ala Pro Val Ala Ala Pro Pro Glu Asn Asp Ile Ile Pro Gly Lys Tyr	
25 30 35	

10336256.txt

ata gtc cag ctg aag cct gat acc gat gtc gca gcg gtc gct gcc cac 1159
 Ile Val Gln Leu Lys Pro Asp Thr Asp Val Ala Ala Val Ala Ala His
 40 45 50

cat cac aaa gtg cgc agc atc cat gcc cgc aac ctg gcc cga cga ggt 1207
 His His Lys Val Arg Ser Ile His Ala Arg Asn Leu Ala Arg Arg Gly
 55 60 65

gac aat tct ccg act ggt gag cca gtg gag cgc gag tac ggg ttc ggc 1255
 Asp Asn Ser Pro Thr Gly Glu Pro Val Glu Arg Glu Tyr Gly Phe Gly
 70 75 80 85

gac ttc aaa ggc tat tct ggg ttt ttc gat gaa gca acc atc gaa gag 1303
 Asp Phe Lys Gly Tyr Ser Gly Phe Phe Asp Glu Ala Thr Ile Glu Glu
 90 95 100

ttg aaa act ctg cca gag gtaatacagg ccccttcata caatgtcaca 1351
 Leu Lys Thr Leu Pro Glu
 105

acctagcaat gctgatataa ttggttag gtg ctt gta gtt gag cca gat ttt atc 1405
 Val Leu Val Val Glu Pro Asp Phe Ile
 110 115

atg agg act tcc gca att gtg tct cag gca agc cca cca tgg ggc ctc 1453
 Met Arg Thr Ser Ala Ile Val Ser Gln Ala Ser Pro Pro Trp Gly Leu
 120 125 130

gct agt atc tcc tcc cgc aca cca gga gct gcc tct tat gtc tac gac 1501
 Ala Ser Ile Ser Ser Arg Thr Pro Gly Ala Ala Ser Tyr Val Tyr Asp
 135 140 145

gac agt gcg ggc caa ggc acc ttt tcc tac gtg at aggtaagtca 1546
 Asp Ser Ala Gly Gln Gly Thr Phe Ser Tyr Val Ile
 150 155 160

aaaacatagt gtagatcttg atttggtggt gacatattat ca a gac acg ggt gtg 1601
 Asp Thr Gly Val

cgc atc acc cac cag gac ttt ggc gga cga gcc atc tgg gga ttt aat 1649
 Arg Ile Thr His Gln Asp Phe Gly Gly Arg Ala Ile Trp Gly Phe Asn
 165 170 175 180

gcc gta aga aac agt cct gat act gat gaa gat gcc cat gga acg 1694
 Ala Val Arg Asn Ser Pro Asp Thr Asp Glu Asp Gly His Gly Thr
 185 190 195

taagccacac ttcatctcac agtggcaata ctcttctgac ataaactagt cac gtt 1750
 His Val

gct gga acc gtt ggc ggt acc aaa tat ggt gtt gcc aag aaa acc acc 1798
 Ala Gly Thr Val Gly Gly Thr Lys Tyr Gly Val Ala Lys Lys Thr Thr
 200 205 210

atc ata agt gtc aag acc ttc ggt ggt agc tca gga agt gca tca gat 1846
 Ile Ile Ser Val Lys Thr Phe Gly Gly Ser Ser Gly Ser Ala Ser Asp
 215 220 225

gtc ttc gca ggg ttc gac tgg acg gtc aac gat atc gtt tcc aag aac 1894
 Val Phe Ala Gly Phe Asp Trp Thr Val Asn Asp Ile Val Ser Lys Asn
 230 235 240 245

cga caa aac att gcc gtc atc aat atg tgc ttc ggt gga tct gcc tct 1942
 Arg Gln Asn Ile Ala Val Ile Asn Met Ser Phe Gly Gly Ser Ala Ser
 250 255 260

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aca acg tgg gac aat gcc att act gca gct tgg aac aaa ggg gta agc 1990
 Thr Thr Trp Asp Asn Ala Ile Thr Ala Ala Trp Asn Lys Gly Val Ser
 265 270 275
 atg gtc gta gca gca gga aac gaa gac gga ccc aca tcc aat cgc tcg 2038
 Met Val Val Ala Ala Gly Asn Glu Asp Gly Pro Thr Ser Asn Arg Ser
 280 285 290
 cca gcc cgc tct ccc gaa gcc atc tgt gtc ggg aac gtc cag agc aac 2086
 Pro Ala Arg Ser Pro Glu Ala Ile Cys Val Gly Asn Val Gln Ser Asn
 295 300 305
 aac aga agg ctc agc ggt gga gga ggc tcc aac tac ggc cct gaa gtg 2134
 Asn Arg Arg Leu Ser Gly Gly Gly Ser Asn Tyr Gly Pro Glu Val
 310 315 320 325
 gat atc ttc gct gca ggc acc ctc atc gtc tcc gca tcc cat ctg agc 2182
 Asp Ile Phe Ala Ala Gly Thr Leu Ile Val Ser Ala Ser His Leu Ser
 330 335 340
 gac aca gga aca acc act aag aac ggt act tcc atg gcg gct cct cac 2230
 Asp Thr Gly Thr Thr Lys Asn Gly Thr Ser Met Ala Ala Pro His
 345 350 355
 gta gct ggt ctg atc tca tac ctt cgt ggc ctt gag ggt ccc tcg act 2278
 Val Ala Gly Leu Ile Ser Tyr Leu Arg Gly Leu Glu Gly Pro Ser Thr
 360 365 370
 gcg gcg gcc att aag gcg agg gtg tat caa ctg gcc acg cct ggt gtc 2326
 Ala Ala Ala Ile Lys Ala Arg Val Tyr Gln Leu Ala Thr Pro Gly Val
 375 380 385
 gtg aca gac gca atg ggc tca gtc aat cta ctg gca tac aac ggt aac 2374
 Val Thr Asp Ala Met Gly Ser Val Asn Leu Leu Ala Tyr Asn Gly Asn
 390 395 400 405
 aaa taatcgcat tctcatgaac gaggatccta gaattgcggt aatctacgat 2427
 Lys
 tttatgattg ggatgtaatc tacttccttg cctgggctct tttctgtata tattatgtgt 2487
 tgaataacta ccaattatcc gattttatcc aagtcacttt caatgcttca aagttgtagt 2547
 atgacttggt tagactaacc tgtaatgttc tagaagtcac gctgtctacc aatccaactc 2607
 gaactcgaca gtgactcgga aggccttcga aaacacaagc tcttgaacga agggaaacaca 2667
 agcgcttcatt tttttactac tcgtctcgaa tcgattcctt cacaatgtta ttgaaaggaa 2727
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 aaggatatact tagcagcttg gcgcgcgtcaa aaaatgtcaa caccaaccgg acatgtcgaa 2907
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 acatccagag tgtaatgcat ggcagcgac tacacgcagc tacatattgg ggcgaaaaat 3267
 gcaaagctgg agcttctaatt gtcaaaattc gatatcaagc agctccaaga tccgtacaac 3327
 cagactctac tctcgtaggc tgcaggcggt ggccagcctc atactgctaa 3377

<210> 225

<211> 107

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 225

Met Arg Phe Phe Thr Arg Phe Thr Ala Leu Val Thr Ala Ala Ala Pro
 1 5 10 15
 Phe Ile Ala Leu Ala Ala Pro Val Ala Ala Pro Pro Glu Asn Asp Ile
 20 25 30
 Ile Pro Gly Lys Tyr Ile Val Gln Leu Lys Pro Asp Thr Asp Val Ala

10336256.txt

35 40 45
 Ala Val Ala Ala His His His Lys Val Arg Ser Ile His Ala Arg Asn
 50 55 60
 Leu Ala Arg Arg Gly Asp Asn Ser Pro Thr Gly Glu Pro Val Glu Arg
 65 70 75 80
 Glu Tyr Gly Phe Gly Asp Phe Lys Gly Tyr Ser Gly Phe Phe Asp Glu
 85 90 95
 Ala Thr Ile Glu Glu Leu Lys Thr Leu Pro Glu
 100 105

<210> 226

<211> 53

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 226

Val Leu Val Val Glu Pro Asp Phe Ile Met Arg Thr Ser Ala Ile Val
 1 5 10 15
 Ser Gln Ala Ser Pro Pro Trp Gly Leu Ala Ser Ile Ser Ser Arg Thr
 20 25 30
 Pro Gly Ala Ala Ser Tyr Val Tyr Asp Asp Ser Ala Gly Gln Gly Thr
 35 40 45
 Phe Ser Tyr Val Ile
 50

<210> 227

<211> 35

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 227

Asp Thr Gly Val Arg Ile Thr His Gln Asp Phe Gly Gly Arg Ala Ile
 1 5 10 15
 Trp Gly Phe Asn Ala Val Arg Asn Ser Pro Asp Thr Asp Glu Asp Gly
 20 25 30
 His Gly Thr
 35

<210> 228

<211> 211

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 228

His Val Ala Gly Thr Val Gly Gly Thr Lys Tyr Gly Val Ala Lys Lys
 1 5 10 15
 Thr Thr Ile Ile Ser Val Lys Thr Phe Gly Gly Ser Ser Gly Ser Ala
 20 25 30
 Ser Asp Val Phe Ala Gly Phe Asp Trp Thr Val Asn Asp Ile Val Ser
 35 40 45
 Lys Asn Arg Gln Asn Ile Ala Val Ile Asn Met Ser Phe Gly Gly Ser
 50 55 60
 Ala Ser Thr Thr Trp Asp Asn Ala Ile Thr Ala Ala Trp Asn Lys Gly
 65 70 75 80
 Val Ser Met Val Val Ala Ala Gly Asn Glu Asp Gly Pro Thr Ser Asn
 85 90 95
 Arg Ser Pro Ala Arg Ser Pro Glu Ala Ile Cys Val Gly Asn Val Gln
 100 105 110
 Ser Asn Asn Arg Arg Leu Ser Gly Gly Gly Gly Ser Asn Tyr Gly Pro
 115 120 125
 Glu Val Asp Ile Phe Ala Ala Gly Thr Leu Ile Val Ser Ala Ser His
 130 135 140
 Leu Ser Asp Thr Gly Thr Thr Thr Lys Asn Gly Thr Ser Met Ala Ala
 145 150 155 160
 Pro His Val Ala Gly Leu Ile Ser Tyr Leu Arg Gly Leu Glu Gly Pro
 165 170 175
 Ser Thr Ala Ala Ala Ile Lys Ala Arg Val Tyr Gln Leu Ala Thr Pro
 180 185 190

10336256.txt

Gly Val Val Thr Asp Ala Met Gly Ser Val Asn Leu Leu Ala Tyr Asn
 195 200 205
 Gly Asn Lys
 210

<210> 229

<211> 1218

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1218)

<400> 229

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ttc att gct ctt gct gct ccc gtc gca gca cct cca gag aat gac ata	96
Phe Ile Ala Leu Ala Ala Pro Val Ala Ala Pro Pro Glu Asn Asp Ile	
20 25 30	
att cct gga aaa tac ata gtc cag ctg aag cct gat acc gat gtc gca	144
Ile Pro Gly Lys Tyr Ile Val Gln Leu Lys Pro Asp Thr Asp Val Ala	
35 40 45	
gcg gtc gct gcc cac cat cac aaa gtg cgc agc atc cat gcc cgc aac	192
Ala Val Ala Ala His His His Lys Val Arg Ser Ile His Ala Arg Asn	
50 55 60	
ctg gcc cga cga ggt gac aat tct ccg act ggt gag cca gtg gag cgc	240
Leu Ala Arg Arg Gly Asp Asn Ser Pro Thr Gly Glu Pro Val Glu Arg	
65 70 75 80	
gag tac ggg ttc ggc gac ttc aaa ggc tat tct ggg ttt ttc gat gaa	288
Glu Tyr Gly Phe Gly Asp Phe Lys Gly Tyr Ser Gly Phe Phe Asp Glu	
85 90 95	
gca acc atc gaa gag ttg aaa act ctg cca gag gtg ctt gta gtt gag	336
Ala Thr Ile Glu Glu Leu Lys Thr Leu Pro Glu Val Leu Val Val Glu	
100 105 110	
cca gat ttt atc atg agg act tcc gca att gtg tct cag gca agc cca	384
Pro Asp Phe Ile Met Arg Thr Ser Ala Ile Val Ser Gln Ala Ser Pro	
115 120 125	
cca tgg ggc ctc gct agt atc tcc tcc cgc aca cca gga gct gcc tct	432
Pro Trp Gly Leu Ala Ser Ile Ser Ser Arg Thr Pro Gly Ala Ala Ser	
130 135 140	
tat gtc tac gac gac agt gcg ggc caa ggc acc ttt tcc tac gtg ata	480
Tyr Val Tyr Asp Asp Ser Ala Gly Gln Gly Thr Phe Ser Tyr Val Ile	
145 150 155 160	
gac acg ggt gtg cgc atc acc cac cag gac ttt ggc gga cga gcc atc	528
Asp Thr Gly Val Arg Ile Thr His Gln Asp Phe Gly Gly Arg Ala Ile	
165 170 175	
tgg gga ttt aat gcc gta aga aac agt cct gat act gat gaa gat ggc	576
Trp Gly Phe Asn Ala Val Arg Asn Ser Pro Asp Thr Asp Glu Asp Gly	
180 185 190	
cat gga acg cac gtt gct gga acc gtt ggc ggt acc aaa tat ggt gtt	624
His Gly Thr His Val Ala Gly Thr Val Gly Gly Thr Lys Tyr Gly Val	
195 200 205	
gcc aag aaa acc acc atc ata agt gtc aag acc ttc ggt ggt agc tca	672

10336256.txt

Ala	Lys	Lys	Thr	Thr	Ile	Ile	Ser	Val	Lys	Thr	Phe	Gly	Gly	Ser	Ser	
210						215					220					
gga	agt	gca	tca	gat	gtc	ttc	gca	ggg	ttc	gac	tgg	acg	gtc	aac	gat	720
Gly	Ser	Ala	Ser	Asp	Val	Phe	Ala	Gly	Phe	Asp	Trp	Thr	Val	Asn	Asp	
225					230				235						240	
atc	gtt	tcc	aag	aac	cga	caa	aac	att	gcc	gtc	atc	aat	atg	tcg	ttc	768
Ile	Val	Ser	Lys	Asn	Arg	Gln	Asn	Ile	Ala	Val	Ile	Asn	Met	Ser	Phe	
				245					250					255		
ggt	gga	tct	gcc	tct	aca	acg	tgg	gac	aat	gcc	att	act	gca	gct	tgg	816
Gly	Gly	Ser	Ala	Ser	Thr	Thr	Trp	Asp	Asn	Ala	Ile	Thr	Ala	Ala	Trp	
			260					265					270			
aac	aaa	ggg	gta	agc	atg	gtc	gta	gca	gca	gga	aac	gaa	gac	gga	ccc	864
Asn	Lys	Gly	Val	Ser	Met	Val	Val	Ala	Ala	Gly	Asn	Glu	Asp	Gly	Pro	
		275					280					285				
aca	tcc	aat	cgc	tcg	cca	gcc	cgc	tct	ccc	gaa	gcc	atc	tgt	gtc	ggg	912
Thr	Ser	Asn	Arg	Ser	Pro	Ala	Arg	Ser	Pro	Glu	Ala	Ile	Cys	Val	Gly	
	290					295				300						
aac	gtc	cag	agc	aac	aac	aga	agg	ctc	agc	ggt	gga	gga	ggc	tcc	aac	960
Asn	Val	Gln	Ser	Asn	Asn	Arg	Arg	Leu	Ser	Gly	Gly	Gly	Gly	Ser	Asn	
305					310					315					320	
tac	ggc	cct	gaa	gtg	gat	atc	ttc	gct	gca	ggc	acc	ctc	atc	gtc	tcc	1008
Tyr	Gly	Pro	Glu	Val	Asp	Ile	Phe	Ala	Ala	Gly	Thr	Leu	Ile	Val	Ser	
				325				330						335		
gca	tcc	cat	ctg	agc	gac	aca	gga	aca	acc	act	aag	aac	ggt	act	tcc	1056
Ala	Ser	His	Leu	Ser	Asp	Thr	Gly	Thr	Thr	Thr	Lys	Asn	Gly	Thr	Ser	
			340					345					350			
atg	gcg	gct	cct	cac	gta	gct	ggt	ctg	atc	tca	tac	ctt	cgt	ggc	ctt	1104
Met	Ala	Ala	Pro	His	Val	Ala	Gly	Leu	Ile	Ser	Tyr	Leu	Arg	Gly	Leu	
		355					360					365				
gag	ggt	ccc	tcg	act	gcg	gcg	gcc	att	aag	gcg	agg	gtg	tat	caa	ctg	1152
Glu	Gly	Pro	Ser	Thr	Ala	Ala	Ala	Ile	Lys	Ala	Arg	Val	Tyr	Gln	Leu	
	370					375				380						
gcc	acg	cct	ggt	gtc	gtg	aca	gac	gca	atg	ggc	tca	gtc	aat	cta	ctg	1200
Ala	Thr	Pro	Gly	Val	Val	Thr	Asp	Ala	Met	Gly	Ser	Val	Asn	Leu	Leu	
385					390					395					400	
gca	tac	aac	ggt	aac	aaa											1218
Ala	Tyr	Asn	Gly	Asn	Lys											
				405												

<210> 230

<211> 406

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> SIGNAL

<222> (1)...(21)

<221> DOMAIN

<222> (35)...(120)

<223> Subtilisin N-terminal region

<221> DOMAIN

<222> (134)...(397)

<223> Subtilase family

10336256.txt

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<400> 230
Met Arg Phe Phe Thr Arg Phe Thr Ala Leu Val Thr Ala Ala Ala Pro
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Phe Ile Ala Leu Ala Ala Pro Val Ala Ala Pro Pro Glu Asn Asp Ile
20      25      30
Ile Pro Gly Lys Tyr Ile Val Gln Leu Lys Pro Asp Thr Asp Val Ala
35      40      45
Ala Val Ala Ala His His His Lys Val Arg Ser Ile His Ala Arg Asn
50      55      60
Leu Ala Arg Arg Gly Asp Asn Ser Pro Thr Gly Glu Pro Val Glu Arg
65      70      75      80
Glu Tyr Gly Phe Gly Asp Phe Lys Gly Tyr Ser Gly Phe Phe Asp Glu
85      90      95
Ala Thr Ile Glu Glu Leu Lys Thr Leu Pro Glu Val Leu Val Val Glu
100      105      110
Pro Asp Phe Ile Met Arg Thr Ser Ala Ile Val Ser Gln Ala Ser Pro
115      120      125
Pro Trp Gly Leu Ala Ser Ile Ser Ser Arg Thr Pro Gly Ala Ala Ser
130      135      140
Tyr Val Tyr Asp Asp Ser Ala Gly Gln Gly Thr Phe Ser Tyr Val Ile
145      150      155      160
Asp Thr Gly Val Arg Ile Thr His Gln Asp Phe Gly Gly Arg Ala Ile
165      170      175
Trp Gly Phe Asn Ala Val Arg Asn Ser Pro Asp Thr Asp Glu Asp Gly
180      185      190
His Gly Thr His Val Ala Gly Thr Val Gly Gly Thr Lys Tyr Gly Val
195      200      205
Ala Lys Lys Thr Thr Ile Ile Ser Val Lys Thr Phe Gly Gly Ser Ser
210      215      220
Gly Ser Ala Ser Asp Val Phe Ala Gly Phe Asp Trp Thr Val Asn Asp
225      230      235      240
Ile Val Ser Lys Asn Arg Gln Asn Ile Ala Val Ile Asn Met Ser Phe
245      250      255
Gly Gly Ser Ala Ser Thr Thr Trp Asp Asn Ala Ile Thr Ala Ala Trp
260      265      270
Asn Lys Gly Val Ser Met Val Val Ala Ala Gly Asn Glu Asp Gly Pro
275      280      285
Thr Ser Asn Arg Ser Pro Ala Arg Ser Pro Glu Ala Ile Cys Val Gly
290      295      300
Asn Val Gln Ser Asn Asn Arg Arg Leu Ser Gly Gly Gly Gly Ser Asn
305      310      315      320
Tyr Gly Pro Glu Val Asp Ile Phe Ala Ala Gly Thr Leu Ile Val Ser
325      330      335
Ala Ser His Leu Ser Asp Thr Gly Thr Thr Lys Asn Gly Thr Ser
340      345      350
Met Ala Ala Pro His Val Ala Gly Leu Ile Ser Tyr Leu Arg Gly Leu
355      360      365
Glu Gly Pro Ser Thr Ala Ala Ile Lys Ala Arg Val Tyr Gln Leu
370      375      380
Ala Thr Pro Gly Val Val Thr Asp Ala Met Gly Ser Val Asn Leu Leu
385      390      395      400
Ala Tyr Asn Gly Asn Lys
405

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<210> 231

<211> 3206

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (883)...(948)

<223> Exon

<221> CDS

<222> (1010)...(3106)

<223> Exon

10336256.txt

<400> 231

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gtagggtgtaa	tatgctgaca	cgaaaataca	gtcgaatcga	gccagatcta	ggcctggcaa	180
ggcaggtata	gatgtcaatc	tgctcacgga	catgttaggc	gtgcaaaagg	cccaagccag	240
accaaggatg	ccaagaaata	tcatgcagtc	ccgcccctctc	aattccgcga	ggatgcattc	300
cagcagccag	ccagcgccgt	ggatgtggag	gatctatgtg	taacctcatg	ttggactttt	360
tttcgacctg	cctttttggg	tgaccggttt	atccgccaca	aattagttgg	tgattagcgt	420
gagctgtggg	catgcgccac	caatcgcat	gtgggcttgg	tggagctact	acacaccaa	480
gatacccacc	cataaacgcc	aagtcagtc	atccagcgac	tctcaagtgg	accaagttgc	540
gataggacga	cacggaaaca	tgctttctgg	caatccacct	aggacgagct	tgtttttgtc	600
cccgcgcac	tagccctgat	cgggcaggag	acatggtgca	aaacgtctat	cttttgacgt	660
ctatggacta	gtcgctactg	cattgcctat	ggaatgatgg	catcgctact	tcaggtaacc	720
gtcccgaag	gacgtggccc	actgcctgga	tggcgacatg	ccctgcggca	ggggcctcgg	780
gcttagctct	ttgtacaaat	aattcgatg	ccctgcacatg	ccttcttctg	gtcatcgacc	840
tcgtccaatt	gagcttttac	gaagctggtc	gcatactgca	ca atg gct	cgt tac	894
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				1		

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Leu Ser Val Ala Ala Ala Leu Ala Ala Thr Gly Ala Cys Ala Phe Thr	
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Pro Glu	

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Ser Pro Asp Gly Ser Val Ala Leu Phe Ser Tyr Thr Gln Tyr Ser Phe	
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Glu Glu His Ala Arg Thr Ala Gly Met Asn Leu Ile Asp Leu Lys Thr	
55 60 65	

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Gly Glu Val Thr Lys Ser Gly Leu Asp Pro Ser Glu Val Asn Glu Val	
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Ala Trp Ile Pro Gly Thr Glu Thr Gly Ile Ile Tyr Ile Asn Gly Thr	
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Asn Glu Glu Ile Pro Gly Gly Val Thr Leu Trp Ile Gly Asp Ile Lys	
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Asp Pro Ser Ala Ser Thr Leu Val Ala Ser Leu Asp Ala Pro Tyr Ser	
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ggc ttg aag gtt gcc aac acc tct act ggt gac ttg cat ttc ttg gtc	1384
Gly Leu Lys Val Ala Asn Thr Ser Thr Gly Asp Leu His Phe Leu Val	
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Asn Ser Leu Ala Tyr Pro Asn Gly Thr Ala Val Asn Pro Glu Thr Glu	
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Val Lys Pro Thr Ser Thr Ala Arg Tyr Tyr Ser Asp Ile Tyr Val Arg	
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aca Thr	ctt Leu	tcc Ser	aag Lys	aac Asn 200	agc Ser	agt Ser	tat Tyr	gct Ala	ctc Leu 205	tct Ser	ggc Gly	gct Ala	ggc Gly	gtg Val 210	cgc Arg	1576
aac Asn	atc Ile	caa Gln	agt Ser 215	ggt Gly	atc Ile	aaa Lys	ttc Phe	acc Thr 220	gct Ala	act Thr	cag Gln	cct Pro	gag Glu 225	act Thr	ccc Pro	1624
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ctg Leu	tac Tyr 325	acc Thr	tac Tyr	gac Asp	gtt Val	gct Ala 330	gtc Val	gag Glu	ggc Gly	caa Gln	ggc Gly 335	gtg Val	gcc Ala	gct Ala	agc Ser	1960
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ccc Pro 420	aac Asn	gaa Glu	tgg Trp	tac Tyr	atc Ile 425	ctc Leu	gcc Ala	gac Asp	ggc Gly	aac Asn 430	aag Lys	aag Lys	acg Thr	ctt Leu	ctt Leu 435	2248
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Leu	Gln	Ala	Tyr	Val	Val	Lys	Pro	Thr	Phe	Tyr	Gln	Glu	Asn	Val	Thr	
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tac	ccc	ctt	gct	ttc	ctg	att	cac	ggg	ggg	cct	cag	ggc	aac	tgg	ggc	2440
Tyr	Pro	Leu	Ala	Phe	Leu	Ile	His	Gly	Gly	Pro	Gln	Gly	Asn	Trp	Gly	
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aac	agc	tgg	tca	aac	cgc	tgg	aac	ccg	cag	gtc	tgg	gcc	gac	caa	ggc	2488
Asn	Ser	Trp	Ser	Asn	Arg	Trp	Asn	Pro	Gln	Val	Trp	Ala	Asp	Gln	Gly	
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tac	atc	gtc	gtc	gca	cct	aac	ccg	act	ggg	tct	aca	agt	ttc	gga	cag	2536
Tyr	Ile	Val	Val	Ala	Pro	Asn	Pro	Thr	Gly	Ser	Thr	Ser	Phe	Gly	Gln	
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Tyr	Leu	Ile	Asp	Ser	Ile	Gln	Gly	Glu	Trp	Gly	Ser	Trp	Pro	Tyr	Glu	
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gac	ctg	gtc	aat	gcc	tgg	aac	tac	atc	aac	tcc	acc	atg	acg	tgg	atc	2632
Asp	Leu	Val	Asn	Ala	Trp	Asn	Tyr	Ile	Asn	Ser	Thr	Met	Thr	Trp	Ile	
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gac	acc	gag	aac	ggg	atc	gcc	gcc	ggg	gcc	tcc	tac	ggg	gga	tac	atg	2680
Asp	Thr	Glu	Asn	Gly	Ile	Ala	Ala	Gly	Ala	Ser	Tyr	Gly	Gly	Tyr	Met	
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acc	aac	tgg	atc	cag	tcc	aat	gac	ctc	ggc	aac	gag	ttc	aag	gct	ctc	2728
Thr	Asn	Trp	Ile	Gln	Ser	Asn	Asp	Leu	Gly	Asn	Glu	Phe	Lys	Ala	Leu	
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gtc	acc	cat	gac	ggg	atc	tcc	aac	acc	gag	ggg	gcc	tgg	gcg	tcc	gag	2776
Val	Thr	His	Asp	Gly	Ile	Ser	Asn	Thr	Glu	Gly	Ala	Trp	Ala	Ser	Glu	
				600					605					610		
gag	ctc	tgg	ttc	atc	cgc	cac	gac	tac	gat	ggc	aac	atc	tgg	gac	tca	2824
Glu	Leu	Trp	Phe	Ile	Arg	His	Asp	Tyr	Asp	Gly	Asn	Ile	Trp	Asp	Ser	
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ccc	gcc	tac	cgc	cag	tgg	aac	ccc	cag	aac	cac	att	gcc	aac	tgg	tcc	2872
Pro	Ala	Tyr	Arg	Gln	Trp	Asn	Pro	Gln	Asn	His	Ile	Ala	Asn	Trp	Ser	
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act	ccc	cag	ttc	gtc	atc	cac	aac	acg	ctc	gac	tac	cgt	ctc	ccc	gag	2920
Thr	Pro	Gln	Phe	Val	Ile	His	Asn	Thr	Leu	Asp	Tyr	Arg	Leu	Pro	Glu	
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Ser	Arg	Phe	Leu	Asn	Phe	Pro	Asp	Glu	Asn	His	Trp	Val	Leu	Lys	Gln	
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gag	aac	agc	ttg	gtt	tgg	cac	act	gag	att	ttc	aac	tgg	atc	aac	cac	3064
Glu	Asn	Ser	Leu	Val	Trp	His	Thr	Glu	Ile	Phe	Asn	Trp	Ile	Asn	His	
			695					700					705			
tgg	tcc	aag	ggg	gag	cct	ttg	agc	act	acc	ccg	att	ggc	aac			3106
Trp	Ser	Lys	Gly	Glu	Pro	Leu	Ser	Thr	Thr	Pro	Ile	Gly	Asn			
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 Cys Ala Phe Thr Pro Glu
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 35 40 45
 Thr Lys Ser Gly Leu Asp Pro Ser Glu Val Asn Glu Val Ala Trp Ile
 50 55 60
 Pro Gly Thr Glu Thr Gly Ile Ile Tyr Ile Asn Gly Thr Asn Glu Glu
 65 70 75 80
 Ile Pro Gly Gly Val Thr Leu Trp Ile Gly Asp Ile Lys Asp Pro Ser
 85 90 95
 Ala Ser Thr Leu Val Ala Ser Leu Asp Ala Pro Tyr Ser Gly Leu Lys
 100 105 110
 Val Ala Asn Thr Ser Thr Gly Asp Leu His Phe Leu Val Asn Ser Leu
 115 120 125
 Ala Tyr Pro Asn Gly Thr Ala Val Asn Pro Glu Thr Glu Val Lys Pro
 130 135 140
 Thr Ser Thr Ala Arg Tyr Tyr Ser Asp Ile Tyr Val Arg His Trp Asp
 145 150 155 160
 Thr Trp Leu Thr Lys Asn Arg Tyr Gln Leu Phe Ala Gly Thr Leu Ser
 165 170 175
 Lys Asn Ser Ser Tyr Ala Leu Ser Gly Ala Gly Val Arg Asn Ile Gln
 180 185 190
 Ser Gly Ile Lys Phe Thr Ala Thr Gln Pro Glu Thr Pro Val Gln Pro
 195 200 205
 Phe Gly Asp Ser Ser Asp Tyr Asp Ile Ser Pro Asp Gly Ser Met Tyr
 210 215 220
 Ala Phe Ile Ser Lys Ala Pro Gln Leu Asn Lys Ala Asn Tyr Thr Ala
 225 230 235 240
 Ser Tyr Leu Tyr Val Gly Ala Phe Ala Ser Asn Glu Ala Pro Val Ala
 245 250 255
 Leu Asn Gly Pro Asp Ser Glu Ala Phe Lys Ala Gly His Gln Gly Ala
 260 265 270
 Ser Gly Leu Pro Ser Phe Ser Gly Asp Ser Cys Lys Leu Ala Tyr Val
 275 280 285
 Gln Gln Asp Glu Asp Tyr Tyr Glu Ser Asp Arg Phe Lys Leu Tyr Thr
 290 295 300
 Tyr Asp Val Ala Val Glu Gly Gln Gly Val Ala Ala Ser Asn Trp Lys
 305 310 315 320
 Ser Leu Ser Glu Gly Phe Asp Arg Trp Val Gln Gly Pro Ile Thr Trp
 325 330 335
 Ala His Asp Asp Ser Ser Ile Tyr Val Thr Ala Asp Asp Tyr Ala Arg
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 Asn Lys Ile Phe Asn Phe Pro Ile Thr Ala Asp Glu Lys Phe Val Pro
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 Glu Pro Leu Thr Gly Asn Thr Ser Val Ser Ala Phe Ser Leu Leu Pro
 370 375 380

10336256.txt

Asp Gly Ser Leu Phe Val Ala Ala Thr Ala Ile Trp Thr Pro Asn Glu
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 Trp Tyr Ile Leu Ala Asp Gly Asn Lys Lys Thr Leu Leu Asp Ala Ser
 405 410 415
 Gln Val Asp Pro Asn Leu Ala Gly Leu Ser Ser Lys Thr Val Ser Glu
 420 425 430
 Ile Phe Phe Asn Gly Ser Asn Pro Asp Leu Lys Gln Gln Leu Gln Ala
 435 440 445
 Tyr Val Val Lys Pro Thr Phe Tyr Gln Glu Asn Val Thr Tyr Pro Leu
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 Ala Phe Leu Ile His Gly Gly Pro Gln Gly Asn Trp Gly Asn Ser Trp
 465 470 475 480
 Ser Asn Arg Trp Asn Pro Gln Val Trp Ala Asp Gln Gly Tyr Ile Val
 485 490 495
 Val Ala Pro Asn Pro Thr Gly Ser Thr Ser Phe Gly Gln Tyr Leu Ile
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 Asp Ser Ile Gln Gly Glu Trp Gly Ser Trp Pro Tyr Glu Asp Leu Val
 515 520 525
 Asn Ala Trp Asn Tyr Ile Asn Ser Thr Met Thr Trp Ile Asp Thr Glu
 530 535 540
 Asn Gly Ile Ala Ala Gly Ala Ser Tyr Gly Gly Tyr Met Thr Asn Trp
 545 550 555 560
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 565 570 575
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 580 585 590
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 595 600 605
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 610 615 620
 Phe Val Ile His Asn Thr Leu Asp Tyr Arg Leu Pro Glu Ser Asp Gly
 625 630 635 640
 Ile Ser Leu Phe Asn Ile Leu Gln Ala Arg Gly Ile Pro Ser Arg Phe
 645 650 655
 Leu Asn Phe Pro Asp Glu Asn His Trp Val Leu Lys Gln Glu Asn Ser
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 Cys Ala Phe Thr 20 Pro Glu Leu Leu 25 Ser Thr Val Arg 30 Ala Ala

gcc gat ccc agt cca gat ggc tca gtc gcg ctc ttc tcg tac acg cag 144
 Ala Asp Pro 35 Ser Pro Asp Gly Ser Val Ala Leu Phe Ser Tyr Thr Gln

tac tcc ttc gag gaa cat gcg cgc acg gct ggc atg aac ctc atc gat 192
 Tyr Ser 50 Phe Glu Glu His Ala Arg Thr Ala Gly Met 60 Asn Leu Ile Asp

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 Page 230

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gag Glu 225	act Thr	ccc Pro	gtc Val	cag Gln	cct Pro 230	ttt Phe	ggc Gly	gac Asp	tcg Ser	agc Ser 235	gat Asp	tat Tyr	gac Asp	atc Ile	agt Ser 240	720
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gct Ala	gga Gly 290	cac His	cag Gln	ggg Gly	gct Ala	tcc Ser 295	ggg Gly	cta Leu	cca Pro	tcc Ser	ttc Phe 300	tcc Ser	ggg Gly	gac Asp	agc Ser	912
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gat Asp 385	gag Glu	aag Lys	ttt Phe	gtt Val	ccc Pro 390	gag Glu	ccg Pro	cta Leu	act Thr	gga Gly 395	aac Asn	act Thr	tca Ser	gtt Val	tcg Ser 400
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tcc Ser	aag Lys 450	act Thr	gtc Val	tct Ser	gag Glu	att Ile 455	ttc Phe	ttc Phe	aat Asn	ggc Gly	tcc Ser 460	aac Asn	ccc Pro	gat Asp	ctc Leu
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gga Gly	tac Tyr	atg Met	acc Thr 580	aac Asn	tgg Trp	atc Ile	cag Gln	tcc Ser 585	aat Asn	gac Asp	ctc Leu	ggc Gly	aac Asn 590	gag Glu	ttc Phe
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Ala 610	Ser	Glu	Glu	Leu	Trp	Phe 615	Ile	Arg	His	Asp	Tyr 620	Asp	Gly	Asn	Ile	
tgg 625	gac Trp	tca Asp	ccc Ser	gcc Pro	tac Ala	cgc Tyr 630	cag Arg	tgg Gln	aac Trp	ccc Asn	cag Pro 635	aac Gln	cac Asn	att His	gcc Ile 640	1920
aac 645	tgg Asn	tcc Trp	act Ser	ccc Thr	cag Pro 645	ttc Gln	gtc Phe	atc Val	cac Ile	aac His 650	acg Asn	ctc Thr	gac Leu	tac Asp	cgt Tyr 655	1968
ctc 660	ccc Leu	gag Pro	agc Glu	gac Ser 660	ggc Asp	atc Gly	agc Ile	ctg Ser	ttc Leu 665	aac Phe	atc Asn	ctc Ile	cag Leu	gcg Ala 670	cg Arg	2016
ggt 680	atc Gly	ccc Ile	agt Pro	cgc Ser 675	ttc Arg	ctc Phe	aac Leu	ttc Asn 680	ccc Phe	gac Pro	gag Asp	aac Glu	cac Asn 685	tgg His	gtc Trp Val	2064
ctc 690	aag Leu	cag Lys	gag Gln	aac Glu	agc Asn	ttg Ser	ggt Leu 695	tgg Val	cac Trp	act His	gag Thr	att Glu 700	ttc Ile	aac Phe	tgg Asn Trp	2112
atc 705	aac Ile	cac Asn	tgg His	tcc Trp	aag Lys 710	ggt Gly	gag Glu	cct Pro	ttg Leu	agc Ser 715	act Thr	acc Thr	ccg Pro	att Ile	ggc Gly 720	2160
aac 725	Asn															2163

<210> 235

<211> 721

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 235

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Cys	Ala	Phe	Thr 20	Pro	Glu	Leu	Leu	Leu 25	Ser	Thr	Val	Arg	Arg 30	Ala	Ala
Ala	Asp	Pro 35	Ser	Pro	Asp	Gly	Ser 40	Val	Ala	Leu	Phe	Ser 45	Tyr	Thr	Gln
Tyr	Ser	Phe 50	Glu	Glu	His	Ala 55	Arg	Thr	Ala	Gly	Met 60	Asn	Leu	Ile	Asp
Leu 65	Lys	Thr	Gly	Glu	Val 70	Thr	Lys	Ser	Gly	Leu 75	Asp	Pro	Ser	Glu	Val 80
Asn	Glu	Val	Ala	Trp 85	Ile	Pro	Gly	Thr	Glu 90	Thr	Gly	Ile	Ile	Tyr 95	Ile
Asn	Gly	Thr	Asn 100	Glu	Glu	Ile	Pro	Gly 105	Gly	Val	Thr	Leu	Trp 110	Ile	Gly
Asp	Ile	Lys 115	Asp	Pro	Ser	Ala	Ser 120	Thr	Leu	Val	Ala	Ser 125	Leu	Asp	Ala
Pro	Tyr 130	Ser	Gly	Leu	Lys	Val 135	Ala	Asn	Thr	Ser	Thr 140	Gly	Asp	Leu	His
Phe 145	Leu	Val	Asn	Ser	Leu 150	Ala	Tyr	Pro	Asn	Gly 155	Thr	Ala	Val	Asn	Pro 160
Glu	Thr	Glu	Val	Lys 165	Pro	Thr	Ser	Thr	Ala 170	Arg	Tyr	Tyr	Ser	Asp 175	Ile
Tyr	Val	Arg	His 180	Trp	Asp	Thr	Trp	Leu 185	Thr	Lys	Asn	Arg	Tyr 190	Gln	Leu
Phe	Ala	Gly 195	Thr	Leu	Ser	Lys	Asn 200	Ser	Ser	Tyr	Ala	Leu 205	Ser	Gly	Ala
Gly	Val 210	Arg	Asn	Ile	Gln	Ser 215	Gly	Ile	Lys	Phe	Thr 220	Ala	Thr	Gln	Pro
Glu 225	Thr	Pro	Val	Gln	Pro 230	Phe	Gly	Asp	Ser	Ser 235	Asp	Tyr	Asp	Ile	Ser 240

10336256.txt

Pro	Asp	Gly	Ser	Met	Tyr	Ala	Phe	Ile	Ser	Lys	Ala	Pro	Gln	Leu	Asn
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Lys	Ala	Asn	Tyr	Thr	Ala	Ser	Tyr	Leu	Tyr	Val	Gly	Ala	Phe	Ala	Ser
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Asn	Glu	Ala	Pro	Val	Ala	Leu	Asn	Gly	Pro	Asp	Ser	Glu	Ala	Phe	Lys
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Ala	Gly	His	Gln	Gly	Ala	Ser	Gly	Leu	Pro	Ser	Phe	Ser	Gly	Asp	Ser
	290					295					300				
Cys	Lys	Leu	Ala	Tyr	Val	Gln	Gln	Asp	Glu	Asp	Tyr	Tyr	Glu	Ser	Asp
305					310					315					320
Arg	Phe	Lys	Leu	Tyr	Thr	Tyr	Asp	Val	Ala	Val	Glu	Gly	Gln	Gly	Val
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Ala	Ala	Ser	Asn	Trp	Lys	Ser	Leu	Ser	Glu	Gly	Phe	Asp	Arg	Trp	Val
			340					345					350		
Gln	Gly	Pro	Ile	Thr	Trp	Ala	His	Asp	Asp	Ser	Ser	Ile	Tyr	Val	Thr
		355					360					365			
Ala	Asp	Asp	Tyr	Ala	Arg	Asn	Lys	Ile	Phe	Asn	Phe	Pro	Ile	Thr	Ala
	370					375					380				
Asp	Glu	Lys	Phe	Val	Pro	Glu	Pro	Leu	Thr	Gly	Asn	Thr	Ser	Val	Ser
385					390					395					400
Ala	Phe	Ser	Leu	Leu	Pro	Asp	Gly	Ser	Leu	Phe	Val	Ala	Ala	Thr	Ala
				405					410					415	
Ile	Trp	Thr	Pro	Asn	Glu	Trp	Tyr	Ile	Leu	Ala	Asp	Gly	Asn	Lys	Lys
			420					425					430		
Thr	Leu	Leu	Asp	Ala	Ser	Gln	Val	Asp	Pro	Asn	Leu	Ala	Gly	Leu	Ser
		435					440					445			
Ser	Lys	Thr	Val	Ser	Glu	Ile	Phe	Phe	Asn	Gly	Ser	Asn	Pro	Asp	Leu
	450					455					460				
Lys	Gln	Gln	Leu	Gln	Ala	Tyr	Val	Val	Lys	Pro	Thr	Phe	Tyr	Gln	Glu
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Asn	Val	Thr	Tyr	Pro	Leu	Ala	Phe	Leu	Ile	His	Gly	Gly	Pro	Gln	Gly
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Asn	Trp	Gly	Asn	Ser	Trp	Ser	Asn	Arg	Trp	Asn	Pro	Gln	Val	Trp	Ala
			500					505					510		
Asp	Gln	Gly	Tyr	Ile	Val	Val	Ala	Pro	Asn	Pro	Thr	Gly	Ser	Thr	Ser
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Phe	Gly	Gln	Tyr	Leu	Ile	Asp	Ser	Ile	Gln	Gly	Glu	Trp	Gly	Ser	Trp
	530					535					540				
Pro	Tyr	Glu	Asp	Leu	Val	Asn	Ala	Trp	Asn	Tyr	Ile	Asn	Ser	Thr	Met
545					550					555					560
Thr	Trp	Ile	Asp	Thr	Glu	Asn	Gly	Ile	Ala	Ala	Gly	Ala	Ser	Tyr	Gly
				565					570					575	
Gly	Tyr	Met	Thr	Asn	Trp	Ile	Gln	Ser	Asn	Asp	Leu	Gly	Asn	Glu	Phe
			580					585					590		
Lys	Ala	Leu	Val	Thr	His	Asp	Gly	Ile	Ser	Asn	Thr	Glu	Gly	Ala	Trp
		595					600					605			
Ala	Ser	Glu	Glu	Leu	Trp	Phe	Ile	Arg	His	Asp	Tyr	Asp	Gly	Asn	Ile
	610					615					620				
Trp	Asp	Ser	Pro	Ala	Tyr	Arg	Gln	Trp	Asn	Pro	Gln	Asn	His	Ile	Ala
625					630					635					640
Asn	Trp	Ser	Thr	Pro	Gln	Phe	Val	Ile	His	Asn	Thr	Leu	Asp	Tyr	Arg
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Leu	Pro	Glu	Ser	Asp	Gly	Ile	Ser	Leu	Phe	Asn	Ile	Leu	Gln	Ala	Arg
			660					665					670		
Gly	Ile	Pro	Ser	Arg	Phe	Leu	Asn	Phe	Pro	Asp	Glu	Asn	His	Trp	Val
		675					680					685			
Leu	Lys	Gln	Glu	Asn	Ser	Leu	Val	Trp	His	Thr	Glu	Ile	Phe	Asn	Trp
	690					695					700				
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705					710					715					720
Asn															

<210> 236

<211> 3434

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

10336256.txt

<220>
 <221> CDS
 <222> (1001)... (1318)
 <223> Exon

<221> CDS
 <222> (1382)... (1645)
 <223> Exon

<221> CDS
 <222> (1711)... (1887)
 <223> Exon

<221> CDS
 <222> (1940)... (2437)
 <223> Exon

<221> misc_feature
 <222> (1)... (3434)
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 tgcaagtggg catggtgggg ggagtgcatg tgaggataag gatgaggggt cggtagtgaa 180
 ggggtatagg gcgagttatt ggctcatggt tgggtatatg gtggtgtgca tggggattgc 240
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 gttttgccct tgtgtattct gctaccatgt cgtatgtaat actagcatct acctcgacg 360
 cagcactttc agcaccttct cagcccacat cctgacaccg atccgtactc cacagctaca 420
 cccggtccct ccacgcgcaa aggggaagggt cgcagtccgc ctccaccgat gcgtcaccgg 480
 taccattcca tcttccacag catacttatg ggcccacacg tacagtatcc ccgcaagtca 540
 ttcgcacatc gcaggcgtag cctacatggt gcgcgttacc caatgtggca gttggctggt 600
 ctgccaaggc gcaaatcccc tgcagatcac catctaggca cataaggctt gagctggacc 660
 acccaggctt atctcgacgc aagcaacgat attactacc tgcccggccat gtcgacccaa 720
 tacctacaca gaatatggga gaccagcttc ccaagcaagg ttgctgcccc ggccagcggc 780
 caaggccagt cgggcagggt tgaggggaatg gtaggctgtc caaggcccaa tgtggaatga 840
 agccgtcgtg ctgcatcggc gggcatgtac ttttgtcatg agagcaattt gactttgttt 900
 cgaggcgatt atatattaga gggtaggcga agcctgagaa tgttctttcc tcaggccacg 960
 cttctccctc tcacctttct ctgtcttcaa tcttgtagcc atg aag ctc ctc agc 1015
 Met Lys Leu Leu Ser
 1 5

gtc acc ctg gcc tcg ctg ggc ctc gcc tcc gcc gcc acc gtt gcc aag 1063
 Val Thr Leu Ala Ser 10 Leu Gly Leu Ala Ser 15 Ala Ala Thr Val Ala Lys 20

aaa gtg acc tac gac gac tgg aag gtc gtc cgt gtc aat gtc ggc gca 1111
 Lys Val Thr Tyr 25 Asp Asp Trp Lys Val 30 Val Arg Val Asn Val 35 Gly Ala

gac gct gct aag ctc gaa aat gta atg agc aag ctg cag ctt gag ctg 1159
 Asp Ala Ala 40 Lys Leu Glu Asn Val 45 Met Ser Lys Leu Gln Leu Glu Leu 50

tgg aag ggc aag cct gcg tca agc gat gtc gtc gat gtt atg gtg ccg 1207
 Trp Lys 55 Gly Lys Pro Ala Ser 60 Ser Asp Val Val Asp 65 Val Met Val Pro

ccg tcg tcg gtc aag gac ttt gag gct cag act cag ggt ttc gaa aca 1255
 Pro Ser Ser Val Lys 75 Asp Phe Glu Ala Gln Thr 80 Gln Gly Phe Glu Thr 85

aaa gtc atg cat gag aat ctt ggc ctt tct atc gca gac gag cag agt 1303
 Lys Val Met His 90 Glu Asn Leu Gly Leu Ser 95 Ile Ala Asp Glu Gln Ser 100

ttt ggc aca tat gcc ggtacgcttg ttttccccgc cctgtaaatt gaagaggtga 1358
 Phe Gly Thr Tyr Ala

10336256.txt

105

catgggaagt cctaactctg tca gct ggt ctt gca cca aac tcg acg tgg ttt 1411
Ala Gly Leu Ala Pro Asn Ser Thr Trp Phe
110 115

aac tcc tac cac tcc att gct gat cac atg caa tgg att agc gat ctt 1459
Asn Ser Tyr His Ser Ile Ala Asp His Met Gln Trp Ile Ser Asp Leu
120 125 130

gcg gct gca tac ccc aag aac gca gaa gtc att tct gca ggc aag tcg 1507
Ala Ala Ala Tyr Pro Lys Asn Ala Glu Val Ile Ser Ala Gly Lys Ser
135 140 145

gtt gag ggc cgt gat atc aag ggt atc cac atc tgg ggt agt ggt ggt 1555
Val Glu Gly Arg Asp Ile Lys Gly Ile His Ile Trp Gly Ser Gly Gly
150 155 160

aag gga tct cag aag ggt gta gta tgg cac ggc act gtg cac gca cgt 1603
Lys Gly Ser Gln Lys Gly Val Val Trp His Gly Thr Val His Ala Arg
165 170 175 180

gaa tgg atc acg aca atg gta aat tcc ctt ttc aaa aaa aaa 1645
Glu Trp Ile Thr Thr Met Val Asn Ser Leu Phe Lys Lys Lys
185 190

aacaggaaca aaggaaagga agaattgtgc taacacactt acaggtgggc gaatatgcag 1705
catac caa ctc ctt acc tcc act gac gcc aca acc gcc ggc ttc aaa gac 1755
Gln Leu Leu Thr Ser Thr Asp Ala Thr Thr Ala Gly Phe Lys Asp
195 200 205

tcg tac gac ttc tac atc ttc ccc atc gtc aac cca gat ggc ttc gcc 1803
Ser Tyr Asp Phe Tyr Ile Phe Pro Ile Val Asn Pro Asp Gly Phe Ala
210 215 220 225

tac agt cag acc acc gac cgc atg tgg cgc aag aac cgc cag act act 1851
Tyr Ser Gln Thr Thr Asp Arg Met Trp Arg Lys Asn Arg Gln Thr Thr
230 235 240

ccc agc gcc tca tgc gta ggc cgg gac atc aac cgt aagttctctc 1897
Pro Ser Ala Ser Cys Val Gly Arg Asp Ile Asn Arg
245 250

ccgtcccccc aagcatatat acatctaacc gatcatcaag gc aac tgg ccc tct 1951
Asn Trp Pro Ser
255

cac tgg aac cag gcc aac ggt gcc tcc acc tcg ccc tgc gac caa gac 1999
His Trp Asn Gln Ala Asn Gly Ala Ser Thr Ser Pro Cys Asp Gln Asp
260 265 270

tac aaa ggc ccc tca gcc ggc gac ggc gta gaa acc aaa gcc ctg aaa 2047
Tyr Lys Gly Pro Ser Ala Gly Asp Gly Val Glu Thr Lys Ala Leu Lys
275 280 285

gcg cac ctc gac agc atc gcc gcc ggc aaa ggc ata acc ctc tac atg 2095
Ala His Leu Asp Ser Ile Ala Ala Gly Lys Gly Ile Thr Leu Tyr Met
290 295 300 305

gac atc cac gcc tac agc caa ctc tgg atg tac ccc tac ggc tac acc 2143
Asp Ile His Ala Tyr Ser Gln Leu Trp Met Tyr Pro Tyr Gly Tyr Thr
310 315 320

tgc tcc ggc gct ctc ccc aac tcc gca aag tac tct tcg ctg acc aac 2191
Cys Ser Gly Ala Leu Pro Asn Ser Ala Lys Tyr Ser Ser Leu Thr Asn
325 330 335

ggt gcc att gcc gcg gtc aag gca gtg cat gga acg gcg ttc acg ggc 2239

10336256.txt

Gly Ala Ile Ala Ala Val Lys Ala Val His Gly Thr Ala Phe Thr Gly
 340 345 350

ggc ccg att tgc aat acc atc tat cag gtt agt ggc gat agt gtg gat 2287
 Gly Pro Ile Cys Asn Thr Ile Tyr Gln Val Ser Gly Asp Ser Val Asp
 355 360 365

tat gcg ttt gag gtc gca aag gcg acg tat agt atg acg gtc gag ttg 2335
 Tyr Ala Phe Glu Val Ala Lys Ala Thr Tyr Ser Met Thr Val Glu Leu
 370 375 380 385

agg gat acg ggt aag tat ggg ttt gtc ctg ccg aaa gag cag att gtg 2383
 Arg Asp Thr Gly Lys Tyr Gly Phe Val Leu Pro Lys Glu Gln Ile Val
 390 400

ccg agt gcc gag gag atg tgg gct ggt ttg agg tac ttg gtg aag aat 2431
 Pro Ser Ala Glu Glu Met Trp Ala Gly Leu Arg Tyr Leu Val Lys Asn
 405 410 415

atg taa ggtggtagag gggaatatat gtatatatcga gtgtggggat gtattttttt 2487
 Met *

tggtgggctg gggggccttct ggaagatttt gagttggcgg ggggagcccc attgtagata 2547
 tatttttctag aggatgaaaa atcttgagag cagagagaga gagaattggc gttaaaaaag 2607
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 aagaatggag tggtaatagt accaaaaagt gtgtacacct cttgaaagggt atgcacctat 2787
 caggtacgat aatcaaatta atcatgattg cgatgaacgt aactgaatag caaactatgg 2847
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 aaccaccaat caagccgctt acatctctta aaaaaccact ataccattcc tctccaccac 3087
 cacataagaa cagcaacaac aaaaaatcaa gcnnnnnnnn nnnnnnnnnn nnaccctcct 3147
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 ctgctccaac acgacctgca cgctctcac agacgcctgc gtagaatcct ccacgcaatg 3387
 cgcgacactg ctctcgcacg gctacaacgg catcgccgtg tgccgcg 3434

<210> 237

<211> 106

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 237

Met Lys Leu Leu Ser Val Thr Leu Ala Ser Leu Gly Leu Ala Ser Ala
 1 5 10 15
 Ala Thr Val Ala Lys Lys Val Thr Tyr Asp Asp Trp Lys Val Val Arg
 20 25 30
 Val Asn Val Gly Ala Asp Ala Ala Lys Leu Glu Asn Val Met Ser Lys
 35 40 45
 Leu Gln Leu Glu Leu Trp Lys Gly Lys Pro Ala Ser Ser Asp Val Val
 50 55 60
 Asp Val Met Val Pro Pro Ser Ser Val Lys Asp Phe Glu Ala Gln Thr
 65 70 75 80
 Gln Gly Phe Glu Thr Lys Val Met His Glu Asn Leu Gly Leu Ser Ile
 85 90 95
 Ala Asp Glu Gln Ser Phe Gly Thr Tyr Ala
 100 105

<210> 238

<211> 88

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 238

Ala Gly Leu Ala Pro Asn Ser Thr Trp Phe Asn Ser Tyr His Ser Ile
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1 5 10 15
 Ala Asp His Met Gln Trp Ile Ser Asp Leu Ala Ala Tyr Pro Lys
 20 25 30
 Asn Ala Glu Val Ile Ser Ala Gly Lys Ser Val Glu Gly Arg Asp Ile
 35 40 45
 Lys Gly Ile His Ile Trp Gly Ser Gly Lys Gly Ser Gln Lys Gly
 50 55 60
 Val Val Trp His Gly Thr Val His Ala Arg Glu Trp Ile Thr Thr Met
 65 70 75 80
 Val Asn Ser Leu Phe Lys Lys Lys
 85

<210> 239

<211> 59

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 239

Gln Leu Leu Thr Ser Thr Asp Ala Thr Thr Ala Gly Phe Lys Asp Ser
 1 5 10 15
 Tyr Asp Phe Tyr Ile Phe Pro Ile Val Asn Pro Asp Gly Phe Ala Tyr
 20 25 30
 Ser Gln Thr Thr Asp Arg Met Trp Arg Lys Asn Arg Gln Thr Thr Pro
 35 40 45
 Ser Ala Ser Cys Val Gly Arg Asp Ile Asn Arg
 50 55

<210> 240

<211> 165

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 240

Asn Trp Pro Ser His Trp Asn Gln Ala Asn Gly Ala Ser Thr Ser Pro
 1 5 10 15
 Cys Asp Gln Asp Tyr Lys Gly Pro Ser Ala Gly Asp Gly Val Glu Thr
 20 25 30
 Lys Ala Leu Lys Ala His Leu Asp Ser Ile Ala Ala Gly Lys Gly Ile
 35 40 45
 Thr Leu Tyr Met Asp Ile His Ala Tyr Ser Gln Leu Trp Met Tyr Pro
 50 55 60
 Tyr Gly Tyr Thr Cys Ser Gly Ala Leu Pro Asn Ser Ala Lys Tyr Ser
 65 70 75 80
 Ser Leu Thr Asn Gly Ala Ile Ala Ala Val Lys Ala Val His Gly Thr
 85 90 95
 Ala Phe Thr Gly Gly Pro Ile Cys Asn Thr Ile Tyr Gln Val Ser Gly
 100 105 110
 Asp Ser Val Asp Tyr Ala Phe Glu Val Ala Lys Ala Thr Tyr Ser Met
 115 120 125
 Thr Val Glu Leu Arg Asp Thr Gly Lys Tyr Gly Phe Val Leu Pro Lys
 130 135 140
 Glu Gln Ile Val Pro Ser Ala Glu Glu Met Trp Ala Gly Leu Arg Tyr
 145 150 155 160
 Leu Val Lys Asn Met
 165

<210> 241

<211> 1254

<212> DNA

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1254)

<400> 241

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 Met Lys Leu Leu Ser Val Thr Leu Ala Ser Leu Gly Leu Ala Ser Ala

10336256.txt																
1			5			10			15							
gcc Ala	acc Thr	gtt Val	gcc Ala 20	aag Lys	aaa Lys	gtg Val	acc Thr	tac Tyr 25	gac Asp	gac Asp	tgg Trp	aag Lys	gtc Val 30	gtc Val	cgt Arg	96
gtc Val	aat Asn	gtc Val 35	ggc Gly	gca Ala	gac Asp	gct Ala	gct Ala 40	aag Lys	ctc Leu	gaa Glu	aat Asn	gta Val 45	atg Met	agc Ser	aag Lys	144
ctg Leu	cag Gln 50	ctt Leu	gag Glu	ctg Leu	tgg Trp	aag Lys 55	ggc Gly	aag Lys	cct Pro	gcg Ala	tca Ser 60	agc Ser	gat Asp	gtc Val	gtc Val	192
gat Asp 65	gtt Val	atg Met	gtg Val	ccg Pro	ccg Pro 70	tcg Ser	tcg Ser	gtc Val	aag Lys	gac Asp 75	ttt Phe	gag Glu	gct Ala	cag Gln	act Thr 80	240
cag Gln	ggg Gly	ttc Phe	gaa Glu	aca Thr 85	aaa Lys	gtc Val	atg Met	cat His	gag Glu 90	aat Asn	ctt Leu	ggc Gly	ctt Leu	tct Ser 95	atc Ile	288
gca Ala	gac Asp	gag Glu	cag Gln 100	agt Ser	ttt Phe	ggc Gly	aca Thr	tat Tyr 105	gcc Ala	gct Ala	ggg Gly	ctt Leu	gca Ala 110	cca Pro	aac Asn	336
tcg Ser	acg Thr	tgg Trp 115	ttt Phe	aac Asn	tcc Ser	tac Tyr	cac His 120	tcc Ser	att Ile	gct Ala	gat Asp	cac His 125	atg Met	caa Gln	tgg Trp	384
att Ile	agc Ser 130	gat Asp	ctt Leu	gcg Ala	gct Ala	gca Ala 135	tac Tyr	ccc Pro	aag Lys	aac Asn	gca Ala 140	gaa Glu	gtc Val	att Ile	tct Ser	432
gca Ala 145	ggc Gly	aag Lys	tcg Ser	gtt Val	gag Glu 150	ggc Gly	cgt Arg	gat Asp	atc Ile	aag Lys 155	ggg Gly	atc Ile	cac His	atc Ile	tgg Trp 160	480
ggg Gly	agt Ser	ggg Gly	ggg Gly	aag Lys 165	gga Gly	tct Ser	cag Gln	aag Lys	ggg Gly 170	gta Val	gta Val	tgg Trp	cac His	ggc Gly 175	act Thr	528
gtg Val	cac His	gca Ala	cgt Arg 180	gaa Glu	tgg Trp	atc Ile	acg Thr	aca Thr 185	atg Met	gta Val	aat Asn	tcc Ser	ctt Leu 190	ttc Phe	aaa Lys	576
aaa Lys	aaa Lys	caa Gln 195	ctc Leu	ctt Leu	acc Thr	tcc Ser	act Thr 200	gac Asp	gcc Ala	aca Thr	acc Thr	gcc Ala 205	ggc Gly	ttc Phe	aaa Lys	624
gac Asp	tcg Ser 210	tac Tyr	gac Asp	ttc Phe	tac Tyr	atc Ile 215	ttc Phe	ccc Pro	atc Ile	gtc Val	aac Asn 220	cca Pro	gat Asp	ggc Gly	ttc Phe	672
gcc Ala 225	tac Tyr	agt Ser	cag Gln	acc Thr	acc Thr 230	gac Asp	cgc Arg	atg Met	tgg Trp	cgc Arg 235	aag Lys	aac Asn	cgc Arg	cag Gln	act Thr 240	720
act Thr	ccc Pro	agc Ser	gcc Ala	tca Ser 245	tgc Cys	gta Val	ggc Gly	cgg Arg	gac Asp 250	atc Ile	aac Asn	cgt Arg	aac Asn	tgg Trp 255	ccc Pro	768
tct Ser	cac His	tgg Trp	aac Asn 260	cag Gln	gcc Ala	aac Asn	ggg Gly	gcc Ala 265	tcc Ser	acc Thr	tcg Ser	ccc Pro	tgc Cys 270	gac Asp	caa Gln	816
gac Asp	tac Tyr	aaa Lys	ggc Gly	ccc Pro	tca Ser	gcc Ala	ggc Gly	gac Asp	ggc Gly	gta Val	gaa Glu	acc Thr	aaa Lys	gcc Ala	ctg Leu	864

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10336256.txt

275	280	285	
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atg gac atc cac gcc tac agc caa ctc tgg atg tac ccc tac ggc tac Met Asp Ile His Ala Tyr Ser Gln Leu Trp Met Tyr Pro Tyr Gly Tyr			960
acc tgc tcc ggc gct ctc ccc aac tcc gca aag tac tct tcg ctg acc Thr Cys Ser Gly Ala Leu Pro Asn Ser Ala Lys Tyr Ser Ser Leu Thr			1008
aac ggt gcc att gcc gcg gtc aag gca gtg cat gga acg gcg ttc acg Asn Gly Ala Ile Ala Ala Val Lys Ala Val His Gly Thr Ala Phe Thr			1056
ggc ggc ccg att tgc aat acc atc tat cag gtt agt ggc gat agt gtg Gly Gly Pro Ile Cys Asn Thr Ile Tyr Gln Val Ser Gly Asp Ser Val			1104
gat tat gcg ttt gag gtc gca aag gcg acg tat agt atg acg gtc gag Asp Tyr Ala Phe Glu Val Ala Lys Ala Thr Tyr Ser Met Thr Val Glu			1152
ttg agg gat acg ggt aag tat ggg ttt gtc ctg ccg aaa gag cag att Leu Arg Asp Thr Gly Lys Tyr Gly Phe Val Leu Pro Lys Glu Gln Ile			1200
gtg ccg agt gcc gag gag atg tgg gct ggt ttg agg tac ttg gtg aag Val Pro Ser Ala Glu Glu Met Trp Ala Gly Leu Arg Tyr Leu Val Lys			1248
aat atg Asn Met			1254

<210> 242

<211> 418

<212> PRT

<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>

<221> SIGNAL

<222> (1)...(20)

<221> DOMAIN

<222> (117)...(321)

<223> Zinc carboxypeptidase

<400> 242

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1 10
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15 20 25
Leu Gln Leu Glu Leu Trp Lys Gly Lys Pro Ala Ser Ser Asp Val Val
30 35 40
Asp Val Met Val Pro Pro Ser Ser Val Lys Asp Phe Glu Ala Gln Thr
45 50 55 60
Gln Gly Phe Glu Thr Lys Val Met His Glu Asn Leu Gly Leu Ser Ile
65 70 75
Ala Asp Glu Gln Ser Phe Gly Thr Tyr Ala Ala Gly Leu Ala Pro Asn
80 85 90
Ser Thr Trp Phe Asn Ser Tyr His Ser Ile Ala Asp His Met Gln Trp

10336256.txt

95 100 105
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 110 115 120
 Ala Gly Lys Ser Val Glu Gly Arg Asp Ile Lys Gly Ile His Ile Trp
 125 130 135 140
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 145 150 155
 Val His Ala Arg Glu Trp Ile Thr Thr Met Val Asn Ser Leu Phe Lys
 160 165 170
 Lys Lys Gln Leu Leu Thr Ser Thr Asp Ala Thr Thr Ala Gly Phe Lys
 175 180 185
 Asp Ser Tyr Asp Phe Tyr Ile Phe Pro Ile Val Asn Pro Asp Gly Phe
 190 195 200
 Ala Tyr Ser Gln Thr Thr Asp Arg Met Trp Arg Lys Asn Arg Gln Thr
 205 210 215 220
 Thr Pro Ser Ala Ser Cys Val Gly Arg Asp Ile Asn Arg Asn Trp Pro
 225 230 235
 Ser His Trp Asn Gln Ala Asn Gly Ala Ser Thr Ser Pro Cys Asp Gln
 240 245 250
 Asp Tyr Lys Gly Pro Ser Ala Gly Asp Gly Val Glu Thr Lys Ala Leu
 255 260 265
 Lys Ala His Leu Asp Ser Ile Ala Ala Gly Lys Gly Ile Thr Leu Tyr
 270 275 280
 Met Asp Ile His Ala Tyr Ser Gln Leu Trp Met Tyr Pro Tyr Gly Tyr
 285 290 295 300
 Thr Cys Ser Gly Ala Leu Pro Asn Ser Ala Lys Tyr Ser Ser Leu Thr
 305 310 315
 Asn Gly Ala Ile Ala Ala Val Lys Ala Val His Gly Thr Ala Phe Thr
 320 325 330
 Gly Gly Pro Ile Cys Asn Thr Ile Tyr Gln Val Ser Gly Asp Ser Val
 335 340 345
 Asp Tyr Ala Phe Glu Val Ala Lys Ala Thr Tyr Ser Met Thr Val Glu
 350 355 360
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 Asn Met

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 <223> Exon

<221> CDS
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 <222> (2834)...(3597)
 <223> Exon

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 ctcccgcaca cctgttctgg aacgggtcag agacgccgaa gttgaggtat ttgcccgga 180
 ccgaaagcgt ctggtcctcg atcttgaagg tgaaatctgg cagtgtggcg ttgcatggga 240
 aggtattact accgccaagt gtcaactcgt agtctggaac ctgactgtag tagttggcga 300

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 tggccggtcc aaaggttttg ttgccgcgc catactctcc aactgctatg gtccaatgct 420
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 gctgtgcaga cgacgatggg aagtagtagg ttttgtccgg accctgcata gttgatgtct 840
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 cagtttagca tgtgtagcag atgtaaggcc gacaatctta cacggcaaca atggatacct 1380
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 gcttgcttga cgtgggaaat ggggtgccga tccagagcgt gcattaatgt gaaagtggac 1680
 taggagagaa g atg gcg cca atc aag ttg gtc ggg tgg aaa tgg cgg act 1730
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ggc tgg ccg ggg ata att cgg cta gcg ggc tgg gag agg aag gag ctc 1778
 Gly Trp Pro Gly Ile Ile Arg Leu Ala Gly Trp Glu Arg Lys Glu Leu
 15 20 25

gtg ttg aca cga tgc agc gtc cac ttt ggc atc cat gaa aca cgc atc 1826
 Val Leu Thr Arg Cys Ser Val His Phe Gly Ile His Glu Thr Arg Ile
 30 35 40 45

cga tat att gtt ctc caa aaa ccg gga ccc ccg caa acc cac aag cc 1873
 Arg Tyr Ile Val Leu Gln Lys Pro Gly Pro Pro Gln Thr His Lys Pro
 50 55 60

gtcaagataa gtacacacct gcacaacggc aaagacaagg tacagtggtc cgtgccacac 1933
 acacagcata gccaaactca aatccatcgt actcgtattg ctacattccc ggcacggccc 1993
 gactcagtc gtagccaact taccatgtag cgttgtaata agctttggcc actctcttgg 2053
 cag t gca tac gct ctg gag atc aca gtc gac cgt cca cac ccc aca ctc 2102
 Ala Tyr Ala Leu Glu Ile Thr Val Asp Arg Pro His Pro Thr Leu
 65 70 75

agg agt gcc ctg ggt cgg tca gcc gag aga cag gca tct ggt act cac 2150
 Arg Ser Ala Leu Gly Arg Ser Ala Glu Arg Gln Ala Ser Gly Thr His
 80 85 90

ata aag acc tgc cat ggc tcc gtc ttc cct tgc ctt gcc cgc atc tgc 2198
 Ile Lys Thr Cys His Gly Ser Val Phe Pro Cys Leu Ala Arg Ile Cys
 95 100 105

gca atc ttg ctc tca cac tca aca atc atg cct gat tcc aag atg gtc 2246
 Ala Ile Leu Leu Ser His Ser Thr Ile Met Pro Asp Ser Lys Met Val
 110 115 120

tca cgc gcc ctt ctc gcc gcc ctt gca ctc cct gct gtc tct gcc gag 2294
 Ser Arg Ala Leu Leu Ala Ala Leu Ala Leu Pro Ala Val Ser Ala Glu
 125 130 135 140

ctt ccc cca ggc gcc att gct gtg ccc ctg atc cga gac gcc gaa ctc 2342
 Leu Pro Pro Gly Ala Ile Ala Val Pro Leu Ile Arg Asp Ala Glu Leu
 145 150 155

gac gca tac tac gca gag ttc cag gtc gga acg ccc ccg cag aag gaa 2390
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		175					180					185				
cgc	aac	caa	gaa	tgt	gtc	tcg	gat	cca	gcg	tca	tgc	act	act	ttt	ggc	2486
Arg	Asn	Gln	Glu	Cys	Val	Ser	Asp	Pro	Ala	Ser	Cys	Thr	Thr	Phe	Gly	
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act	ttt	gac	aac	ttg	acc	tct	tc	gtaagtaatc atctttggct tcttttttta								2539
Thr	Phe	Asp	Asn	Leu	Thr	Ser	Ser									
205					210											
ttaaaaaaag aagcccccaa aaagattgca agcgctaatt ctacatcttc cag a act																2596
														Thr		
tgt	cgt	tat	gaa	gga	cct	ggc	ttc	tac	gat	gaa	ctc	tac	gca	tta	gga	2644
Cys	Arg	Tyr	Glu	Gly	Pro	Gly	Phe	Tyr	Asp	Glu	Leu	Tyr	Ala	Leu	Gly	
	215					220					225					
ttt	ggc	gat	tac	ctc	agt	gac	acc	ttg	gtc	ctg	ggc	ggg	gtc	acc	atg	2692
Phe	Gly	Asp	Tyr	Leu	Ser	Asp	Thr	Leu	Val	Leu	Gly	Gly	Val	Thr	Met	
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ccc	aac	atg	tat	ttc	ggg	tac	acg	tcc	aat	tat	acg	gcc	gga	aaa	gta	2740
Pro	Asn	Met	Tyr	Phe	Gly	Tyr	Thr	Ser	Asn	Tyr	Thr	Ala	Gly	Lys	Val	
				250					255					260		
gtt	cca	gaa	cca	att	caa	act	att	ctg	g gtatgtcaag acacccgtgt							2788
Val	Pro	Glu	Pro	Ile	Gln	Thr	Ile	Leu								
			265					270								
tcttcgtgca cgactgcagt ctaactgttt gattgcgaaa tctag gc ctg tct ctc																2844
											Gly	Leu	Ser	Leu		
gaa	tgt	tat	ccg	gag	gag	cct	gac	tgc	atg	tcc	aaa	ggg	gca	tat	ttt	2892
Glu	Cys	Tyr	Pro	Glu	Glu	Pro	Asp	Cys	Met	Ser	Lys	Gly	Ala	Tyr	Phe	
275					280					285					290	
cta	cca	gag	ttg	aag	aac	gcc	tca	ctg	att	gac	gtc	atg	gca	aca	agt	2940
Leu	Pro	Glu	Leu	Lys	Asn	Ala	Ser	Leu	Ile	Asp	Val	Met	Ala	Thr	Ser	
				295					300					305		
atg	tac	ctt	ggg	ccg	gat	gaa	ttc	aac	gtc	acc	aat	gcc	cag	atg	atc	2988
Met	Tyr	Leu	Gly	Pro	Asp	Glu	Phe	Asn	Val	Thr	Asn	Ala	Gln	Met	Ile	
			310				315					320				
att	ggg	ggc	gcc	tat	gac	aag	gca	aag	gtg	gac	ggg	gac	atg	ttc	acg	3036
Ile	Gly	Gly	Ala	Tyr	Asp	Lys	Ala	Lys	Val	Asp	Gly	Asp	Met	Phe	Thr	
		325					330				335					
ctg	gag	atg	gtg	gat	cca	ttc	tcc	aca	ctc	acc	ggc	gaa	caa	acg	aac	3084
Leu	Glu	Met	Val	Asp	Pro	Phe	Ser	Thr	Leu	Thr	Gly	Glu	Gln	Thr	Asn	
		340				345					350					
tac	gtg	aac	gtc	act	gca	atg	gaa	gtt	gta	ctt	gac	ggc	ggc	aac	cgc	3132
Tyr	Val	Asn	Val	Thr	Ala	Met	Glu	Val	Val	Leu	Asp	Gly	Gly	Asn	Arg	
355					360				365						370	
acg	tca	caa	acc	ttt	gga	gat	aag	ggg	gtt	ggg	gtc	ccc	atc	ttg	ctc	3180
Thr	Ser	Gln	Thr	Phe	Gly	Asp	Lys	Gly	Val	Gly	Val	Pro	Ile	Leu	Leu	
				375					380					385		
gac	acg	ggc	att	gca	acc	tgg	tac	gtg	act	gat	acc	att	ttc	ggc	gcc	3228
Asp	Thr	Gly	Ile	Ala	Thr	Trp	Tyr	Val	Thr	Asp	Thr	Ile	Phe	Gly	Ala	

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390	395	400	
gtc tcc tac gga ttg ggt att acc gcc ttc caa cct gga aaa cag gtg Val Ser Tyr 405 Gly Leu Gly Ile Thr 410 Ala Phe Gln Pro Gly 415 Lys Gln Val			3276
acc tct gtt gac tgc aag tac cgg gac ccc aac aat gcc aag ggc tac Thr 420 Ser Val Asp Cys Lys Tyr 425 Arg Asp Pro Asn Asn 430 Ala Lys Gly Tyr			3324
atc tct gtc gaa ttc ggc gct agt ggc aag att gac gtt ccg ctg cac Ile 435 Ser Val Glu Phe Gly 440 Ala Ser Gly Lys Ile 445 Asp Val Pro Leu His 450			3372
gaa att atc tct ctg ttt gct aat agc acg tgt ggc gtc tac atg gag Glu Ile Ile Ser Leu 455 Phe Ala Asn Ser Thr 460 Cys Gly Val Tyr Met 465 Glu			3420
cct cgc tcg gaa acc gat att ggc gta ctc gca gac ccc ttt att cgt Pro Arg Ser Glu 470 Thr Asp Ile Gly Val 475 Leu Ala Asp Pro Phe 480 Ile Arg			3468
gca att tac gca atc ttc gac cag acc cac agg acc atc aca atg ggc Ala Ile Tyr 485 Ala Ile Phe Asp Gln Thr His Arg Thr 495 Ile Thr Met Gly			3516
aaa gca aaa tac aca act gag cag aac att gtg ccc ttc ccc gag gga Lys Ala Lys Tyr Thr Thr Glu 505 Gln Asn Ile Val Pro 510 Phe Pro Glu Gly			3564
ggg ttc aca gtg ggc tcc aag gtc agc tct tag Gly Phe Thr Val Gly Ser 520 Lys Val Ser Ser *	acacggcaca	tgtatatatt	3617
tgtaatccgg ttagaatgta catattcaag ttgggattgt gagatccaag cgctcttatg caagaggaaa cgcgacagat gatgtttaat gatgtcgtgg ttaccaatct tgacacattc caatgatgca tttcaactcg taaagattta tttcaagttg ttgaggccat atctacattt ccatgataca taccaaagcg ggtccactag aaatggacaa cacagcagtg ccaagaaaat gattacaacg aatacgagtc aagacactga actctgtagt gaagattagt gctgaccttt gttgataatg gacatgaact acgttggcgc tgcggggcgg aatatccaca tattaagaga catctttacct cccgtaataa ggcttaattg atgggtgcatt acaagcccac ctatgactct tgtctggaag aaagtgttta gatttgcgct ttagctgcaa aggctattta gtctgactgt actactcgtt ctatgtagca aggggtgcgta tggttaagtag atgtcgcgtg agaatcgcg taacgtaaca cggagatccc tgtcaactag gtaagagtg ggagagcaag tggcagtaga gtttggagct actagtatgt aaattctaatt tcttcgtgca accaaagccc tgggggggagc atggatacgg ggcagggtact gtgaacataa tgtcgcgaatt atattcatca tgtcgttact atagccggca atgaactgat taacaagcaa ccccgcgatg atatcatctt atagctcccc accctcagt caaccccatc catataacacc ccagccatgg caacggtcag tgaggcggag gcgccacagc ctagggaagg tgtctttgat ctaccaactg cagatgggtac atcccaagcc accgttactt tacaagaaaa tgaagatgcc accaaaccgc ccttgctact cgacatcacc aaacgagctc tcgaccc			3677 3737 3797 3857 3917 3977 4037 4097 4157 4217 4277 4337 4397 4457 4517 4577 4594

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<211> 61

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<213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<400> 244

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 35 40 45
 Val Leu Gln Lys Pro Gly Pro Pro Gln Thr His Lys Pro
 50 55 60

<210> 245

10336256.txt

<211> 151

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 245

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 20 25 30
 Lys Thr Cys His Gly Ser Val Phe Pro Cys Leu Ala Arg Ile Cys Ala
 35 40 45
 Ile Leu Leu Ser His Ser Thr Ile Met Pro Asp Ser Lys Met Val Ser
 50 55 60
 Arg Ala Leu Leu Ala Ala Leu Ala Leu Pro Ala Val Ser Ala Glu Leu
 65 70 75 80
 Pro Pro Gly Ala Ile Ala Val Pro Leu Ile Arg Asp Ala Glu Leu Asp
 85 90 95
 Ala Tyr Tyr Ala Glu Phe Gln Val Gly Thr Pro Pro Gln Lys Glu Tyr
 100 105 110
 Leu Lys Val Asp Thr Gly Ser Pro Arg Tyr Ser Phe Leu Asn Pro Arg
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 Asn Gln Glu Cys Val Ser Asp Pro Ala Ser Cys Thr Thr Phe Gly Thr
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 Phe Asp Asn Leu Thr Ser Ser
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<210> 246

<211> 58

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 246

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 20 25 30
 Met Pro Asn Met Tyr Phe Gly Tyr Thr Ser Asn Tyr Thr Ala Gly Lys
 35 40 45
 Val Val Pro Glu Pro Ile Gln Thr Ile Leu
 50 55

<210> 247

<211> 254

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 247

Gly Leu Ser Leu Glu Cys Tyr Pro Glu Glu Pro Asp Cys Met Ser Lys
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 Gly Ala Tyr Phe Leu Pro Glu Leu Lys Asn Ala Ser Leu Ile Asp Val
 20 25 30
 Met Ala Thr Ser Met Tyr Leu Gly Pro Asp Glu Phe Asn Val Thr Asn
 35 40 45
 Ala Gln Met Ile Ile Gly Gly Ala Tyr Asp Lys Ala Lys Val Asp Gly
 50 55 60
 Asp Met Phe Thr Leu Glu Met Val Asp Pro Phe Ser Thr Leu Thr Gly
 65 70 75 80
 Glu Gln Thr Asn Tyr Val Asn Val Thr Ala Met Glu Val Val Leu Asp
 85 90 95
 Gly Gly Asn Arg Thr Ser Gln Thr Phe Gly Asp Lys Gly Val Gly Val
 100 105 110
 Pro Ile Leu Leu Asp Thr Gly Ile Ala Thr Trp Tyr Val Thr Asp Thr
 115 120 125
 Ile Phe Gly Ala Val Ser Tyr Gly Leu Gly Ile Thr Ala Phe Gln Pro
 130 135 140
 Gly Lys Gln Val Thr Ser Val Asp Cys Lys Tyr Arg Asp Pro Asn Asn
 145 150 155 160
 Ala Lys Gly Tyr Ile Ser Val Glu Phe Gly Ala Ser Gly Lys Ile Asp
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Val Pro Leu His Glu Ile Ile Ser Leu Phe Ala Asn Ser Thr Cys Gly
 Val Tyr Met Glu Pro Arg Ser Glu Thr Asp Ile Gly Val Leu Ala Asp
 Pro Phe Ile Arg Ala Ile Tyr Ala Ile Phe Asp Gln Thr His Arg Thr
 Ile Thr Met Gly Lys Ala Lys Tyr Thr Thr Glu Gln Asn Ile Val Pro
 Phe Pro Glu Gly Gly Phe Thr Val Gly Ser Lys Val Ser Ser

<210> 248

<211> 1575

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1575)

<400> 248

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ggg ata att cgg cta gcg ggc tgg gag agg aag gag ctc gtg ttg aca	96
Gly Ile Ile Arg Leu Ala Gly Trp Glu Arg Lys Glu Leu Val Leu Thr	
20 25 30	
cga tgc agc gtc cac ttt ggc atc cat gaa aca cgc atc cga tat att	144
Arg Cys Ser Val His Phe Gly Ile His Glu Thr Arg Ile Arg Tyr Ile	
35 40 45	
gtt ctc caa aaa ccg gga ccc ccg caa acc cac aag cct gca tac gct	192
Val Leu Gln Lys Pro Gly Pro Pro Gln Thr His Lys Pro Ala Tyr Ala	
50 55 60	
ctg gag atc aca gtc gac cgt cca cac ccc aca ctc agg agt gcc ctg	240
Leu Glu Ile Thr Val Asp Arg Pro His Pro Thr Leu Arg Ser Ala Leu	
65 70 75 80	
ggt cgg tca gcc gag aga cag gca tct ggt act cac ata aag acc tgc	288
Gly Arg Ser Ala Glu Arg Gln Ala Ser Gly Thr His Ile Lys Thr Cys	
85 90 95	
cat ggc tcc gtc ttc cct tgc ctt gcc cgc atc tgc gca atc ttg ctc	336
His Gly Ser Val Phe Pro Cys Leu Ala Arg Ile Cys Ala Ile Leu Leu	
100 105 110	
tca cac tca aca atc atg cct gat tcc aag atg gtc tca cgc gcc ctt	384
Ser His Ser Thr Ile Met Pro Asp Ser Lys Met Val Ser Arg Ala Leu	
115 120 125	
ctc gcc gcc ctt gca ctc cct gct gtc tct gcc gag ctt ccc cca ggc	432
Leu Ala Ala Leu Ala Leu Pro Ala Val Ser Ala Glu Leu Pro Pro Gly	
130 135 140	
gcc att gct gtg ccc ctg atc cga gac gcc gaa ctc gac gca tac tac	480
Ala Ile Ala Val Pro Leu Ile Arg Asp Ala Glu Leu Asp Ala Tyr Tyr	
145 150 155 160	
gca gag ttc cag gtc gga acg ccc ccg cag aag gaa tac ctc aaa gtc	528
Ala Glu Phe Gln Val Gly Thr Pro Pro Gln Lys Glu Tyr Leu Lys Val	
165 170 175	
gat act ggc agc cca cga tat tcc ttt ctt aac ccg cgc aac caa gaa	576
Asp Thr Gly Ser Pro Arg Tyr Ser Phe Leu Asn Pro Arg Asn Gln Glu	

10336256.txt																
180						185						190				
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ttg Leu	acc Thr 210	tct Ser	tca Ser	act Thr	tgt Cys	cgt Arg 215	tat Tyr	gaa Glu	gga Gly	cct Pro	ggc Gly 220	ttc Phe	tac Tyr	gat Asp	gaa Glu	672
ctc Leu 225	tac Tyr	gca Ala	tta Leu	gga Gly	ttt Phe 230	ggc Gly	gat Asp	tac Tyr	ctc Leu	agt Ser 235	gac Asp	acc Thr	ttg Leu	gtc Val	ctg Leu 240	720
ggc Gly	ggt Gly	gtc Val	acc Thr	atg Met 245	ccc Pro	aac Asn	atg Met	tat Tyr	ttc Phe 250	ggg Gly	tac Tyr	acg Thr	tcc Ser	aat Asn 255	tat Tyr	768
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	Met Gly Lys Ala Lys Tyr Thr Thr Glu Gln Asn Ile Val Pro Phe Pro	
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<220>

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cctccccccc ctccctccac tccctgcaat cagaaaatgt gaacataatc taatcatctg	5508
gagatacaaa catcgctctg atcaccacaga tcccggctcg ctatgtacgg cagtatatgtg	5568
aatactgcgt tgattatcac ttttacgtga atccgttttg gaaaagcaac ctaccaagca	5628
tcttaaaatt gcctatttga gtgattgctt ctaggataca ggaatgtaga tgacaaagcg	5688
agagcatgct tagttattca ttactagaac cagcatttcc ttctactac atcccggcag	5748
cttcgcccctc tcaactccttt tttcatccaa actgaaatct tctgcgcaga aagctattag	5808
aggagcgcct tgaatctttc tcaactgtagt ttatcgatga agaattgggtt ggatgtcctt	5868
ttgtaaccacaa cggtgatgtc tgacccacag catcgctcat atcgcgactc cagttcacat	5928
tcagagatgg cggatcgcgc acgcataatg aagcacaatc atgggtgatag ttttctgcat	5988
tttcgacttt atcaatatcg cttcgtatca ggccctagaa cctgggggtat gcgagatggt	6048
cataacatag acgaagct	6066

<210> 251

<211> 64

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 251

10336256.txt

Met Lys Leu Leu Ser Val Phe Gly Ser Phe Leu Cys Ala Ser Ala Ala
 1 5 10 15
 Leu Ala Ala Asn Ala Pro Arg Phe Leu Arg Pro Asn Arg Val His Arg
 20 25 30
 Pro Asn Pro Val Ile Glu Lys Arg Val Pro Gly Gln Asp Phe Gln Asn
 35 40 45
 Pro Glu Ile Asn Lys Arg Ala His Thr Phe Leu Asn Ala Lys Thr Gln
 50 55 60

<210> 252

<211> 54

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 252

Pro Phe Ala Val Asp Gly Lys Asn Val Pro Leu Ala Asn Phe Asp Leu
 1 5 10 15
 Gly Glu Ser Tyr Ala Gly Leu Leu Pro Ile Ser Asn Asp Lys Asn Glu
 20 25 30
 Thr Arg Lys Leu Phe Phe Trp Phe Phe Pro Ser Thr Gln Ala Lys Thr
 35 40 45
 Pro Glu Glu Ile Val Met
 50

<210> 253

<211> 429

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 253

Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Ser Gly Leu Leu Gln Glu
 1 5 10 15
 Asn Gly Pro Phe Leu Trp Gln Asp Gly Thr Leu Ala Pro Thr Gln Asn
 20 25 30
 Pro Tyr Ser Trp His Asn Leu Thr Asn Met Leu Trp Val Glu Gln Pro
 35 40 45
 Val Gly Val Gly Tyr Ser Glu Gly Glu Pro Asp Ile Ser Asn Glu Tyr
 50 55 60
 Glu Leu Ser Asp Gln Phe Arg Gly Phe Tyr Lys Asn Phe Val Asp Leu
 65 70 75 80
 Phe Gly Val Trp Asn Trp Lys Thr Tyr Val Thr Gly Glu Ser Tyr Ala
 85 90 95
 Gly Phe Tyr Val Pro Tyr Ile Ala Asp Ser Phe Ile Arg Ala Asn Asp
 100 105 110
 Lys Lys Tyr Phe Asn Leu Gly Gly Ile Ala Ile Asn Asp Pro Ile Ile
 115 120 125
 Gly Thr Asp Thr Val Gln Gln Gln Ile Val Ile Arg Pro Tyr Val Glu
 130 135 140
 Phe Trp Gln Asn Val Phe Tyr Leu Asn Gln Thr Phe Leu Glu Arg Ala
 145 150 155 160
 Arg Lys Arg Asp Leu Glu Cys Gly Tyr Thr Gln Tyr Tyr Glu Lys Tyr
 165 170 175
 Phe Lys Phe Pro Pro Lys Gly Pro Phe Pro Asn Leu Pro Asp Pro
 180 185 190
 Phe Asp Ser Thr Gly Asp Val Pro Ile Cys Asp Gln Phe Asp Asn Tyr
 195 200 205
 Ala Gln Ala Ile Ala Glu Val Asn Pro Cys Phe Asp Val Tyr His Ile
 210 215 220
 Thr Glu Thr Cys Pro Phe Lys Ser Thr Pro Leu Gly Gly Thr Asn Pro
 225 230 235 240
 Gly Asp Tyr Val Ala Pro Gly Thr Glu Val Tyr Phe Asp Arg Ala Asp
 245 250 255
 Val Lys Lys Ala Leu His Ala Ser Pro Asn Ser Thr Trp Met Leu Cys
 260 265 270
 Thr Asp Lys Asn Val Phe Ala Gly Ala Gly Val Asn Gly Ser Asp Thr
 275 280 285
 Ser Val Pro Pro Ala Asn Ser Gly Val Leu Gln Asn Val Ile Glu Lys
 290 295 300

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Thr Asn Asn Val Met Ile Gly Ser Gly Asp Leu Asp Ile Leu Leu Ser
 305 310 315 320
 Thr Asn Gly Thr Leu Ala Leu Gln Asn Met Thr Trp Asn Gly Ala
 325 330 335
 Gln Gly Leu Thr Arg Tyr Pro Ser Gln Asn Leu Tyr Val Pro Tyr His
 340 345 350
 Pro Glu Phe Asn Gly Gly Ala Leu Ala Gly Tyr Gln Gly Leu
 355 360 365
 Trp Thr Lys Glu Arg Gly Leu Thr Phe Tyr Thr Ala Arg Leu Ala Gly
 370 375 380
 His Glu Leu Pro Gly Tyr Thr Pro Gly Val Gly Tyr Arg Met Leu Glu
 385 390 395 400
 Ile Leu Leu Gly Arg Ile Ser Asp Phe Ser Thr Arg Asp Phe Thr
 405 410 415
 Thr Gln Thr Gly Asn Phe Thr Gly Thr Thr Asp Leu Tyr
 420 425

<210> 254

<211> 1644

<212> DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> CDS

<222> (1)...(1644)

<400> 254

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Met Lys Leu Leu Ser Val Phe Gly Ser Phe Leu Cys Ala Ser Ala Ala	
1 5 10 15	
ctc gct gca aat gcc cct cgc ttt ctc aga cct aac aga gtc cat cgc	96
Leu Ala Ala Asn Ala Pro Arg Phe Leu Arg Pro Asn Arg Val His Arg	
20 25 30	
ccc aat cca gtc att gag aag cgt gtc cct gga cag gac ttt cag aac	144
Pro Asn Pro Val Ile Glu Lys Arg Val Pro Gly Gln Asp Phe Gln Asn	
35 40 45	
cca gag atc aac aag aga gct cat acc ttc ctc aac gca aag acc caa	192
Pro Glu Ile Asn Lys Arg Ala His Thr Phe Leu Asn Ala Lys Thr Gln	
50 55 60	
ccc ttt gct gtc gat ggc aag aat gtc ccc ttg gcc aat ttc gac tta	240
Pro Phe Ala Val Asp Gly Lys Asn Val Pro Leu Ala Asn Phe Asp Leu	
65 70 75 80	
ggt gag agt tat gct ggc tta cta ccc atc tcc aac gac aaa aac gaa	288
Gly Glu Ser Tyr Ala Gly Leu Leu Pro Ile Ser Asn Asp Lys Asn Glu	
85 90 95	
acg cgc aag ctt ttt ttc tgg ttc ttt cca tct acc cag gcc aag aca	336
Thr Arg Lys Leu Phe Phe Trp Phe Phe Pro Ser Thr Gln Ala Lys Thr	
100 105 110	
ccg gag gaa atc gtc atg ctt aat ggt ggc cct gga tgt agt tca ctc	384
Pro Glu Glu Ile Val Met Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu	
115 120 125	
agc ggt ttg ctc caa gag aac ggc ccg ttc ttg tgg caa gac ggc act	432
Ser Gly Leu Leu Gln Glu Asn Gly Pro Phe Leu Trp Gln Asp Gly Thr	
130 135 140	
ctt gcc cca act cag aac cct tat tca tgg cac aac ctc acc aac atg	480
Leu Ala Pro Thr Gln Asn Pro Tyr Ser Trp His Asn Leu Thr Asn Met	
145 150 155 160	
ctt tgg gtc gaa cag cct gtt ggt gtc ggc tat tcg gaa ggc gag ccc	528

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Leu	Trp	Val	Glu	Gln	Pro	Val	Gly	Val	Gly	Tyr	Ser	Glu	Gly	Glu	Pro
				165					170					175	
gat	atc	agc	aac	gaa	tac	gaa	ctc	agt	gac	caa	ttc	cgc	ggc	ttt	tac
Asp	Ile	Ser	Asn	Glu	Tyr	Glu	Leu	Ser	Asp	Gln	Phe	Arg	Gly	Phe	Tyr
			180					185					190		
aag	aac	ttt	gtc	gat	ctc	ttt	ggg	gtc	tgg	aac	tgg	aag	act	tat	gtt
Lys	Asn	Phe	Val	Asp	Leu	Phe	Gly	Val	Trp	Asn	Trp	Lys	Thr	Tyr	Val
		195					200					205			
acc	gga	gag	tca	tat	gct	ggc	ttt	tac	gtt	cct	tac	att	gct	gac	agc
Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Phe	Tyr	Val	Pro	Tyr	Ile	Ala	Asp	Ser
	210					215					220				
ttc	atc	cgt	gcc	aat	gac	aag	aaa	tac	ttc	aat	ctt	ggg	ggc	atc	gca
Phe	Ile	Arg	Ala	Asn	Asp	Lys	Lys	Tyr	Phe	Asn	Leu	Gly	Gly	Ile	Ala
	225				230					235					240
atc	aac	gac	ccc	atc	atc	ggg	act	gat	act	gtc	caa	cag	cag	atc	gtc
Ile	Asn	Asp	Pro	Ile	Ile	Gly	Thr	Asp	Thr	Val	Gln	Gln	Gln	Ile	Val
				245					250					255	
atc	cgg	ccc	tac	gtc	gaa	ttc	tgg	caa	aat	gtc	ttc	tac	ttg	aac	cag
Ile	Arg	Pro	Tyr	Val	Glu	Phe	Trp	Gln	Asn	Val	Phe	Tyr	Leu	Asn	Gln
			260					265					270		
act	ttc	tta	gaa	aga	gcc	cga	aag	cgc	gac	ctg	gaa	tgc	ggg	tac	acc
Thr	Phe	Leu	Glu	Arg	Ala	Arg	Lys	Arg	Asp	Leu	Glu	Cys	Gly	Tyr	Thr
		275					280					285			
cag	tat	tat	gaa	aaa	tac	ttc	aaa	ttc	cct	ccg	cca	aag	ggg	ccc	ttc
Gln	Tyr	Tyr	Glu	Lys	Tyr	Phe	Lys	Phe	Pro	Pro	Pro	Lys	Gly	Pro	Phe
	290					295					300				
cca	aat	ctc	cct	gac	cca	ttc	gac	agt	acg	ggg	gat	gtc	cca	att	tgc
Pro	Asn	Leu	Pro	Asp	Pro	Phe	Asp	Ser	Thr	Gly	Asp	Val	Pro	Ile	Cys
	305				310					315					320
gac	cag	ttc	gat	aac	tac	gcc	caa	gcc	att	gcc	gag	gta	aat	cct	tgc
Asp	Gln	Phe	Asp	Asn	Tyr	Ala	Gln	Ala	Ile	Ala	Glu	Val	Asn	Pro	Cys
				325					330					335	
ttt	gac	gtc	tac	cac	atc	acc	gaa	acc	tgt	ccg	ttc	aag	tcg	acg	ccg
Phe	Asp	Val	Tyr	His	Ile	Thr	Glu	Thr	Cys	Pro	Phe	Lys	Ser	Thr	Pro
			340					345					350		
ctc	ggg	gga	acc	aac	cca	gga	gat	tat	gtc	gca	cca	ggc	acg	gaa	gtc
Leu	Gly	Gly	Thr	Asn	Pro	Gly	Asp	Tyr	Val	Ala	Pro	Gly	Thr	Glu	Val
		355				360						365			
tat	ttt	gac	cgc	gca	gat	gtc	aag	aag	gct	ctt	cat	gcc	agt	cct	aac
Tyr	Phe	Asp	Arg	Ala	Asp	Val	Lys	Lys	Ala	Leu	His	Ala	Ser	Pro	Asn
	370					375					380				
agc	aca	tgg	atg	ttg	tgc	aca	gat	aag	aac	gtc	ttc	gcc	ggg	gcc	ggc
Ser	Thr	Trp	Met	Leu	Cys	Thr	Asp	Lys	Asn	Val	Phe	Ala	Gly	Ala	Gly
					390					395					400
gta	aac	ggc	tca	gac	acg	tct	gtc	cca	ccc	gcc	aac	agc	ggc	gtc	ctc
Val	Asn	Gly	Ser	Asp	Thr	Ser	Val	Pro	Pro	Ala	Asn	Ser	Gly	Val	Leu
				405					410					415	
caa	aac	gtt	att	gaa	aaa	aca	aac	aac	gtc	atg	atc	ggc	tct	gga	gac
Gln	Asn	Val	Ile	Glu	Lys	Thr	Asn	Asn	Val	Met	Ile	Gly	Ser	Gly	Asp
			420					425					430		
ctc	gac	ata	ctt	ctc	agc	aca	aac	ggc	acc	ctc	ctc	gcc	ctt	caa	aac
									Page 255						

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Leu	Asp	Ile	Leu	Leu	Ser	Thr	Asn	Gly	Thr	Leu	Leu	Ala	Leu	Gln	Asn	
		435					440					445				
atg	act	tgg	aac	ggc	gca	caa	ggg	cta	acc	aga	tac	ccc	tcc	caa	aac	1392
Met	Thr	Trp	Asn	Gly	Ala	Gln	Gly	Leu	Thr	Arg	Tyr	Pro	Ser	Gln	Asn	
		450				455					460					
ctc	tac	gtg	cct	tac	cac	ccc	gaa	ttc	aac	ggc	ggg	gca	cta	gct	ggc	1440
Leu	Tyr	Val	Pro	Tyr	His	Pro	Glu	Phe	Asn	Gly	Gly	Ala	Leu	Ala	Gly	
		465			470					475					480	
gct	gga	tac	cag	ggc	tta	tgg	acc	aaa	gaa	cgc	ggg	ctg	acc	ttc	tac	1488
Ala	Gly	Tyr	Gln	Gly	Leu	Trp	Thr	Lys	Glu	Arg	Gly	Leu	Thr	Phe	Tyr	
				485					490					495		
act	gcg	cgt	ctt	gca	ggg	cat	gag	ttg	cca	ggg	tac	acg	cct	ggc	gtc	1536
Thr	Ala	Arg	Leu	Ala	Gly	His	Glu	Leu	Pro	Gly	Tyr	Thr	Pro	Gly	Val	
			500					505					510			
gga	tac	cgc	atg	ttg	gag	att	ctg	ctc	ggg	cgc	atc	tcc	gat	ttt	agc	1584
Gly	Tyr	Arg	Met	Leu	Glu	Ile	Leu	Leu	Gly	Arg	Ile	Ser	Asp	Phe	Ser	
		515					520					525				
agc	acc	cgc	gat	ttc	acc	acc	caa	aca	ggg	aat	ttt	act	ggg	acc	acc	1632
Ser	Thr	Arg	Asp	Phe	Thr	Thr	Gln	Thr	Gly	Asn	Phe	Thr	Gly	Thr	Thr	
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gat	ctc	tat	tag													1644
Asp	Leu	Tyr	*													
545																

<210> 255

<211> 547

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>

<221> SIGNAL

<222> (1)...(18)

<221> DOMAIN

<222> (74)...(522)

<223> Serine carboxypeptidase

<400> 255

Met	Lys	Leu	Leu	Ser	Val	Phe	Gly	Ser	Phe	Leu	Cys	Ala	Ser	Ala	Ala	
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Leu	Ala	Ala	Asn	Ala	Pro	Arg	Phe	Leu	Arg	Pro	Asn	Arg	Val	His	Arg	
			20					25					30			
Pro	Asn	Pro	Val	Ile	Glu	Lys	Arg	Val	Pro	Gly	Gln	Asp	Phe	Gln	Asn	
		35					40					45				
Pro	Glu	Ile	Asn	Lys	Arg	Ala	His	Thr	Phe	Leu	Asn	Ala	Lys	Thr	Gln	
	50					55					60					
Pro	Phe	Ala	Val	Asp	Gly	Lys	Asn	Val	Pro	Leu	Ala	Asn	Phe	Asp	Leu	
65				70						75					80	
Gly	Glu	Ser	Tyr	Ala	Gly	Leu	Leu	Pro	Ile	Ser	Asn	Asp	Lys	Asn	Glu	
			85						90					95		
Thr	Arg	Lys	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ser	Thr	Gln	Ala	Lys	Thr	
			100					105					110			
Pro	Glu	Glu	Ile	Val	Met	Leu	Asn	Gly	Gly	Pro	Gly	Cys	Ser	Ser	Leu	
		115					120					125				
Ser	Gly	Leu	Leu	Gln	Glu	Asn	Gly	Pro	Phe	Leu	Trp	Gln	Asp	Gly	Thr	
	130					135					140					
Leu	Ala	Pro	Thr	Gln	Asn	Pro	Tyr	Ser	Trp	His	Asn	Leu	Thr	Asn	Met	
145					150					155					160	
Leu	Trp	Val	Glu	Gln	Pro	Val	Gly	Val	Gly	Tyr	Ser	Glu	Gly	Glu	Pro	
				165					170					175		

10336256.txt

Asp Ile Ser Asn Glu Tyr Glu Leu Ser Asp Gln Phe Arg Gly Phe Tyr
 180 185 190
 Lys Asn Phe Val Asp Leu Phe Gly Val Trp Asn Trp Lys Thr Tyr Val
 195 200 205
 Thr Gly Glu Ser Tyr Ala Gly Phe Tyr Val Pro Tyr Ile Ala Asp Ser
 210 215 220
 Phe Ile Arg Ala Asn Asp Lys Lys Tyr Phe Asn Leu Gly Gly Ile Ala
 225 230 235 240
 Ile Asn Asp Pro Ile Ile Gly Thr Asp Thr Val Gln Gln Gln Ile Val
 245 250 255
 Ile Arg Pro Tyr Val Glu Phe Trp Gln Asn Val Phe Tyr Leu Asn Gln
 260 265 270
 Thr Phe Leu Glu Arg Ala Arg Lys Arg Asp Leu Glu Cys Gly Tyr Thr
 275 280 285
 Gln Tyr Tyr Glu Lys Tyr Phe Lys Phe Pro Pro Pro Lys Gly Pro Phe
 290 295 300
 Pro Asn Leu Pro Asp Pro Phe Asp Ser Thr Gly Asp Val Pro Ile Cys
 305 310 315 320
 Asp Gln Phe Asp Asn Tyr Ala Gln Ala Ile Ala Glu Val Asn Pro Cys
 325 330 335
 Phe Asp Val Tyr His Ile Thr Glu Thr Cys Pro Phe Lys Ser Thr Pro
 340 345 350
 Leu Gly Gly Thr Asn Pro Gly Asp Tyr Val Ala Pro Gly Thr Glu Val
 355 360 365
 Tyr Phe Asp Arg Ala Asp Val Lys Lys Ala Leu His Ala Ser Pro Asn
 370 375 380
 Ser Thr Trp Met Leu Cys Thr Asp Lys Asn Val Phe Ala Gly Ala Gly
 385 390 395 400
 Val Asn Gly Ser Asp Thr Ser Val Pro Pro Ala Asn Ser Gly Val Leu
 405 410 415
 Gln Asn Val Ile Glu Lys Thr Asn Asn Val Met Ile Gly Ser Gly Asp
 420 425 430
 Leu Asp Ile Leu Leu Ser Thr Asn Gly Thr Leu Leu Ala Leu Gln Asn
 435 440 445
 Met Thr Trp Asn Gly Ala Gln Gly Leu Thr Arg Tyr Pro Ser Gln Asn
 450 455 460
 Leu Tyr Val Pro Tyr His Pro Glu Phe Asn Gly Gly Ala Leu Ala Gly
 465 470 475 480
 Ala Gly Tyr Gln Gly Leu Trp Thr Lys Glu Arg Gly Leu Thr Phe Tyr
 485 490 495
 Thr Ala Arg Leu Ala Gly His Glu Leu Pro Gly Tyr Thr Pro Gly Val
 500 505 510
 Gly Tyr Arg Met Leu Glu Ile Leu Leu Gly Arg Ile Ser Asp Phe Ser
 515 520 525
 Ser Thr Arg Asp Phe Thr Thr Gln Thr Gly Asn Phe Thr Gly Thr Thr
 530 535 540
 Asp Leu Tyr
 545